

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 6, 2006, 15:56:11 ; Search time 163 Seconds  
(without alignments)  
4207.199 Million cell updates/sec

Title: US-10-642-248-2  
Perfect score: 5108  
Sequence: 1 MNTLSQAIKAYNSDYQLAL.....SAKGENIPVKNFIINSITL 972

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5108	100.0	972	HAS_PASMU	Q7blv3 p hyaluro
2	4310.5	84.4	965	CHS_PASMU	Q8emp0 p chondroit
3	2209	43.2	686	CHS_ECOLI	Q810v4 e chondroit
4	1306	25.6	253	Q847L4_PASMU	Q847L4 pasteurella
5	1303	25.5	253	Q847L2_PASMU	Q847L2 pasteurella
6	1148.5	22.5	220	Q847L3_PASMU	Q847L3 pasteurella
7	305	6.0	602	Q4UM29_RICPE	Q4um29 rickettsia
8	298.5	5.8	327	Q8Y828_LISMO	Q8y828 listeria mo
9	297	5.8	804	Q7U8H3_SYNPX	Q7u8h3 synchococc
10	295	5.8	604	Q7PB12_RICSI	Q7pb12 rickettsia
11	293	5.7	604	Q92IF9_RICCN	Q92if9 rickettsia
12	289	5.7	337	Q9CLR9_PASMU	Q9clr9 pasteurella
13	287.5	5.6	836	Q831L3_ENTFA	Q831l3 enterococc
14	282.5	5.5	350	Q9ALS8_CAMJE	Q9als8 campylobact
15	278.5	5.5	1127	Q7B951_BACST	Q7b951 bacillus st
16	276.5	5.4	326	Q8XN37_CLOPE	Q8xn37 clostridium
17	276.5	5.4	696	Q97P72_STRPN	Q97p72 streptococc
18	276.5	5.4	851	Q637U5_BACCCZ	Q637u5 bacillus ce
19	273.5	5.4	851	Q81YG7_BACAN	Q81yg7 bacillus an
20	273.5	5.4	851	Q6HFS0_BACHK	Q6hfs0 bacillus th
21	271	5.3	325	Q7N2R1_PHOLL	Q7n2r1 photorhabd
22	268.5	5.3	295	Q74BU3_GEOSL	Q74bu3 geobacter s
23	267.5	5.2	713	Q832P1_ENTFA	Q832p1 enterococc
24	267	5.2	323	Q8ABR0_BACTN	Q8abr0 bacteroides
25	265.5	5.2	341	Q4K1L9_STRPN	Q4kl19 streptococc
26	264.5	5.2	319	Q5NGN8_FRATT	Q5ngn8 francisella
27	263.5	5.2	323	Q8YSL7_ANASP	Q8ysl7 anabaena sp
28	262	5.1	315	Q93T15_STRAG	Q93t15 streptococc
29	261.5	5.1	706	Q88090_ENTFA	Q88090 enterococc
30	261	5.1	342	Q8XN57_CLOPE	Q8xn57 clostridium
31	260.5	5.1	324	Q8YSL1_ANASP	Q8ysl1 anabaena sp

## RESULT 1

ID	HAS_PASMU	STANDARD	PRT	972 AA
AC	Q7BLV3	O68389	O85457	
DT	10-MAY-2005	(Rel. 47, Created)		
DT	10-MAY-2005	(Rel. 47, Last sequence update)		
DT	13-SEP-2005	(Rel. 48, Last annotation update)		
DE	Hyaluronan synthase (EC 2.4.1.212) [Includes: Glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-beta-N-acetylglucosaminyltransferase (UDP-GlcNAc transferase); N-acetylglucosaminyl-proteoglycan 3-beta-glucuronosyltransferase (EC 2.4.1.226) (UDP-GlcUA transferase)].			
GN	Name=hyad;			
OS	Pasteurella multocida.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC	Pasteurellaceae; Pasteurella.			
OK	NCBI_TaxID=747;			
RP	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=Serogroup A:1 / X73;			
RC	MEDLINE=98442423; PubMed=9770287;			
RA	Chung J.Y., Zhang Y., Adler B.;			
RT	"The capsule biosynthetic locus of Pasteurella multocida A:1.";			
RL	FEMS Microbiol. Lett. 166:289-296(1998).			
RP	[2]			
RP	SEQUENCE REVISION TO 855-972.			
RA	Chung J.Y., Zhang Y., Adler B.;			
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
RP	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=P1059 / ATCC 15742;			
RC	MEDLINE=98192645; PubMed=9525958; DOI=10.1074/jbc.273.14.8454;			
RA	DeAngelis P.L., Jing W., Drake R.R., Achyuthan A.M.;			
RT	"Identification and molecular cloning of a unique hyaluronan synthase from Pasteurella multocida.";			
RL	J. Biol. Chem. 273:8454-8458(1998).			
RP	[4]			
RP	SEQUENCE REVISION TO 43.			
RA	DeAngelis P.L., Jing W., Achyuthan A.M.;			
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.			
RP	[5]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Fuller T.E., Kennedy M.J., Lowery D.E.;			
RT	"Identification of Pasteurella multocida virulence genes in a septicemic mouse model using signature-tagged mutagenesis.";			
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			
RP	[6]			
RP	CHARACTERIZATION, AND MUTAGENESIS OF ASP-196 AND ASP-477.			
RC	STRAIN=P1059 / ATCC 15742;			
RC	PubMed=10988250; DOI=10.1093/glycob/10.9.883;			
RA	Jing W., DeAngelis P.L.;			
RT	"Dissection of the two transerase activities of the Pasteurella multocida hyaluronan synthase: two active sites exist in one polypeptide.";			
RL	Glycobiology 10:883-889(2000).			

Q8xn34 clostridium  
Q9k616 bacillus ha  
Q64w33 bacteroides  
Q4jyv4 streptococc  
Q93ti7 streptococc  
Q86893 streptococc  
Q9uz16 lactococcus  
Q06035 lactococcus  
Q4jzb4 streptococc  
Q81em5 bacillus ce  
Q9afh3 streptococc  
Q8dz90 streptococc  
Q8xn54 clostridium  
Q4jz68 streptococc

## ALIGNMENTS

[7]  
 RP CHARACTERIZATION, AND MUTAGENESIS OF ASP-247; ASP-249; GLU-369;  
 RP ASP-370; ASP-527; ASP-529 AND ASP-563.  
 RX PubMed=12799342; DOI=10.1093/glycob/cwg085;  
 RA "Analysis of the two active sites of the hyaluronan synthase and the  
 RT chondroitin synthase of Pasteurella multocida.";  
 RL Glycobiology 13:661-671 (2003).  
 CC -1- FUNCTION: Catalyzes the polymerization of hyaluronan, a  
 CC polysaccharide composed of a repeating disaccharide of N-  
 CC acetylglucosamine (GlcNAc) and glucuronic acid (GlcUA) units. Each  
 CC unit has the composition in beta-(1->3)-GlcUA-beta-(1->3)-GlcNAc.  
 CC -1- CATALYTIC ACTIVITY: n UDP-N-acetyl-D-glucosamine + n UDP-D-  
 CC glucuronate = (beta-N-acetyl-D-glucosaminyl(1->4)-beta-D-  
 CC glucuronosyl(1->3)) (n) + 2n UDP.  
 CC -1- COFACTOR: Magnesium or cobalt.  
 CC -1- BIOPHYSICOCHEMICAL PROPERTIES:  
 CC Kinetic parameters:  
 CC KM=160 uM for UDP-N-acetyl-D-glucosamine;  
 CC KM=140 uM for UDP-D-glucuronate;  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.  
 CC -1- SIMILARITY: Belongs to the glycosyltransferase 2 family. CS/HAS  
 C. subfamily.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC -----  
 CC ENBL; AF067175; AAC67250.2; -; Genomic DNA.  
 CC ENBL; AF036004; AAC38318.2; -; Genomic DNA.  
 CC ENBL; AF237926; AAF68412.1; -; Genomic DNA.  
 CC PIR; T09595; T09595.  
 CC HSSP; P39621; 1QQQ.  
 CC InterPro; IPR001173; Glyco trans 2.  
 CC Pfam; PF00535; Glycos transf\_2; 2.  
 CC Glycosyltransferase; Membrane; Multifunctional enzyme; Repeat;  
 KW transferase.  
 KW REGION 152 325 A1.  
 FT REGION 432 604 A2.  
 FT MUTAGEN 196 196 D->E,K,N: Complete loss of GlcNAc  
 FT transferase activity.  
 FT MUTAGEN 247 247 D->E,K,N: Complete loss of GlcNAc  
 FT transferase activity.  
 FT MUTAGEN 249 249 D->E,K,N: Complete loss of GlcNAc  
 FT transferase activity.  
 FT MUTAGEN 369 369 E->D: Complete loss of GlcNAc transferase  
 FT activity. Regains 10% of wild type  
 FT activity at high UDP-GlcNAc  
 FT concentrations.  
 FT MUTAGEN 369 369 E->H,Q: Complete loss of GlcNAc  
 FT transferase activity.  
 FT MUTAGEN 370 370 D->E,K,N: Complete loss of GlcNAc  
 FT transferase activity.  
 FT MUTAGEN 477 477 D->E,K,N: Complete loss of GlcUA  
 FT transferase activity.  
 FT MUTAGEN 527 527 D->E,K,N: Complete loss of GlcUA  
 FT transferase activity.  
 FT MUTAGEN 529 529 D->E: 90% loss of GlcUA transferase  
 FT activity.  
 FT MUTAGEN 529 529 D->K,N: Complete loss of GlcUA  
 FT transferase activity.  
 FT MUTAGEN 563 563 D->E,K,N: No effect.  
 FT CONFLICT 17 17 Q -> E (in Ref. 1).  
 FT CONFLICT 43 43 K -> Q (in Ref. 5).  
 SQ SEQUENCE 972 AA; 111839 MW; D933BD8C1E923685 CRC64;

Query Match 100.0%; Score 5108; DB 1; Length 972;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-272;  
 Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNTLSQAIKAYNSNDYQLALKLFEKSAEYIGRKIVFQITKCKEKLSAHPSVNSAHL SVN 60

Db 1 MNTLSQAIKAYNSNDYQLALKLFEKSAEYIGRKIVFQITKCKEKLSAHPSVNSAHL SVN 60  
 Qy 61 KEEKVNVCDSPDLATQQLLSNVKVLSDSEKNTLNKWKLLTEKSENAEYRAVALVP 120  
 Db 61 KEEKVNVCDSPDLATQQLLSNVKVLSDSEKNTLNKWKLLTEKSENAEYRAVALVP 120  
 Qy 121 KDFPKDLVLAPLDPHVNDFTWYKKRKLGIKPEHGHVGLSIIIVTFNRPAILSLTACL 180  
 Db 121 KDFPKDLVLAPLDPHVNDFTWYKKRKLGIKPEHGHVGLSIIIVTFNRPAILSLTACL 180  
 Qy 181 VNOKTHYPEVIVTDDGSQEDLSPIIROYENKLDIRYVRQKONGFOASARNNGRLAKY 240  
 Db 181 VNOKTHYPEVIVTDDGSQEDLSPIIROYENKLDIRYVRQKONGFOASARNNGRLAKY 240  
 Qy 241 DFIGLLDCDMPNPLMVHVSVAELLEDLTIIGPKYIDTQIDPKDFLNNASLLESPL 300  
 Db 241 DFIGLLDCDMPNPLMVHVSVAELLEDLTIIGPKYIDTQIDPKDFLNNASLLESPL 300  
 Qy 301 EVKTNNSVAAKGEGTVSLDWRLSEQPEKTENLRUSDSPFFFAAGNVAFAKKWLNKSGFFD 360  
 Db 301 EVKTNNSVAAKGEGTVSLDWRLSEQPEKTENLRUSDSPFFFAAGNVAFAKKWLNKSGFFD 360  
 Qy 361 EEFNHGGEDVEGYRLFRYGSFFKTIIDGIMAHQEPGKENETDREAGNKIITLDMREK 420  
 Db 361 EEFNHGGEDVEGYRLFRYGSFFKTIIDGIMAHQEPGKENETDREAGNKIITLDMREK 420  
 Qy 421 VPIYRKLLPIEDSHINRVPLSVIYIPAYNCANYIQRCDVSALNQTVDLEVCINCDSGT 480  
 Db 421 VPIYRKLLPIEDSHINRVPLSVIYIPAYNCANYIQRCDVSALNQTVDLEVCINCDSGT 480  
 Qy 481 DNTLEVINLKYNNPRVRIMSKPNGGIGASNAAVSAFAGYYIGQLDSDDDYLPDVELC 540  
 Db 481 DNTLEVINLKYNNPRVRIMSKPNGGIGASNAAVSAFAGYYIGQLDSDDDYLPDVELC 540  
 Qy 541 LKEFLDKTKLACVYTTNRNVPDGSIIANGYNWPEFSREKLTAMTAHFRMTITRAHWL 600  
 Db 541 LKEFLDKTKLACVYTTNRNVPDGSIIANGYNWPEFSREKLTAMTAHFRMTITRAHWL 600  
 Qy 601 TDGFNEKIENAVDYMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHVVVN 660  
 Db 601 TDGFNEKIENAVDYMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHVVVN 660  
 Qy 661 QSLNRQGITYYNDEPDDLDESCKYIFNKTAEQEEDIDILKOIITONKDAKIAVSIFYP 720  
 Db 661 QSLNRQGITYYNDEPDDLDESCKYIFNKTAEQEEDIDILKOIITONKDAKIAVSIFYP 720  
 Qy 721 NTNLGLVKKLNNIIEYNKNI FVILHVDKNHLPDIDKKEILAFYHKHQVNILLNNDISYY 780  
 Db 721 NTNLGLVKKLNNIIEYNKNI FVILHVDKNHLPDIDKKEILAFYHKHQVNILLNNDISYY 780  
 Qy 781 TSNRLIKTBAHLSNINKLSQNLNCEYIIFDNHDSLFVRKNSYAYMKKYDVGMNFSALTH 840  
 Db 781 TSNRLIKTBAHLSNINKLSQNLNCEYIIFDNHDSLFVRKNSYAYMKKYDVGMNFSALTH 840  
 Qy 841 DWIEKINAHPPPKKLITKTVFNDNDLKSMMVKASQGMFTYALAHELLITIKKEVITSQS 900  
 Db 841 DWIEKINAHPPPKKLITKTVFNDNDLKSMMVKASQGMFTYALAHELLITIKKEVITSQS 900  
 Qy 901 IDSVPEYNTEDTWQFALLILEKKTGHVFNKSTLTLYMPWERKLOMTNQIESAKRGNI 960  
 Db 901 IDSVPEYNTEDTWQFALLILEKKTGHVFNKSTLTLYMPWERKLOMTNQIESAKRGNI 960  
 Qy 961 PVNKFIIINSITL 972  
 Db 961 PVNKFIIINSITL 972

RESULT 2  
 CHS\_PASMU  
 ID CHS\_PASMU STANDARD; PRT; 965 AA.  
 AC Q9CMP0; Q6P0M8; Q9AHL6; Q9KJ99;  
 DT 10-MAY-2005 (Rel. 47, Created)



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Db 294 ETATNNPSITSGNISLDRLEHFKTDNLRLCDSPFRYFSCGNVAFSEKLNKVGWFD 353
QY 361 EEFNHGGEDEVFGYRLFRVGSFPTKTDIGIMAYHQEPGPKENETDREAGKNITLDMREK 420
Db 354 EEFNHGGEDEVFGYRLFAKGCPRFVLDGGMAYHQEPGPKENETDREAGKSITLKIVKEK 413
QY 421 VPIYRKLLPIEDSHINRVLVSTIYIPAYNCANYIQRCVDSALNQTVDLEVCINCDSGT 480
Db 414 VPIYRKLLPIEDSHIHRIPLVSIYIPAYNCANYIQRCVDSALNQTVDLEVCINCDSGT 473
QY 481 DNTLEVINKLYGNPNRVIRMSKPGGSIASNAVSPAKGYITGQLDSDDYLDLPDAVELC 540
Db 474 DNTLEVINKLYGNPNRVIRMSKPGGSIASNAVSPAKGYITGQLDSDDYLDLPDAVELC 533
QY 541 LKEFLKDKTLACVYTNTRNVNPDGSLIANGYNPFESREKLTAMIAHFMFTIRAWHL 600
Db 534 LKEFLKDKTLACVYTNTRNVNPDGSLIANGYNPFESREKLTAMIAHFMFTIRAWHL 593
QY 601 TDGFNEKIENAVDYMFLKLSYVGKPKHLNKICYNRVLHGDNTSIKKGLOKQKHFPVYN 660
Db 594 TDGFNEKIENAVDYMFLKLSYVGKPKHLNKICYNRVLHGDNTSIKKGLOKQKHFPVYN 653
QY 661 QSLNRQGITVYNYDEPDLDDESRYIFNKTAHYQEEIDILDKIIONKDKAKIAVSIFYP 720
Db 654 QSLNRQGVSNYNYDEPDLDDESRYIFNKTAHYQEEIDILDKIIVQRDKAKVAISIFYP 713
QY 721 NTUNGVLKLNIIIEYNKNIFVILVHVDKVNHLFPDIIKEILAFYKHQVNLINNDISYY 780
Db 714 NRDGLVKKLNIIIEYNKNVLIIVLHDKNHLSIDIKKEILEPHNKNQINILLNNDVSY 773
QY 781 TSNRLIKTEAHLNINKLSOLNCEYIIIFDNHDSLFPKNDISYAYMKKYDVGNNFSAITH 840
Db 774 TNNRLIKTKAHLNMMKNKLQNLNLEYIIIFDNHDSLFIKNDISYHNHIKKYDIGNFSSLTN 833
QY 841 DWIEKINAHPPFKLLIKTYFENDNLDKSMNVKGSQGMFTYALAHELLITIKKEVITSCQS 900
Db 834 DWINKINAHSPFKLLIKTYFENDNLDKTIINNVKGSQGMFTYALAHELLITIKKEVITSCQS 893
QY 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKSTLTLYMPWERKQWNTNEQIESAKRGENI 960
Db 894 TDSVPEYNTEDIWQFALLILEKKTGHVFNKSTLTLYMPWERKQWNTNEQIESAKRGENI 953
QY 961 PVNKFIINSITL 972
Db 954 PVNKFIINSITL 965

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## RESULT 3

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CHS_ECOLI
ID CHS_ECOLI STANDARD; PRT; 686 AA.
AC QBL0V4;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Chondroitin synthase (CS) (Chondroitin polymerase) [Includes:
DE Glucuronosyl-N-acetylgalactosaminyl-proteoglycan 4-beta-N-
DE acetylgalactosaminyltransferase (EC 2.4.1.175) (UDP-GalNac
DE transferase); N-acetylgalactosaminyl-proteoglycan 3-beta-
DE glucuronosyltransferase (EC 2.4.1.226) (UDP-GlcUA transferase)].
GN Name=kfoc;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RC NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND CHARACTERIZATION.
RP STRAIN=05:K4(L):H4 / ATCC 23502;
RX MEDLINE=22050655; PubMed=11943778; DOI=10.1074/jbc.M201719200;
RA Nimomiya T., Sugiura N., Tawada A., Sugimoto K., Watanabe H.,
RA Kimata K.
RT "Molecular cloning and characterization of chondroitin polymerase from
RT Escherichia coli strain K4.";

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RL J. Biol. Chem. 277:21567-21575(2002).
CC -I- FUNCTION: Catalyzes the polymerization of chondroitin, a
CC polysaccharide composed of a repeating disaccharide of N-
CC acetylgalactosamine (GalNAc) and glucuronic acid (GlcUA) units.
CC Each unit has the composition in beta-(1->4)-GlcUA-beta-(1->3)-
CC GalNAc.
CC -I- CATALYTIC ACTIVITY: UDP-alpha-D-glucuronate + N-acetyl-beta-D-
CC galactosaminyl-(1->4)-beta-D-glucuronosyl-proteoglycan = UDP +
CC beta-D-glucuronosyl-(1->3)-N-acetyl-beta-D-galactosaminyl-(1->4)-
CC beta-D-glucuronosyl-proteoglycan.
CC -I- CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + beta-D-
CC glucuronosyl-(1->3)-N-acetyl-beta-D-galactosaminyl-proteoglycan =
CC UDP + N-acetyl-beta-D-galactosaminyl-(1->4)-beta-D-glucuronosyl-
CC (1->3)-N-acetyl-beta-D-galactosaminyl-proteoglycan.
CC -I- COFACTOR: Manganese.
CC -I- BIOPHYSICOCHEMICAL PROPERTIES:
CC Kinetic parameters:
CC KM=3.44 uM for UDP-GlcUA;
CC KM=31.6 uM for UDP-GalNAc;
CC pH dependence:
CC Optimum pH is 7-7.5;
CC Temperature dependence:
CC Optimum temperature is 30 degrees Celsius for highest reaction
CC speed, and 25 degrees Celsius to obtain highest molecular weight
CC of product chondroitin;
CC -I- SIMILARITY: Belongs to the glycosyltransferase 2 family. CS/HAS
CC subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB079602; BAC00523.1; -; Genomic DNA.
CC InterPro; IPR001173; Glyco trans 2.
CC Pfam; PF00535; Glycos transf 2; 2.
CC Glycosyltransferase; Repeat; Transferase.
CC REGION 143 317 A1.
CC FT REGION 424 596 A2.
CC SQ SEQUENCE 686 AA; 79257 MW; 6FB941623D9EC9D4 CRC64;
Query Match 43.2%; Score 2209; DB 1; Length 686;
Best Local Similarity 59.6%; Pred. No. 7.1e-113;
Matches 412; Conservative 117; Mismatches 150; Indels 12; Gaps 4;
QY 1 MNTLSQAIKAYNSNDYQLALKLFKSAEYIGRKIVFQITCKCKELSAHPSVNSAHLVN 60
Db 1 MSILNQAINLYKNVYQALSIFKVAEIVDVSVWEANIKLCQTALNLSEVD----KLN 56
QY 61 KEEKNVVCDSPLDIATQLLLSNVKLVLSDSSEKNTLKNWKLTEKKSSENAEVAVALVP 120
Db 57 RKAVIDI-----DAATKIMCSNAKAIISNEVEKNEIISKYREITAKKSRAELKVEPIP 111
QY 121 KDPFKDLVLAPLPDHVNDFTWYKKRIGIKPEHOHV--GLSIIYVTTNRPAILSIITLA 178
Db 112 LDWPSDLTUPPESTNDIVWAGKRKE-LDDYPRKLIIDGLSIVIPITNRAKILAITLA 170
QY 179 CLVNRKQTHYPPFVIVTDDGSQSDLSPIITRQYENKLDIRYVRQKNGFQASARNMGLRLA 238
Db 171 CLCNQKTIYDEIVVADDSGSKENIEIREFESLLNIKVVRQKDYGYQLCAVRNLGLRAA 230
QY 239 KYDFIGLLDCDMAPNPLWHSVVAELLEDDEDDTITIGPRKYITQHDIDPKDFLNASLLS 298
Db 231 KINYVAILEDCDMAPNPLWVQSYMELLAVDNDVALLIGPRKYIDTSKHTYDLFLSKSLINE 290
QY 299 LPEVTNNSVAAGGECTVSLDWLRFQEKTEENLRISDSPPRFFAAGNVAFAKWLKNSGF 358
Db 291 IFEITINNVAQKVEQNSVDWRIEHFKNTDNLRLCNETFRFFSGGNVAFAPAKKWLFRAG 350
QY 359 FDEEFNHGGEDEVFGYRLFRVGSFPTKTDIGIMAYHQEPGPKENETDREAGKNITLDMR 418
Db 351 FDEEFTHWGGEDEVFGYRLYREGCYFRSVEGAMAYHQEPGPKENETDREAGKNITVOLLQ 410

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Qy 419 EKVPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRVCDSALNOTVVDLEVCICNDG 478
Db 411 QKVPFYRKEKESATLKRVLPSIYIPAYNCISKYIVRCVESALNQTITDLEVCICDDG 470
Qy 479 STDNTLVINKLYGNPRVRIMSPNGIGIASASNAAVSFAGYYIGQLDSDDDVLEPAVE 538
Db 471 STDDTLILQEHYANHRVRFISQKNKGIGASNTAVRLCRGFGYIGQLDSDDDVLEPAVE 530
Qy 539 LCLKEFLKDKTACVYTTNRNVNPDGSLIANGYNWPEFSREKLTMTAMIAHHFRMFTIRAW 598
Db 531 LCLDEFRKDLSLACVYTTNRNIDRGNLISNGYNWPIYSREKLTSMI CHHFRMFTIRAW 590
Qy 599 HLTGDFNEKIENAVDYDMFLKLSVGKFKHLNKLKCYNRVLHGDNTSIKGLGIQKNHFV 658
Db 591 NLTEGFNESISNAVYDMYKLSVGGPKFKHLNKLKCYNRVLHGTISIKKLDIQKNHFV 650
Qy 659 VNQSLNRQGIYYNYDFDDIDESRKYIFNK 689
Db 651 VNESLSRLGIKKYKYSPLTNLNECRKYTWK 681

RESULT 4
Q847L4_PASMU PRELIMINARY; PRT; 253 AA.
AC Q847L4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Knt1 (Fragment).
GN Name=hvad;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jabbari A.R., Emaeliazad M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225345; AAO63009.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 253 AA; 29539 MW; A6BF4E189802367D CRC64;

Query Match 25.6%; Score 1306; DB 2; Length 253;
Best Local Similarity 98.4%; Pred. No. 7.1e-64;
Matches 248; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 721 NTGLVKKLNNIIEYKNKIFVILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY 780
Db 2 SVLSNVLNLANIIEYKNKIFVILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY 61
Qy 781 TSNRLIKTEAHLNSINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKYDVGMNFSALTH 840
Db 62 TSNRLIKTEAHLNSINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKYDVGMNFSALTH 121
Qy 841 DWIEKINAHPPPKLIKTYFNDNDLKSVMKVGASQGMFTYALAHELLTIKEVITSCOS 900
Db 122 DWIEKINAHPPPKLIKTYFNDNDLKSVMKVGASQGMFTYALAHELLTIKEVITSCOS 181
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLTQWNEQIESAKRGNI 960
Db 182 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLTQWNEQIESAKRGNI 241
Qy 961 PVNKFIINSITL 972
Db 242 PVNKFIINSITL 253

RESULT 5
Q847L2_PASMU PRELIMINARY; PRT; 253 AA.
AC Q847L2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
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DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Knt1 (Fragment).
GN Name=hvad;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jabbari A.R., Emaeliazad M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225347; AAO63011.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 253 AA; 29638 MW; 38946AAD8FCC178F CRC64;

Query Match 25.5%; Score 1303; DB 2; Length 253;
Best Local Similarity 98.4%; Pred. No. 1e-63;
Matches 246; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 723 NLGLVKKLNNIIEYKNKIFVILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYYS 782
Db 4 NLGLVKKLNNIIEYKNKIFVILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYYS 63
Qy 783 NRLIKTEAHLNSINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKYDVGMNFSALTHDW 842
Db 64 NRLIKTEAHLNSINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKYDVGMNFSALTHDW 123
Qy 843 IEKINAHPPPKLIKTYFNDNDLKSVMKVGASQGMFTYALAHELLTIKEVITSCOSID 902
Db 124 IEKINAHPPPKLIKTYFNDNDLKSVMKVGASQGMFTYALAHELLTIKEVITSCOSID 183
Qy 903 SVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLTQWNEQIESAKRGNI 962
Db 184 SVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLTQWNEQIESAKRGNI 243
Qy 963 NKFIINSITL 972
Db 244 NKFIINSITL 253

RESULT 6
Q847L3_PASMU PRELIMINARY; PRT; 220 AA.
AC Q847L3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Knt1 (Fragment).
GN Name=hvad;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jabbari A.R., Emaeliazad M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225346; AAO63010.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 220 AA; 25709 MW; 4A04535EB0CE5C14 CRC64;

Query Match 22.5%; Score 1148.5; DB 2; Length 220;
Best Local Similarity 99.1%; Pred. No. 2.6e-55;
Matches 219; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 752 LTPDIKKEILAFYHKHQVNILLNNDISYYSNRLIKTEAHLNSINKLSQNLNCEYIIFD 811
Db 1 LTP-VKKEILAFYHKHQVNILLNNDISYYSNRLIKTEAHLNSINKLSQNLNCEYIIFD 59
Qy 812 NHDLSLFVKNDSYAYMKYDVGMNFSALTHDWIEKINAHPPPKLIKTYFNDNDLKSVMK 871
Db 60 NHDLSLFVKNDSYAYMKYDVGMNFSALTHDWIEKINAHPPPKLIKTYFNDNDLKSVMK 119
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QY 872 GASQGMPTYALAHLLTIKEVITSQSIDSVPYNTDINWQFALLILEKKTGHVFNK 931
Db 120 GASQGMPTYALAHLLTIKEVITSQSIDSVPYNTDINWQFALLILEKKTGHVFNK 179
QY 932 TSLTYMPWPKLQWNEQIESAKRGENIPVKNFIINSITL 972
Db 180 TSLTYMPWPKLQWNEQIESAKRGENIPVKNFIINSITL 220

RESULT 7
ID Q4UM29_RICFE PRELIMINARY; PRT; 602 AA.
AC Q4UM29_
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Two-domain glycosyltransferase (BC 2.4.1.-).
GN OrderedLocusNames=RF_0543;
OS Rickettsia felis (Rickettsia azadi).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia; spotted fever group.
OX NCBI_TaxID=42862;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=URRWXcal2; DOI=10.1371/journal.pbio.0030248;
RX PubMed=15984913; PubMed=11679669; DOI=10.1126/science.1063447;
RA Ogata H., Renato P., Audic S., Robert C., Blanc G., Fournier P.-E.,
RA Parinello H., Claverie J.-M., Raoult D.;
RT "The genome sequence of Rickettsia felis identifies the first putative
RT conjugative plasmid in an obligate intracellular parasite.";
RL PLOS Biol. 3:E248-E248(2005).
DR EMBL; CP000053; AAY61394.1; -; Genomic_DNA.
DR InterPro; IPR001173; Glyco_trans_2.
DR InterPro; IPR002035; VWF_A.
DR PFAM; PF00535; Glycos_transf_2; 2.
DR PRINTS; PR00453; VWFADOMAIN.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 602 AA; 68869 MW; D503EF1CA372BAF0 CRC64;

Query Match 6.0%; Score 305; DB 2; Length 602;
Best Local Similarity 26.3%; Pred. No. 2e-08;
Matches 119; Conservative 73; Mismatches 195; Indels 66; Gaps 18;

QY 440 PLVSIYIPAYNCANYIQCVDNALNTQVVDLEVCICNDGSTDN-TLEVINKLVGNPRVR 498
Db 14 PLVSIIPVYNGANGYREADISALAQTYENIEIVVNDGSKNGETENVALSYGD--KIR 71
QY 499 IMSKPNGGIASASNAVSPAKGYIIGOLDSDDDVLEPDAVE---LCLKEFLKDKTLACVY 554
Db 72 YFHKNGCGSALNYGKWKGEYFSLSHDDIYYPNKIEHQVNLNKLNDKDTIYGGY 131
QY 555 -----TTNRNVPDGLSIANGYNWPEFSREKLTAMIAHHFRMFTIRAWHLTDGFGNEK 607
Db 132 ELIDEGSSRLYKPDVSLPINKLN---ISLLPLRLGLHGCSLLIPAKYFHEIGIFNEA 188
QY 608 IENAVDYDMLKSEVCKFKHLNKCYNRVLHGDNSTSIKKLGQKQNFVNVNQSINROG 667
Db 189 LPTQDYDLWFKILRVAPIHFDESILIKSRFHSQGS-KKI-----SNH-----NEECNVLW 239
QY 668 ITYN--YDFDLDLDESRYIFNKTA-----EYOEEDILKDKIKIONKDAKTAIVI 717
Db 240 SSFELHTEEMTKMEDSPYLFTRTATFUSNNTPYKACDLANTWAKQVLDHDTKVSVII 299
QY 718 FYENTLNLGLVKLNNI-IENKNIFVIVLH-----VDKNHLTPDIKKE-ILAFYHKHQVNI 771
Db 300 PVYNRINWAIEAESVLIOTHKNEFILLIDGSTDSDISELTSICKKDXRIRYFHK----- 354
QY 772 LNDISYYSNRLIKTEAHLNINKLSQNLNCEYIIFNHDLSLFVNDNSYAMKKYDV 831
Db 355 -----KNEGPAARN-LGKINAKGVIAFLDSDDLFYK-DKIBIQLKFME 397
QY 832 GNMFSALTDHWIEKINAHPPFKLIKT-YFNDN 863
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Db 398 ENNF-IFSHTSQKINEKOKYIESVHSGFFSGN 429
||| :||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY828 LISMO
ID QY828_LISMO PRELIMINARY; PRT; 327 AA.
AC QY828;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lmo1090 protein.
GN OrderedLocusNames=lmo1090;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dusauguet O.,
RA Entian K.-D., Feibi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krett J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Norddick G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluetter T., Simoes N., Tierrez A.,
RA Vazquez-Roland J.-A., Voss H., Wehlund J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591977; CAC99168.1; -; Genomic_DNA.
DR PIR; AB1211; AB1211.
DR Listlist; LMO1090; -.
DR InterPro; IPR001173; Glyco_trans_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Complete proteome.
SQ SEQUENCE 327 AA; 37843 MW; F7480656043EC2FC CRC64;

Query Match 5.8%; Score 298.5; DB 2; Length 327;
Best Local Similarity 28.0%; Pred. No. 2.1e-08;
Matches 99; Conservative 49; Mismatches 130; Indels 75; Gaps 11;

QY 440 PLVSIYIPAYNCANYIQCVDNALNTQVVDLEVCICNDGSTDN-TLEVINKLVGNPRVR 499
Db 3 PLVSIIPVYNGANGYREADISALAQTYENIEIVVNDGSKNGETENVALSYGD--RIRY 60
QY 500 MSKPNGGIASASNAVSPAKGYIIGOLDSDDDVLEPDAVELCLEFLKDKTLACVYTNRN 559
Db 61 FEKENGQATARNFGLDVATGDIYVMVSDDYISKNLVETCL-DTQKTNADLVLTFSYN 119
QY 560 VNPDSG-----LIANGYNWPEFSREKLTAMIAHHFRMFTIRAWHLTDGFG--- 604
Db 120 VNOEGKQYIKDKGKIKVLDAGTTPNKFYQADLWKG-----SRFPVGYWYEDLGIIPV 173
QY 605 -----NEKIENAVDY-----DMFLKLSEVCKFKHLNKCYNRVLHGDNSTSIKKLGQKQNF 654
Db 174 VTLKAKNPVKIQDALYYITDRADSQSNIQQVDHFLDVI--MLENVETELKKLGI---- 227
QY 655 HFVVVNQSLNRQGITTYNDDEPDLDDESRYIFNKTAEQEIEDILKDKIKIONKDAKIA 714
Db 228 -----YEEKSD-----QLAYLYIEHLIYRL---VLURKAIYITNKQER-- 261
QY 715 VSIFYPNTLNLGLVKLNNIIEYNKNIFVIVLHVDKNHLTPDIKKEILAFYHKH 767
Db 262 -----KXLIKLISTIOEKFPMWGSYPYQAGSKLTATLKKKALWLYLHH 305

RESULT 9
QYU8H3_SYNPX
ID QYU8H3_SYNPX PRELIMINARY; PRT; 804 AA.
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AC Q7U8H3; Putative two-domain glycosyltransferase.  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Putative glycosyltransferase family 2 protein.  
 GN OrderedLocusNames=SYNW0645;  
 OS Synechococcus sp. (strain WH8102).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
 OX NCBI\_TaxID=84588;  
 RN NUCLEOTIDE SEQUENCE.  
 RP Malek J.A., Eremeeva M.E., Dasch G.A.;  
 RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RX Palenik B., Brahamah B., Latimer F.W., Land M.L., Hauser L.,  
 RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J.,  
 RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.,  
 RT "The genome of a motile marine Synechococcus."  
 RL EMBL; BX569690; CAB07160.1; -; Genomic\_DNA.  
 DR NBL; BX569690; CAB07160.1; -; Genomic\_DNA.  
 DR HSP; P39621; I170.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR InterPro; IPR001173; Glyco\_transf\_2.  
 DR Pfam; PF00535; Glycos\_transf\_2; 2.  
 KW Complete proteome; Transferase.  
 SQ SEQUENCE 804 AA; 92268 MW; FE49920809F9F22C CRC64;  
 Query Match 5.8%; Score 297; DB 2; Length 804;  
 Best Local Similarity 22.2%; Pred. No. 8.2e-08;  
 Matches 119; Conservative 103; Mismatches 210; Indels 104; Gaps 23;  
 QY 366 WGGDEVEFGYRL--FRYGSFPTKIDGIMAYHQBPQKNETDRAGKNI-----TLDIMR 418  
 DB 176 WRTQI---YRLAQIRHQWPKT-----PSDKPTQ-ETDERYENYKEIBELDHNE 224  
 QY 419 EKVPYIKLPIEDSHINRVPLSVIIPAYNC-ANVIQRCVDSALNQTVVDLEVCIND 477  
 DB 225 EQI-----REWLQNOD----APLISIIPTNTNSHLRECIESVCRQSYPNWELCICDD 276  
 QY 478 GSTDNTLEVINLY-GNNPRV-IMSKPGKGIASNAASVAFKGYIGOLDSDYLEPD 535  
 DB 277 SSSAVSVKTLRSYQSDPRVKLIIFREKNGHICASNDALRMATGEVALLDHDILADN 336  
 QY 536 AVELCKEFLKDKTLCACVYTTNRNVNPDGSLIANGYNNWPFSSREKLTAMIAHFRFTI 595  
 DB 337 ALYVARELQKQPAQLIYSDKINDGWRACHPK-PARNIDLLSYNFISHLGVYR 395  
 QY 596 RAWHLTDGFNEKIENAVDYDMFLK---SEVGKFKHLNKICYNRVLHGDNTSIKLGIOKK 644  
 DB 396 EILQIGGFRVFGSQDHLALRVLESPPQIIHIPRVLYHWRHSESTASPNDSKDY 455  
 QY 645 IKKLGIOKKHFPVVN-----QSLNRQGITVYNYDEFDLDESRYIFNKTA 692  
 DB 456 TTESGHKAVQHFLOHRRGGVRATARIKAKNRFTQWHIPDKSPSVE-----LIIPTRD 510  
 QY 693 YQEEIDILKO-----IKIIONKDAKIAVSIFYPNTLNGLVKLN-----NII 736  
 DB 511 QAEVLNLAVDIIITTYNTITVDNQSEVATKLPK-----LKVHGEKINIKY 565  
 QY 737 KNHIFVILVHDKNHLTPDIKEILAFYHGHQVNLANDISYTSNRILIKTEAHLNIN 796  
 DB 566 NKKFNYSAIN--NVAVRKSTADIV-----VLVNNDEVISSKWLQBIVSHTSRPD 613  
 QY 797 -----KLSQNLNCEY--IIFD-----NHDLSLFVNDISYAMKYDVGMMFSA 839  
 DB 614 VGCVGAKLYGNRTTHGGVIGIGQVAGHAHKYFPGDSPGVQVRLQVQMTAVT 669  
 RESULT 10  
 Q7PB12\_RICS1 PRELIMINARY; PRT; 604 AA.  
 AC Q7PB12;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Putative two-domain glycosyltransferase.  
 GN Names: sib\_orf.242;  
 OS Rickettsia sibirica.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsia; Rickettsia; spotted fever group;  
 OC Rickettsia sibirica subgroup.  
 OX NCBI\_TaxID=35793;  
 RN NUCLEOTIDE SEQUENCE.  
 RP Malek J.A., Eremeeva M.E., Dasch G.A.;  
 RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RX -; CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABW01000001; EAA25501.1; -; Genomic DNA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR InterPro; IPR001173; Glyco\_transf\_2.  
 DR Pfam; PF00535; Glycos\_transf\_2; 2.  
 KW Transferase.  
 SQ SEQUENCE 604 AA; 69114 MW; AF2201951783E823 CRC64;  
 Query Match 5.8%; Score 295; DB 2; Length 604;  
 Best Local Similarity 24.6%; Pred. No. 7.2e-08;  
 Matches 123; Conservative 73; Mismatches 212; Indels 92; Gaps 19;  
 QY 426 RKLLPIEDSHINRVPLSVIIPAYNCANVIFQRCVDSALNQTVVDLEVCINDGSDN-TL 484  
 DB 4 RKDKPLNIYH---TLVSIIPVYNGANYKMEASALAQTYKNIETIIVVNDGSKNGET 59  
 QY 485 EVINKLYGNNPRVIRMSKPGKGIASNAASVAFKGYIGOLDSDYLEPDVE- 540  
 DB 60 ERVLSYGD--KIRYPHKENGCGSALNYGKMGQEFYFWLSDHDIYYPNKIEHQVDIL 117  
 QY 541 LKEFLKDKTLCACVY-----TTNRNVNPDGSLIANGYNNWPFSSREKLTAMIAHFRMF 593  
 DB 118 NKLDNKDTIYGGYELIDEKNSLRYPKDSVLPINKLN---ISLLPLRLGLIHGCSILM 174  
 QY 594 TIRAWHLTDGFNEKIENAVDYDMFLKSEVGKFKHLNKICYNRVLHGDNTSIKLGIOKK 653  
 DB 175 PAKYFHEVGIFNEALPTQDYDLWFKIFRVAPIHFDESILIKSRFHSEQGS-KKISNHN 233  
 QY 654 N-----HFVVVNSLNROGITVYNYDEFDLDESRYIFNKTAIEBEIDILDKIK 704  
 DB 234 ECNVLSFSLHETEEEMIKMEGSPYL-----FLTRTATFLSNNT-PYKACDLANTMA 286  
 QY 705 IIONKDAKIAVSIFYPNTLNGLVKLNLI-IEYKNIFVILVH-----VDKNHLTPDIKKE 759  
 DB 287 KQVNDIKISVIIPVYNRINWAEIAESVLIQTHKFEILLIDGSDTDDISELTAICKD 346  
 QY 760 -ILAFYHGHQVNLANDISYTSNRILIKTEAHLNINLNSQLNCEYIIFDNDHSLFV 818  
 DB 347 KRIKYFK-----KNEGPAARLN-LGIKNAIGKYIAFLDSDDLFY 385  
 QY 819 KNDISYAMKYDVGMMFSAITDHWIEKINAHPPPKLKIYFNDNDLKSMMVKGASQGMF 878  
 DB 386 K-DKIEIQLFQMEENP-IFSHTSYQKINE-----KGKYESVHSGLF 426  
 QY 879 MYALAHLELLTIKEIVITSC 898  
 DB 427 SG-----NVFPQVQTC 438  
 RESULT 11  
 Q92IF9\_RICCN PRELIMINARY; PRT; 604 AA.  
 ID Q92IF9;  
 AC Q92IF9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Putative two-domain glycosyltransferase [EC:2.4.1.-].  
 GN OrderedLocusNames=RC0461;  
 OS Rickettsia conorii.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;

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OC Rickettsiaceae; Rickettsiae; Rickettsia; spotted fever group.
OX NCBI_TaxID=781;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wallish 7;
RX MEDLINE=211442074; PubMed=11557893; DOI=10.1126/science.1061471;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; A5008609; AAL02999.1; -; Genomic_DNA.
DR PIR; E97757; E97757.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001173; Glyco_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 2.
DR Complete proteome; Transferase.
SQ SEQUENCE 604 AA; 69121 MW; 514CDD81DC3FB3AB CRC64;

Query Match 5.7%; Score 293; DB 2; Length 604;
Best Local Similarity 24.6%; Pred. No. 9.3e-08;
Matches 123; Conservative 72; Mismatches 213; Indels 92; Gaps 19;

QY 426 RKLPIEDSHINRPLVSVIIPAYNCANYIQRQVDSALNQTVDLEVCINCDSGTDN-TL 484
DB 4 RDKPLNIYH-----TLVSIIPVNGANYKKEINSALAQTYKNIIIVVNDGSKNGET 59
QY 485 EVINKLYGNPRVRIMSKPNGGIASNAVSPAKGYIIGQLSDDDYLEPDAVE---LC 540
DB 60 ERVALSYGD-KIRYFVKENGCGSALNYGKMKQGEYFSLSHDDIYYPNKIEHQVDIL 117
QY 541 LKEFLKDKTLACY-----TTRNVNPDGSLIANGYNWPEFSREKLTMTAMAHFRMP 593
DB 118 NKLDNKDTIYGYEYIDKGNLSRYIKPDSVLPINKLN---ISLLPLRLGLHGGSLM 174
QY 594 TTRAWHLTDGFKENAVDYMFLKSEVGKPKHLNKCYNRVLHGDNTSIKKLGIOKK 653
DB 175 PAKYFHEVGIFNEALPTQDYDLWFKIFRVAPHFDESILIKRFSHQGS-KKISNHNE 233
QY 654 N-----HFVVNQSLNRQIYTYNVDPEDDLDESRYIFNKTAEQEIEDILKDIK 704
DB 234 ECNVLWSSFLHETEMIKMEGSPYL-----FLTRTATFLSNNT-PYKKACDLANTWA 286
QY 705 IQNKDAKAVSIFYPNTLNGLVKLNLI-IENKNI FIVLVH-----VDKNHLTPDIKKE 759
DB 287 KOVLNDTKISVIPPVYNRWAIETAKSVLIQTHKNFEILIIDDGSTDISELTAICRCKD 346
QY 760 -ILAFYKHQVNLNNDISYTSNRLIKTEAHLNKNKLSQLNLNCEYIIPDNHDSLFV 818
DB 347 KRIKYFHK-----KNEGPAARLN-LGIKNAIGKYIAFLDSDDLFF 385
QY 819 KNDVAYMKYDVGMMFSAIETHDWIEKINAHPPFKLIKITYFNDNDLKMNVKASQGMF 878
DB 386 K-DKIEIQLKMBENNFI-FSHTSYHKINE-----KGYIESVHSGLF 426
QY 879 MYALAHELLTIKEVITSC 898
DB 427 SG-----NVPPQVIQTC 438

RESULT 12
Q9CLR9_PASMU
ID Q9CLR9_PASMU PRELIMINARY; PRT; 337 AA.
AC Q9CLR9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein Pw1140.
GN OrderedLocusNames=Pw1140;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Pm70;
RX MEDLINE=211445866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; A5006155; AAK03224.1; -; Genomic_DNA.
DR InterPro; IPR001173; Glyco_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 337 AA; 39267 MW; 8639BCFB5F700DB4 CRC64;

Query Match 5.7%; Score 289; DB 2; Length 337;
Best Local Similarity 26.5%; Pred. No. 7.1e-08;
Matches 95; Conservative 72; Mismatches 116; Indels 76; Gaps 17;

QY 440 PLVSIVIPAYNCANYIQRQVDSALNQTVDLEVCINCDSGTDNTLEVINKLYGNPRVRI 499
DB 7 PLVSVLICAYNADKYIEECIDAILNQTYKNIIIVVNDGSTDTTSLKLYFAGKDPRIKI 66
QY 500 M-SKPNGGIASNAAVSPAKGYIIGQLSDDDYLEPDAVELCLKEFLKDKTLACV---YTT 556
DB 67 INNEENKGFASINIGIASINGDYLARTDADDTTPWEIEKILGYMLSHPHQIIAMGSYLT 126
QY 557 NRVNPDGSLIANGY-----NWPE-FSREKLTMTAMAH-----FRMTIRAW 598
DB 127 ILSDGNGSLNANYEHGDEWRNPLSHREIVEAMLFRNPINHNMSIVKSTVTFREHGLR-- 184
QY 599 HLTGDNKIEINAVDYMFLKSEVGKPKHLNKCYNRVLHGDNTSIKKLGIOKKNHV 657
DB 185 -----FDPAYQTEYQFVLEVSRLGELANYPESLVYR-LH--NTQTSLLNKYQN--- 233
QY 658 VVQNQLNRQIYTYNVDPEDDLDESRYIFNKTAEQEIEDI-LKDIKIQNKAIAV- 715
DB 234 LMAKKIRKAINY---LQDLG-----VIHRLGE-----DIFFHDIEIQAELASLSLL 279
QY 716 -----SIYPNTLNGLVKLNLIENYKNVIFVLVDKNHLTPDIKKEILAFYKHQ 768
DB 280 DNCIIRILDYCYLSLVNDKLNILYFLR-----DKNN-----SYFNKKQ 319

RESULT 13
Q831L3_ENTFA
ID Q831L3_ENTFA PRELIMINARY; PRT; 836 AA.
AC Q831L3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glycosyl transferase, group 2 family protein.
GN OrderedLocusNames=EF2491;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 293:2071-2074(2003).
DR EMBL; A5016954; AAO82207.1; -; Genomic_DNA.
DR TIGR; EF2491; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001173; Glyco_transf_2; 2.
DR Pfam; PF00535; Glycos_transf_2; 2.
```

```
KW Complete proteome; Transferase.
SQ SEQUENCE 836 AA; 97409 MW; F62EAF321113083C2 CRC64;

Query Match          5.6%; Score 287.5; DB 2; Length 836;
Best Local Similarity 19.5%; Pred. No. 2.9e-07;
Matches 191; Conservative 147; Mismatches 315; Indels 327; Gaps 42;

Qy 156 QHVLGSIIVTFNRPAILSTIACLVNOKTHYPEVIVTDGSGQEDLSPIROVENKLDI 215
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 ENVKSVIVPVYVETYLEEALMSLKQ-TLKEIEFLIINDGSTDNSQKIEE----- 53

Qy 216 RYVRKQNGFQSAARNMGLRLAKYDFIGLLDCDMPNPLVHVSVAELLEDLDTIIGP 275
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 54 --IAQDDPRFVFNKGG--IGKAFNLGVSEAK-----GEYIAEFSDDDIVALTHAY 101

Qy 276 RKYIDT---QHIDPKDFLNASLLESPEVKTNNSVAAKGEGTVSLD--WRL--EQFEKTE 329
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 102 ERLYNTAKSHAD-----VVRCNWVEFSSEEVERDILWQYDPKYNQLI 145

Qy 330 NLRLSGPFRRFAAGNVAFAKWLKSGF-PDEFNHWGGEDVEFGYRLFRYGSFPK--- 385
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 146 DLKTTDLIVQVY-PWNAIYKKSMEKENVTWDEIKSYGDT-----GLFWKINS 193

Qy 386 -----TIDGIMAYHOBPPCKENETDREAGKNITLDMREKVPYIVR----- 426
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 194 ASQNVIFIKDCLFYRQNP-----NSTVNVATKVPFLPQOFKLIRSNLIEQ 241

Qy 427 -----KLLPIED----- 433
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 NKPERYKGYFYKMPKIFYMAIEKLTHLRDSSEVYEQVAVDPFQALLETDLQNDIDFEY 301

Qy 434 -----SHINRVLVSIYIPAYCANYIQRQVDSALNQTVVDLEVCICND 477
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 IKQFYQIANDPAAYEYEDLKNLYKSVVMPVTHNASKYLRLQTLVTCGSEIREIILVEN 361

Qy 478 GSTNTLEVINLKGNNPRIMSPNGGIASASNAASVAKYVYIGOLDSDDDYLE----- 533
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 362 GSTNTMDIINEFAVKDPRITGISIGKSNPGHARNVGISMARGYQLFLDADDDHEANLL 421

Qy 534 -----PDAVELCLKEFLDKTLACVYTTNRNVNPPGSLIANG--YVWPEFSREK 580
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 422 QDAYYRAYSATDILLFCMKEKLPNGEVHVH-----NP---LLTNGRMSGSEISLDE 472

Qy 581 LTTAMIAHHFRMTIRAWHLTDGFNEKJENAVDYMFL---KLSEVGKFKHLNKCYNRV 637
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 473 VTPVLYDKLFLLEYIKENNLVN-----LEQFVGEDAYFTYALLGTEKIVALNLYLLTRI 527

Qy 638 LHGDNSTIKKLGIOKKNHFVVVNQSL-----NR-----OGITYNYNDEFD--DLDE 681
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 528 VRQDGL-MSTYGMNVRDEFNLHDKRMLEYLKHQAPNRIEAYRLKIINTLNWFIQDMRVYDQ 586

Qy 682 SRKYIFNKTAEQEIDILKDIKIQNKDAKIAVSIFYPNTLNGU--VKLLNNIIEYNKN 739
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 587 AFKERF-----YQE---LKB-KYIQLGLDLVKKEKYSNDPEQVERITRIGNILQYNLE 636

Qy 740 IFVIV---LHVDKNHLPDIIK-----KEILAPYHGHQVN-----ILLNNDISYTS 782
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 637 IYQNIYKDFGMMKFTIIPNVHITQERGKVIQEQETQGTGTAIEMFSIIADND---TS 692

Qy 783 NPLIKTEAHLNKLSQLNCEVIIIPDNHDSLFPKNDVSAYMKKYDVGMNFSALTHDW 842
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 693 N-----ASGVIDFVYMGDNKII-----HOSLVVS-----LLIKKEGTTLSIVLQAEW 736

Qy 843 IEKINAHPPFKKLIKTYFNDNDLKMVMKVGASQGMFTYALAHELL--TIIKEVITSCQS 900
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 737 -----EKG-----YTLQENMYTFVDNVFT--- 757

Qy 901 IDSVPEYNTEDTW-----FQALLILEKKTGHVFNKTSITLYMPWPKLQWNEQI 951
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 758 -----IWAGYTKYAAFDYNNVRLTISREGE-----THFSVVRQNGQYIQT 798

Qy 952 ESAKGENIPVNKFIINSIT 971
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

799 MTSIGNELTPINKIEGNEPT 818

## RESULT 14

Q9ALS8\_CAMJE PRELIMINARY; PRT; 350 AA.

AC Q9ALS8;

DT 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Campylobacter jejuni.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

OC Campylobacteraceae; Campylobacter.

OX NCBI\_TaxID=197;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NCTC 11828;

RX DOI=10.1128/JB.184.8.2100-2107.2002;

RX Oldfield N.J., Moran A.P., Miller L.A., Prendergast M.M., Ketley J.M.;

RT "Characterization of the Campylobacter jejuni heptosyltransferase II

RT gene, waar, provides genetic evidence that extracellular

RT polysaccharide is lipid A core independent.";

RL J. Bacteriol. 184:2100-2107(2002).

DR EMBL; AF343914; AAK12955.1; -; Genomic\_DNA.

DR InterPro; IPR001173; Glyco\_trans\_2.

DR Pfam; PF00535; Glycos\_transf\_2; 1.

DR Hypothetical protein.

KW HYPOHETHELICAL PROTEIN.

SQ SEQUENCE 350 AA; 41616 MW; FB19017F89326E9E CRC64;

Query Match 5.5%; Score 282.5; DB 2; Length 350;

Best Local Similarity 26.2%; Pred. No. 1.7e-07;

Matches 106; Conservative 66; Mismatches 134; Indels 99; Gaps 17;

Qy 440 PLVSIYIPAYCANYIQRQVDSALNQTVVDLEVCICNDGSTDNTLEVINLKGNNPRVI 499

Db 5 PLVSIIPCYNAENFIENCSIINQTYINVEIICVDDGSTDNTLKILKNLSINNSRLKA 64

Qy 500 MSKENGGIAS-ASNAASVFAKYYIGOLSDSDVLEPAVELCLKEFLDKTLACVYT--- 555

Db 65 YSINHGTGPSVVKYNGYGLKAGFEILLDSDDMTIEVLEKGIKGFQDPNPDVILIYPIKF 124

Qy 556 ~-TNRNVNPPGSLIANGVNMPEFSREKLTAMIAHHFRMTIRAWHLTDGFNEKJENAVD 613

Db 125 MFSNNNYKIGGIYNNLSINSDVNLGATNKLISGR-----DAFRNIYNKLI 172

Qy 614 YDMFLKLSVEGKPKHLNKCYNRVVLHGDNSTSIKKLGIOKK-----NHFVVVNQSLNROG 667

Db 173 GPPFVK-KTIDKIINFNEESFN---GDEVSFRHLLQAKKIAFIATDTTEFFVYN--FNQES 225

Qy 668 IT-----YVYDEFPDDLDESRYIEN--KTAE-YQEEIDILKDIKIQNKDAKIAVSIFVP 720

Db 226 ITKKIGVHHWDW-----KTWFNLEKLAQKNYKELIKKIN-----KIRYSIYY- 270

Qy 721 NTNLGLVKLNNIIEYNKNIFVILVHVDKNHLPDIIKKEILAFYHKKHGVNILLNNDISYV 780

Db 271 -----ELCKFKNTEYL-----FSQNEKNIL----- 292

Qy 781 TSNRLIKTEAHLNKLNSQL-LNLNC-----EYIFDNHDSLFVK 819

Db 293 --NKILEKNHLSRINSIFDFLFCCKDEKGYIKFYKTFYFK 335

## RESULT 15

Q7BG51\_BACST

AC Q7BG51; BACST PRELIMINARY; PRT; 1127 AA.

DT 05-JUL-2004 (T-EMBLrel. 27, Created)

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Bacillus stearothermophilus.



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 15:48:30 ; Search time 139 seconds

(without alignments)  
3072.490 Million cell updates/sec

Title: US-10-642-248-2

Perfect score: 5108

Sequence: 1 MNTLSQAIKAYNSNDYQLAL.....SAKGENIPVKNKFIINSITL 972

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5104	99.9	972	2 AAY06212	Aay06212 Pasteurel
2	5104	99.9	972	3 AAY43099	Aay43099 P. multoc
3	5104	99.9	972	7 ABJ72189	Abj72189 Pasteurel
4	5104	99.9	972	7 ADC77479	Adc77479 Pasteurel
5	5104	99.9	972	7 ADD93926	Add93926 Pasteurel
6	4502.5	88.1	965	5 AAM47336	Aam47336 Pasteurel
7	4502.5	88.1	965	7 ADP75651	Adp75651 Pasteurel
8	4502.5	88.1	965	9 AEA04965	Aea04965 Chondroit
9	4490.5	87.9	965	3 AAY96213	Aay96213 P. multoc
10	4490.5	87.9	965	5 AAM47335	Aam47335 Pasteurel
11	4490.5	87.9	965	7 ADP75649	Adp75649 Pasteurel
12	4475.5	87.6	965	8 ADN40555	Adn40555 Glycosami
13	3697	72.4	703	9 AEA04963	Aea04963 Hyaluron
14	3693	72.3	703	7 ADP75656	Adp75656 Pasteurel
15	3690	72.2	703	7 ADP75758	Adp75758 Pasteurel
16	3689	72.2	703	7 ADP75759	Adp75759 Pasteurel
17	3689	72.2	703	7 ADP75742	Adp75742 Pasteurel
18	3689	72.2	703	7 ADP75761	Adp75761 Pasteurel
19	3689	72.2	703	7 ADP75749	Adp75749 Pasteurel
20	3689	72.2	703	7 ADP75746	Adp75746 Pasteurel
21	3689	72.2	703	7 ADP75755	Adp75755 Pasteurel
22	3689	72.2	703	7 ADP75753	Adp75753 Pasteurel
23	3689	72.2	703	7 ADP75762	Adp75762 Pasteurel
24	3689	72.2	703	7 ADP75744	Adp75744 Pasteurel

25	3688	72.2	703	7 ADP75747	Adp75747 Pasteurel
26	3688	72.2	703	7 ADP75760	Adp75760 Pasteurel
27	3688	72.2	703	7 ADP75756	Adp75756 Pasteurel
28	3688	72.2	703	7 ADP75752	Adp75752 Pasteurel
29	3688	72.2	703	7 ADP75740	Adp75740 Pasteurel
30	3688	72.2	703	7 ADP75750	Adp75750 Pasteurel
31	3688	72.2	703	7 ADP75741	Adp75741 Pasteurel
32	3686	72.2	703	7 ADP75751	Adp75751 Pasteurel
33	3686	72.2	703	7 ADP75754	Adp75754 Pasteurel
34	3686	72.2	703	7 ADP75743	Adp75743 Pasteurel
35	3686	72.2	703	7 ADP75745	Adp75745 Pasteurel
36	3686	72.2	703	7 ADP75748	Adp75748 Pasteurel
37	3686	72.2	703	7 ADP75757	Adp75757 Pasteurel
38	3686	72.2	703	7 ADP75763	Adp75763 Pasteurel
39	3673.5	71.9	702	3 AAY96212	Aay96212 P. multoc
40	2209	43.2	686	6 ABR42041	Abra42041 Escherich
41	2209	43.2	686	9 ADY52710	Ady52710 Escherich
42	2202	43.1	686	9 ADY52720	Ady52720 Escherich
43	2202	43.1	686	9 ADY52716	Ady52716 Escherich
44	556	10.9	107	8 ADN40570	Adn40570 Glycosami
45	537.5	10.5	104	8 ADN40571	Adn40571 Glycosami

ALIGNMENTS

RESULT 1

AAY06212

ID AAY06212 standard; protein; 972 AA.

XX

AC AAY06212;

XX

AC

DT 16-AUG-1999 (first entry)

XX

DE Pasteurella multocida hyaluronate synthase pmHAS.

XX

KW Hyaluronate synthase; pmHAS; hyaluronic acid; hyaluronan.

XX

OS Pasteurella multocida.

XX

PN WO9923227-A2.

XX

PD 14-MAY-1999.

XX

PP 30-OCT-1998; 98WO-US023153.

XX

PR 31-OCT-1997; 97US-0064435P.

PR 26-OCT-1998; 98US-00178851.

XX

PA (OKLA ) UNIV OKLAHOMA STATE.

XX

PI Weigel PH, Kumari K, Deangelis P;

XX

XX WPI; 1999-337486/28.

DR N-PSDB; AAX58857.

XX

PT Nucleic acid encoding hyaluronate synthase for production of hyaluronic

XX

PS acid with controlled molecular weight and targeting specificity.

XX

XX Disclosure; Page 123-125; 125pp; English.

XX

XX This present sequence represents the hyaluronate synthase (pmHAS) of

CC Pasteurella multocida Carter Type A. The pmHAS enzyme has different

CC kinetic optima with respect to pH and metal ion dependence, and differ

CC Km values compared with the HAS enzymes of Streptococcus equisimilis (see

CC AAY06206) and Streptococcus pyogenes. Km values are about 2- to 3-fold

CC lower for UDP sugars, and Vmax values are about 2- to 3-fold higher. The

CC invention provides recombinant vectors containing hyaluronate synthase

CC DNA, especially S. equisimilis hyaluronate synthase DNA (see AAX58841),

CC and prokaryotic or eukaryotic host cells which produce the enzyme and its

CC hyaluronic acid product, particularly a product with modified structure

CC or molecular size. The hyaluronate produced this way is purer than

CC that produced by conventional methods

[illegible]

QY 121 KDPKDLVLAPLDHVNDFWYKRRKRLGKPEHQHVGSLSIIVTFRNRPAILSLTACL 180  
DB 121 KDPKDLVLAPLDHVNDFWYKRRKRLGKPEHQHVGSLSIIVTFRNRPAILSLTACL 180  
QY 181 VNQKTHYFFVIVTDDGSQEDLSPIIRQYENKLDIRYVRQKNGFQASAAARNMGLRLAKY 240  
DB 181 VNQKTHYFFVIVTDDGSQEDLSPIIRQYENKLDIRYVRQKNGFQASAAARNMGLRLAKY 240  
QY 241 DFIGLLDCMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHDPKDFLNNASLLESPL 300  
DB 241 DFIGLLDCMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHDPKDFLNNASLLESPL 300  
QY 301 EVKTNNSVAAKGEVTSIDWRLQEFKTEENLRSDSPRFAAGNVAFAKWLKNSGFFD 360  
DB 301 EVKTNNSVAAKGEVTSIDWRLQEFKTEENLRSDSPRFAAGNVAFAKWLKNSGFFD 360  
QY 361 EEFNHWGGEVFGYRLFRYGSFFKTIDGIMAYHQEPGKENETDREAGKNITLIDIMREK 420  
DB 361 EEFNHWGGEVFGYRLFRYGSFFKTIDGIMAYHQEPGKENETDREAGKNITLIDIMREK 420  
QY 421 VPYIYRKLPLIEDSHINRVLVSIYIIPAYNCANYIQRVDSALNQTVDLEVCICNDGST 480  
DB 421 VPYIYRKLPLIEDSHINRVLVSIYIIPAYNCANYIQRVDSALNQTVDLEVCICNDGST 480  
QY 481 DNTLEVINKLGNNPRVIRMSKPGNGIASAANAASVFAKGYIIGQLSDDDYLEPDAVELC 540  
DB 481 DNTLEVINKLGNNPRVIRMSKPGNGIASAANAASVFAKGYIIGQLSDDDYLEPDAVELC 540  
QY 541 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFFRMFTIRAWHL 600  
DB 541 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFFRMFTIRAWHL 600  
QY 601 TDGFNEKIENAVDYMFLKSEVGKFKHLNKCYNRVLHGDNTSIKLGIOKKNHFVVVN 660  
DB 601 TDGFNEKIENAVDYMFLKSEVGKFKHLNKCYNRVLHGDNTSIKLGIOKKNHFVVVN 660  
QY 661 QSLNRQGITVYNYDEFDLDSRSKYFNKTAEOEIDILDKIIONKDKAKIAVSIYP 720  
DB 661 QSLNRQGITVYNYDEFDLDSRSKYFNKTAEOEIDILDKIIONKDKAKIAVSIYP 720  
QY 721 NTNLGLVKLNNIIEYNKNIIFVILHVDKNHLTPDIKKEILAFYHKKHQVNILLNNDISYY 780  
DB 721 NTNLGLVKLNNIIEYNKNIIFVILHVDKNHLTPDIKKEILAFYHKKHQVNILLNNDISYY 780  
QY 781 TSNRLIKTEAHLNSINKLSQNLNCEYIIFONHDSLFVNDSYAYMKKYDVGMPFSALTH 840  
DB 781 TSNRLIKTEAHLNSINKLSQNLNCEYIIFONHDSLFVNDSYAYMKKYDVGMPFSALTH 840  
QY 841 DWIEKINAHPPKKLIKTFFNDNLKSNVKGASQGMFTYALAHELLTIIEKITVTSQOS 900  
DB 841 DWIEKINAHPPKKLIKTFFNDNLKSNVKGASQGMFTYALAHELLTIIEKITVTSQOS 900  
QY 901 IDSVPEYNTEDIWFQFALLILEKTKGHVFNKTSITLTYMPWERKQWNTNEQIESAKRGNI 960  
DB 901 IDSVPEYNTEDIWFQFALLILEKTKGHVFNKTSITLTYMPWERKQWNTNEQIESAKRGNI 960  
QY 961 PVNKFIINSITL 972  
DB 961 PVNKFIINSITL 972

RESULT 3  
ABJ72189  
ID ABJ72189 standard; protein; 972 AA.  
XX  
AC ABJ72189;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Pasteurella multocida hyaluronan synthase protein.  
XX  
KW Hyaluronic acid; glycosaminoglycan; hyaluronan synthase; antirheumatic;  
KW UDP-glucose 6-dehydrogenase; UDP-glucose pyrophosphorylase; orthopaedic;

KW UDP-N-acetylglucosamine; ophthalmological; dermatological; joint surgery;  
KW eye; rheumatology; dermatology; adhesion; development; cell motility;  
KW cancer; angiogenesis; wound healing; enzyme.  
XX  
OS Pasteurella multocida.  
XX WQ2003054163-A2.  
XX 03-JUL-2003.  
XX 20-DEC-2002; 2002WO-US041067.  
XX 21-DEC-2001; 2001US-0342644P.  
XX (NOVO ) NOVOZYMES BIOTECH INC.  
XX Sloma A, Behr R, Widner W, Tang M, Sternberg D, Brown S;  
XX WPI; 2003-559139/52.  
XX DR N-PSDB; ABT44090.  
XX  
XX Producing a hyaluronic acid (e.g. for use in eye and joint surgery,  
XX orthopaedics, rheumatology or dermatology) comprises cultivating a  
XX Bacillus host cell and recovering the hyaluronic acid from the  
XX cultivation medium.  
XX  
XX Claim 10; Page 190-194; 218pp; English.  
XX  
XX The invention relates to a novel method which comprises producing a  
XX hyaluronic acid via cultivating a Bacillus host cell under conditions  
XX suitable for production of the hyaluronic acid and subsequently  
XX recovering the hyaluronic acid from the cultivation medium. The most  
XX abundant heteropolysaccharides of the body are the glycosaminoglycans, of  
XX which hyaluronic acid is an example. A number of enzymes are involved in  
XX the biosynthesis of hyaluronic acid including hyaluronan synthase, UDP-N-  
XX glucose 6-dehydrogenase, UDP-glucose pyrophosphorylase and UDP-N-  
XX acetylglucosamine. The molecules of the invention demonstrate  
XX ophthalmological, antirheumatic and dermatological activities, whilst the  
XX method itself may be useful for producing a hyaluronan in a recombinant  
XX host cell. The hyaluronan generated may be used in eye and joint surgery,  
XX orthopaedics, rheumatology or dermatology and may exhibit further uses  
XX within the fields of adhesion, development, cell motility, cancer,  
XX angiogenesis and wound healing. The current sequence is that of the  
XX protein of the invention which plays a role in the synthesis of  
XX hyaluronic acid  
XX  
SQ Sequence 972 AA;  
  
Query Match 99.9%; Score 5104; DB 7; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MNTLSQAIKAYNSNDYQALALFKESAEIYGRKIVEFOITKCKEKLSAHPSVNSAHLNVN 60  
DB 1 MNTLSQAIKAYNSNDYQALALFKESAEIYGRKIVEFOITKCKEKLSAHPSVNSAHLNVN 60  
QY 61 KEEKVNVCDSPLDIATQLLNSNVKLVLSDESKNTLKNKWLLEKKSSENAEVRVALVP 120  
DB 61 KEEKVNVCDSPLDIATQLLNSNVKLVLSDESKNTLKNKWLLEKKSSENAEVRVALVP 120  
QY 121 KDFPKDLVLAPLDHVNDFWYKRRKRLGKPEHQHVGSLSIIVTFRNRPAILSLTACL 180  
DB 121 KDFPKDLVLAPLDHVNDFWYKRRKRLGKPEHQHVGSLSIIVTFRNRPAILSLTACL 180  
QY 181 VNQKTHYFFVIVTDDGSQEDLSPIIRQYENKLDIRYVRQKNGFQASAAARNMGLRLAKY 240  
DB 181 VNQKTHYFFVIVTDDGSQEDLSPIIRQYENKLDIRYVRQKNGFQASAAARNMGLRLAKY 240  
QY 241 DFIGLLDCMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHDPKDFLNNASLLESPL 300  
DB 241 DFIGLLDCMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHDPKDFLNNASLLESPL 300  
QY 301 EVKTNNSVAAKGEVTSIDWRLQEFKTEENLRSDSPRFAAGNVAFAKWLKNSGFFD 360

Db 301 EVKTNNSVAAKGEGTSLDWRLEQFEKTEKRLRLSDSPFRFAAGNVAFAKKWLKNSGFFD 360  
Qy 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQEPGPKENETDREAGKNITLIDIMREK 420  
Db 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQEPGPKENETDREAGKNITLIDIMREK 420  
Qy 421 VPYIYRKLPIEDSHINRPLVSIYIIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480  
Db 421 VPYIYRKLPIEDSHINRPLVSIYIIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480  
Qy 481 DNTLEVINLKYGNPNRVRIMSKPNGGIASNAASPAKGYIGQLSDDDYLDPAVELC 540  
Db 481 DNTLEVINLKYGNPNRVRIMSKPNGGIASNAASPAKGYIGQLSDDDYLDPAVELC 540  
Qy 541 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFHFMFTIRAWHL 600  
Db 541 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFHFMFTIRAWHL 600  
Qy 601 TDGFNEKIENAVDMPFLKSEVGKFGHLNKI CNRVLHGDNTSIKKLGIOKQKHFFVVVN 660  
Db 601 TDGFNEKIENAVDMPFLKSEVGKFGHLNKI CNRVLHGDNTSIKKLGIOKQKHFFVVVN 660  
Qy 661 QSLNRQGITTYNYDEFDLDESRYIFNKTAEOEEDILDKIIONKDAKIAVSIFYP 720  
Db 661 QSLNRQGITTYNYDEFDLDESRYIFNKTAEOEEDILDKIIONKDAKIAVSIFYP 720  
Qy 721 NTNLGLVKLLNIIIEYNKNIFVILHVDKNHLPDIKKEILAFYHKHQVNILLNNDISYY 780  
Db 721 NTNLGLVKLLNIIIEYNKNIFVILHVDKNHLPDIKKEILAFYHKHQVNILLNNDISYY 780  
Qy 781 TSRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKQDSYAYMKKYDVGWNFSAETH 840  
Db 781 TSRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKQDSYAYMKKYDVGWNFSAETH 840  
Qy 841 DWIEKINAHPEPKLIKTYFNNDNLKSMNVKGASQGMFTYALAHELLTIIKEVITSQS 900  
Db 841 DWIEKINAHPEPKLIKTYFNNDNLKSMNVKGASQGMFTYALAHELLTIIKEVITSQS 900  
Qy 901 IDSVPYNTEDIWQFALLILEKKTGHVFNKTSLTLYMPWERKLOWTNEQIESAKRGENI 960  
Db 901 IDSVPYNTEDIWQFALLILEKKTGHVFNKTSLTLYMPWERKLOWTNEQIESAKRGENI 960  
Qy 961 PVNKFIIINSITL 972  
Db 961 PVNKFIIINSITL 972  
RESULT 4  
ADC77479  
ID ADC77479 standard; protein; 972 AA.  
XX  
AC ADC77479;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Pasteurella multocida hyaluronate synthase (HAS) amino acid sequence.  
XX  
KW hyaluronate synthase; HAS; streptococcal infection;  
KW streptococcal bacteria; phagocytic cell; foreign microorganism;  
KW polysaccharide capsule; hyaluronate acid capsule; HA capsule;  
KW antibacterial compound; bacterial infection; enzyme.  
XX  
OS Pasteurella multocida.  
XX  
US2003092118-A1.  
PN  
XX  
PD 15-MAY-2003.  
XX  
13-JUN-2002; 2002US-00172527.  
XX  
31-OCT-1997; 97US-0064435P.  
PR  
26-OCT-1998; 98US-00178851.  
PR

PR 21-DEC-1999; 99US-00469200.  
PR 13-JUN-2001; 2001US-0297744P.  
PR 13-JUN-2001; 2001US-0297788P.  
XX  
PA (DEAN/) DEANGELIS P L.  
PA (WEIG/) WEIGEL P H.  
PA (KUMA/) KUMARI K.  
XX  
PI Deangelis PL, Weigel PH, Kumari K;  
XX  
DR WPI; 2003-755179/71.  
DR N-PSDB; ADC77478.  
XX  
XX Recombinant host cell is a Bacillus cell comprising a recombinant vector  
PT having purified nucleic acid segment with a coding region encoding  
PT enzymatically active hyaluronan synthase.  
XX  
PS Claim 104; SEQ ID NO 10; 79pp; English.  
XX  
CC This invention relates to a recombinant Bacillus host cell containing a  
CC recombinant vector including a nucleic acid segment with a coding region  
CC encoding enzymatically active hyaluronate synthase (HAS), where the  
CC coding region is under control of a promoter. The incidence of  
CC streptococcal infections is a major health and economic problem  
CC worldwide. Streptococcal bacteria can grow undetected by the body's  
CC phagocytic cells which are responsible for recognising and engulfing  
CC foreign microorganisms. One way the bacteria evades these cells is by  
CC coating themselves with polysaccharide capsules, such as a hyaluronate  
CC acid (HA) capsule. As HA is non-immunogenic, the encapsulated bacteria do  
CC not illicit an immune response. The present invention provides a means of  
CC preparing HA which may prove useful for the identification of novel  
CC antibacterial compounds for the treatment of bacterial infection. The  
CC present sequence is the amino acid sequence of the hyaluronate synthase  
CC (HAS) of Pasteurella multocida, used in the method of the invention.  
XX  
SQ Sequence 972 AA;  
Query Match 99.9%; Score 5104; DB 7; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNTLSQAIKAYNSNDYQLALALKEKSAEYGRKIVFQITKCKEKLSAHPSVNSAHLNVN 60  
Db 1 MNTLSQAIKAYNSNDYQLALALKEKSAEYGRKIVFQITKCKEKLSAHPSVNSAHLNVN 60  
Qy 61 KEEKVNVCDSPDLATQLLLSNVKLVLSDSSEKNTLNKWKLLTEKKSENAEYRAVALVP 120  
Db 61 KEEKVNVCDSPDLATQLLLSNVKLVLSDSSEKNTLNKWKLLTEKKSENAEYRAVALVP 120  
Qy 121 KDFPKDLVLAPLDPHVNDFTWYKKRKRIGIKPEHQHVGLSIIVTFNRPAILISITLACL 180  
Db 121 KDFPKDLVLAPLDPHVNDFTWYKKRKRIGIKPEHQHVGLSIIVTFNRPAILISITLACL 180  
Qy 181 VNOKTHYPEVIVTDDGSOEDLSPIIROYENKLDIRYVROKNGFQASAAARNGLRLAKY 240  
Db 181 VNOKTHYPEVIVTDDGSOEDLSPIIROYENKLDIRYVROKNGFQASAAARNGLRLAKY 240  
Qy 241 DFIGLLDCMAPNPLWVHSYVAELLEDDDLTIIGPRKYIDTQHDIDPKDFLNNALESPL 300  
Db 241 DFIGLLDCMAPNPLWVHSYVAELLEDDDLTIIGPRKYIDTQHDIDPKDFLNNALESPL 300  
Qy 301 EVKTNNSVAAKGEGTSLDWRLEQFEKTEKRLRLSDSPFRFAAGNVAFAKKWLKNSGFFD 360  
Db 301 EVKTNNSVAAKGEGTSLDWRLEQFEKTEKRLRLSDSPFRFAAGNVAFAKKWLKNSGFFD 360  
Qy 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQEPGPKENETDREAGKNITLIDIMREK 420  
Db 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQEPGPKENETDREAGKNITLIDIMREK 420  
Qy 421 VPYIYRKLPIEDSHINRPLVSIYIIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480  
Db 421 VPYIYRKLPIEDSHINRPLVSIYIIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480

QY 481 DNTLEVINKLYGNPRVIMSKPNGGIASASNAVSPAKGYIIGQLSDDDYLEPDAVELC 540  
DB 481 DNTLEVINKLYGNPRVIMSKPNGGIASASNAVSPAKGYIIGQLSDDDYLEPDAVELC 540  
QY 541 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
DB 541 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
QY 601 TDGFNEKIENAVDYDMFLKSEVGKPKHLNKCYNRVLHGDNITSIKLGIQKQKHFFVNVN 660  
DB 601 TDGFNEKIENAVDYDMFLKSEVGKPKHLNKCYNRVLHGDNITSIKLGIQKQKHFFVNVN 660  
QY 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEOEEDILKDIIKIQNKDAKIAVSIFYP 720  
DB 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEOEEDILKDIIKIQNKDAKIAVSIFYP 720  
QY 721 NTNLGLVKLNIIIEYNKNIIFVILVHDKNHLTPDIKEILAFYKHQVNIILLNNDISYY 780  
DB 721 NTNLGLVKLNIIIEYNKNIIFVILVHDKNHLTPDIKEILAFYKHQVNIILLNNDISYY 780  
QY 781 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHSLFVNDISYAYMKKYDVGWNFSAETH 840  
DB 781 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHSLFVNDISYAYMKKYDVGWNFSAETH 840  
QY 841 DWIEKINAHPPFKLIIKTYFNDNDLKSMNVKGASQGMFTYALAHELLTIIKEVITSCOS 900  
DB 841 DWIEKINAHPPFKLIIKTYFNDNDLKSMNVKGASQGMFTYALAHELLTIIKEVITSCOS 900  
QY 901 IDSPEYNTEDIWFQFALLIIEKKTGHVFNKTSILTYPWBRKLTQWNEQIESAKRGNI 960  
DB 901 IDSPEYNTEDIWFQFALLIIEKKTGHVFNKTSILTYPWBRKLTQWNEQIESAKRGNI 960  
QY 961 PVNKFINSITL 972  
DB 961 PVNKFINSITL 972  
RESULT 5  
ID ADD93926 standard; protein; 972 AA.  
XX ADD93926;  
AC ADD93926;  
XX 29-JAN-2004 (first entry)  
XX Pasteurella multocida hyaluronan synthase protein.  
DE hyaluronan synthase; HAS; Streptococcal infection;  
KW Streptococcal bacterium; phagocytic cell; macrophage;  
KW polymorphonuclear cell; PMN; polysaccharide capsule; hyaluronic acid;  
KW HA capsule; vaccine; enzyme.  
XX Pasteurella multocida.  
XX WO2003048330-A2.  
XX 12-JUN-2003.  
XX 03-DEC-2002; 2002WO-US038596.  
XX 03-DEC-2001; 2001US-0336105P.  
PR 11-DEC-2001; 2001US-00011771.  
XX (WEIG/) WEIGEL P H.  
PA (KUMA/) KUMARI K.  
XX Weigel PH, Kumari K;  
PI WPI; 2003-482708/45.  
XX N-PSDB; ADD93925.  
DR Novel functionally active hyaluronan synthase having at least one  
XX modified amino acid residue in it as compared to a corresponding

PT functionally active native hyaluronan synthase, useful for producing  
XX hyaluronic acid.  
PS Claim 22; SEQ ID NO 8; 362pp; English.  
XX This invention relates to a novel functionally active hyaluronan synthase  
CC (HAS) having at least one modified amino acid residue in it or having  
CC altered enzymatic activity as compared to a corresponding functionally  
CC active native hyaluronan synthase. Streptococcal infection is a major  
CC health and economic problem worldwide, particularly in developing  
CC countries. Streptococcal bacteria can grow undetected by the body's  
CC phagocytic cells (macrophages and polymorphonuclear cells; PMNs). The  
CC bacteria can evade detection by coating itself with polysaccharide  
CC capsules, such as a hyaluronic acid (HA) capsule. The invention is useful  
CC for producing hyaluronic acid and may aid the production of therapeutics  
CC and vaccines against Streptococcal infection. The present sequence is  
CC that of the Pasteurella multocida HAS protein which is related to the  
XX invention.  
SQ Sequence 972 AA;

Query Match 99.9%; Score 5104; DB 7; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNTLSQAIKAYNSNDYQALALKEKSAEIIYGRKIVEFQITCKEKL SAHPSVNSAHSVN 60  
DB 1 MNTLSQAIKAYNSNDYQALALKEKSAEIIYGRKIVEFQITCKEKL SAHPSVNSAHSVN 60  
QY 61 KEEKVNVCDSPDLIATQLLLSNVKVLSDSEKVTLNKNWKLTEKKSNAEVRALVLP 120  
DB 61 KEEKVNVCDSPDLIATQLLLSNVKVLSDSEKVTLNKNWKLTEKKSNAEVRALVLP 120  
QY 121 KDFPKDLVLAFLPDHVNDFTWYKKRKLGTKEPHQVGLSIIIVTTFNRPAILSTITLACL 180  
DB 121 KDFPKDLVLAFLPDHVNDFTWYKKRKLGTKEPHQVGLSIIIVTTFNRPAILSTITLACL 180  
QY 181 VNQKTHYPFEVITDDGSQEDLSPIIRQYENKLDIYRVQKDNQFQSAARNMGLRLAKY 240  
DB 181 VNQKTHYPFEVITDDGSQEDLSPIIRQYENKLDIYRVQKDNQFQSAARNMGLRLAKY 240  
QY 241 DFIGLLDCDMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHDIDPKDFLNNASLESIP 300  
DB 241 DFIGLLDCDMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHDIDPKDFLNNASLESIP 300  
QY 301 EVKTNNSVAAKGEGETVSLDWLEQFEKTENLRSDSPERFPAAGNVAFKWLKNSGFPD 360  
DB 301 EVKTNNSVAAKGEGETVSLDWLEQFEKTENLRSDSPERFPAAGNVAFKWLKNSGFPD 360  
QY 361 EEFNHWGGEDEVFGYRLFRYGSFFKTIIDGIMAYHQEPGKNETDREAGKNITLDMREK 420  
DB 361 EEFNHWGGEDEVFGYRLFRYGSFFKTIIDGIMAYHQEPGKNETDREAGKNITLDMREK 420  
QY 421 VPIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRVDSALNQTVDVLEVCINDGST 480  
DB 421 VPIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRVDSALNQTVDVLEVCINDGST 480  
QY 481 DNTLEVINKLYGNPRVIMSKPNGGIASASNAVSPAKGYIIGQLSDDDYLEPDAVELC 540  
DB 481 DNTLEVINKLYGNPRVIMSKPNGGIASASNAVSPAKGYIIGQLSDDDYLEPDAVELC 540  
QY 541 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
DB 541 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
QY 601 TDGFNEKIENAVDYDMFLKSEVGKPKHLNKCYNRVLHGDNITSIKLGIQKQKHFFVNVN 660  
DB 601 TDGFNEKIENAVDYDMFLKSEVGKPKHLNKCYNRVLHGDNITSIKLGIQKQKHFFVNVN 660  
QY 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEOEEDILKDIIKIQNKDAKIAVSIFYP 720  
DB 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEOEEDILKDIIKIQNKDAKIAVSIFYP 720

QY 721 NTNLGLVKLNIIIEYNKNI FVILVHVDKXHLIPDIKKEILAFYHKHVNILLNNDISYY 780  
DB |||||  
QY 721 NTNLGLVKLNIIIEYNKNI FVILVHVDKXHLIPDIKKEILAFYHKHVNILLNNDISYY 780  
DB |||||  
QY 781 TSNRLIKTEAHLNINKLSQLNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAETH 840  
DB |||||  
QY 841 DWIEKINAHPPPKKLIKITYFNDNDLSMNKVGASQGMFTYALAHELLITIIKEVITSCQS 900  
DB |||||  
QY 841 DWIEKINAHPPPKKLIKITYFNDNDLSMNKVGASQGMFTYALAHELLITIIKEVITSCQS 900  
DB |||||  
QY 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSLTLYMPWERKLOWTNEOIESAKGENI 960  
DB |||||  
QY 961 PVNKFIIINSITL 972  
DB |||||  
QY 961 PVNKFIIINSITL 972  
DB |||||  
RESULT 6  
AAW47336  
ID AAW47336 standard; protein; 965 AA.  
XX  
AC AAW47336;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Pasteurella multocida chondroitin synthase #2.  
XX  
KW Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer;  
KW eye application; joint application; moisturiser; drug delivery;  
KW wound dressing; biocompatible film.  
XX  
OS Pasteurella multocida.  
XX  
PN WO200180810-A2.  
XX  
PD 01-NOV-2001.  
XX  
PF 25-APR-2001; 2001WO-US013395.  
XX  
PR 25-APR-2000; 2000US-0199538P.  
XX  
PA (DANG/) DE ANGELIS P L.  
XX  
PI De Angelis PL;  
XX  
DR WPI; 2002-049237/06.  
DR N-PSDB; ABA05098.  
XX  
PT New chondroitin synthase gene obtained from Pasteurella multocida, useful  
PT as hyaluronan polysaccharide substitute in medial or cosmetic  
PT applications, e.g. for eye or joint applications, for moisturizer or  
PT wound dressings.  
XX  
PS Claim 3; Page 122; 125pp; English.  
XX  
CC The present invention relates to the coding sequence of the Pasteurella  
CC multocida chondroitin synthase. A chondroitin polysaccharide may be used  
CC as a hyaluronan polysaccharide substitute in medial or cosmetic  
CC applications, for example in eye or joint applications, for moisturiser  
CC or wound dressings. The enzyme may be used in covalently coupling  
CC specific drugs, proteins or toxins to the structurally modified  
CC chondroitin for general or targeted drug delivery or radiological  
CC procedures, covalently cross linking the hyaluronic acid itself or to  
CC other supports to achieve a gel or other three dimensional biomaterial  
CC with stronger physical properties, and covalently linking hyaluronic acid  
CC to a surface to create a biocompatible film or monolayer. The present  
CC sequence is one version of the protein of the invention  
XX  
SQ Sequence 965 AA;

Query Match 88.1%; Score 4502.5; DB 5; Length 965;  
Best Local Similarity 86.9%; Pred. No. 0;  
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;  
QY 1 MNTLSQAIKAYNSNDYQALAKLFEKSAEYIGRIKVEFQITKCKEKLKSAHPSVNSAHLNVN 60  
DB |||||  
QY 1 MNTLSQAIKAYNSNDYQALAKLFEKSAEYIGRIKVEFQITKCKEKLKSAHPSVNSAHLNVN 60  
DB |||||  
QY 61 KEKVNVCDSPLDIATOLLNSNVKLVLSDESKNTLKNWKLLTEKKESENAEVRVALVP 120  
DB |||||  
QY 54 EDKNSVCDSSLDIATOLLNSNVKLVLSDESKNTLKNWKLLTEKKESENAEVRVALVP 113  
DB |||||  
QY 121 KDFPKDLVLAPLDPHNDFTWYKKRKLIGIKPEHGHVGLSIIIVTFNRPALISITLACL 180  
DB |||||  
QY 114 KDFPKDLVLAPLDPHNDFTWYKKRKLIGIKPEHGHVGLSIIIVTFNRPALISITLACL 173  
DB |||||  
QY 181 VNOKTHYPEVIVTDDGSOEDLSPIIROYENKLDIRYVQKONGFOASARNMGLRLAKY 240  
DB |||||  
QY 174 VNOKTHYPEVIVVADGSKENLLTIYQKYEOKLDIYVQKONGFOASARNMGLRLAKY 233  
DB |||||  
QY 241 DFIGLLDCDMPNPLVWHSYVAELLEDLTIIGPRKYIDTOHIDPKDFLNNASLESPL 300  
DB |||||  
QY 234 DFVSILDCDMPNPLVWHSYVAELLEDLTIIGPRKYIDTOHIDPKDFLNNASLESPL 293  
DB |||||  
QY 301 EVKTNNSVAAKGEVTSVLSWRLEQPEKTENLRSDSPRFAAGNVAFAKWLKNGSFPD 360  
DB |||||  
QY 294 ETATNNPSITSGNISLDMRLEHFKKTDNLRCDSPFRYFCGNVAFSKELNKGWGF 353  
DB |||||  
QY 361 EEPNHWGGEDVEFGYRLFRYGSFFKTDIGIMAHQBPFGKENETDREAGNITLDMREK 420  
DB |||||  
QY 354 EEPNHWGGEDVEFGYRLFRYGSFFKTDIGIMAHQBPFGKENETDREAGNITLDMREK 413  
DB |||||  
QY 421 VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRVDSALNTQVLDVLCINDGST 480  
DB |||||  
QY 414 VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRVDSALNTQVLDVLCINDGST 473  
DB |||||  
QY 481 DNTLEVINKLYGNPRVIRMSKPNNGIASASNAVSAFAGYIIGQLDSDDDYLEPDAVELC 540  
DB |||||  
QY 474 DNTLEVINKLYGNPRVIRMSKPNNGIASASNAVSAFAGYIIGQLDSDDDYLEPDAVELC 533  
DB |||||  
QY 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
DB |||||  
QY 534 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 593  
DB |||||  
QY 601 TDGFNEKIENAVDYMFLKLSVGVKPKHLNKICYNRVLHGDNTSIKKLGQKQHFVNVN 660  
DB |||||  
QY 594 TDGFNEKIENAVDYMFLKLSVGVKPKHLNKICYNRVLHGDNTSIKKLGQKQHFVNVN 653  
DB |||||  
QY 661 QSLNRQGITYYNYDEPDDLDESRRKYIFNKTAEYQEBIDILKDIKTONKDAKIAVSIFYP 720  
DB |||||  
QY 654 QSLNRQGITYYNYDEPDDLDESRRKYIFNKTAEYQEBIDILKDIKTONKDAKIAVSIFYP 713  
DB |||||  
QY 721 NTNLGLVKLNIIIEYNKNI FVILVHVDKXHLIPDIKKEILAFYHKHVNILLNNDISYY 780  
DB |||||  
QY 714 NTNLGLVKLNIIIEYNKNI FVILVHVDKXHLIPDIKKEILAFYHKHVNILLNNDISYY 773  
DB |||||  
QY 781 TSNRLIKTEAHLNINKLSQLNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAETH 840  
DB |||||  
QY 774 TSNRLIKTEAHLNINKLSQLNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAETH 833  
DB |||||  
QY 841 DWIEKINAHPPPKKLIKITYFNDNDLSMNKVGASQGMFTYALAHELLITIIKEVITSCQS 900  
DB |||||  
QY 834 DWIEKINAHPPPKKLIKITYFNDNDLSMNKVGASQGMFTYALAHELLITIIKEVITSCQS 893  
DB |||||  
QY 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSLTLYMPWERKLOWTNEOIESAKGENI 960  
DB |||||  
QY 894 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSLTLYMPWERKLOWTNEOIESAKGENI 953  
DB |||||  
QY 961 PVNKFIIINSITL 972  
DB |||||  
QY 954 PVNKFIIINSITL 965



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XX (DEAN/) DEANGELIS P L.
PA Deangelis PL;
XX WPI; 2005-417007/42.
PI N-PSDB; AEA04966.
XX
PT Elongating a functional acceptor (e.g. hyaluronic acid or chondroitin),
PT useful in polysaccharide polymer grafting, comprises providing hyaluronic
PT acid synthase, UDP-GlcUA and/or UDP-GlcNAc sugars to elongate the
PT functional acceptor.
XX
PS Disclosure; SEQ ID NO 3; 41pp; English.
XX
CC The present invention relates to a method for elongating a functional
CC acceptor. The method comprises providing a hyaluronic acid (HA) synthase
CC (PmHAS; AEA04963) capable of elongating the functional acceptor and
CC providing UDP-GlcUA and UDP-GlcNAc sugars such that the hyaluronic acid
CC synthase elongates the functional acceptor. PmHAS adds sequence to the
CC nonreducing end of a growing polymer chain. The PmHAS sequence is
CC significantly different from the other known HA synthases: there appears
CC to be only two short potential sequence motifs (AEA04967 and AEA04968) in
CC common between PmHAS and the other HA synthases. The method is useful in
CC polysaccharide polymer grafting, which may be utilized in the development
CC of biotechnological medical improvements. These may be used for producing
CC hybrid polysaccharides or for forming polysaccharide coatings. Also
CC disclosed is chondroitin synthase (PmCS; AEA04965) and its coding
CC sequence (AEA04966) from Pasteurella multocida. Type A P. multocida
CC produces a HA capsule [GlcUA-GlcNAc repeats] and possesses the PmHAS
CC enzyme. On the other hand, Type P P. multocida produce a chondroitin or
CC chondroitin-like polymer capsule [GlcUA-GalNAc repeats] using PmCS.
CC Either HA or chondroitin chains can serve as acceptors for PmCS as both
CC acceptors serve well for PmHAS.
XX
SQ Sequence 965 AA;

Query Match      88.18; Score 4502.5; DB 9; Length 965;
Best Local Similarity 86.94; Pred. No. 0;
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

QY 1 MNTLSQAIKAYNSNDYQALALFEKSAEYGRKIVEFQITCKEKLSAHPSVNSAHSVN 60
DB 1 MNTLSQAIKAYNSNDYELALFEKSAEYGRKIVEFQIIKCKEKL----STNS---YVS 53
QY 61 KESEKVVCDSPDLIATOLLISNVKKVLVSDSEKNTLKNKKLTKTEKSENAEVRVALVP 120
DB 54 EDKNSVCDSSLDTATQLLSNVKKLTLSESEKNSLKNKWSITGKSENAEIRKVELVP 113
QY 121 KDFPKDLVLAPLPDHVNDFTWYKKRKLGLKPEHQHVGLSIIVTTENRPAIISITLACL 180
DB 114 KDFPKDLVLAPLPDHVNDFTWYKRRKSLGLKPKVKNKGISLIIPFNRRRIIDITUACL 173
QY 181 VNQKTHYFVEVIVTDDGSQBDLSPRIIRQYENKLDIRYVRQKMGFQASAAARNMGLRLAKY 240
DB 174 VNQKTHYFVEVIVVADDSKENLITVQYEQGLDIKYVRQDYGQYQLCAVRNLGLRTAKY 233
QY 241 DFTGLDCMAPNPLVHVSVAELLEDLDTITIGPKYIDTOHIDPKDFLNASLESPL 300
DB 234 DFVSILDCMAPQQLVAHVSYLELLEDNDIVLIGPKRYVDTHNITABQFLNDPYLEISLP 293
QY 301 EVKTNNSVAAKGEGTVSLDRLSQFETENLRISDSPPRFPAAGNVAFKWLNKSGFFD 360
DB 294 ETATNNPSITSNGISLDRLRLEHFKKTDNRLCDSPPRFYFCNGVAFSKEWLNVKGWFD 353
QY 361 EEFNHMGGEVVEGYRLFRYGSFKTIDIGIMAYHQEPGPKENETDREAGKNITLIDIMREK 420
DB 354 EEFNHMGGEVVEGYRLFANGCFPRVIDGGWAYHQEPGPKENETDREAGKSITLKIYKEK 413
QY 421 VPYIYRKLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVICNDGST 480
DB 414 VPYIYRKLPIEDSHIHRIPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVICNDGST 473

RESULT 9
AA996213
ID AA996213 standard; protein; 965 AA.
XX
AC AA996213;
XX
DT 17-AUG-2000 (first entry)
XX
DE P. multocida chondroitin synthase.
XX
KW Chondroitin synthase; CS; enzyme; hyaluronic acid; ulcer;
KW tissue abrasion; viscoelastic replacement; bioadhesive.
XX
OS Pasteurella multocida.
XX
PN WO200027437-A2.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-US026501.
XX
PR 11-NOV-1998; 98US-0107929P.
PR 01-APR-1999; 99US-00283402.
XX
PA (OKLA ) UNIV OKLAHOMA STATE.
XX
PI Deangelis PL;
XX
DR WPI; 2000-376319/32.
DR N-PSDB; AAA27449.
XX
PT Novel method for the enzymatic transfer of sugar molecules to an
PT acceptor, useful for synthesis of e.g. polysaccharide bioadhesives or
PT drug delivery systems, including hybrid molecules.
XX
PS Claim 15; Page 85; 86pp; English.
```

XX The present sequence is the Pasteurella multocida chondroitin synthase  
CC PmCS. PmCS catalyses glycosaminoglycan polymerisation to produce  
CC chondroitin: a linear polysaccharide which has viscoelastic properties  
CC which makes it useful for a number of applications. Chondroitin can be  
CC used with hyaluronic acid (HA) to coat medical devices e.g. catheters and  
CC sensors to reduce tissue abrasion. In addition, they can be used as  
CC broadsides for haemostatic sealing and healing of wounds and surgical  
CC incisions; and as biomaterials that provide sustained delivery of  
CC encapsulated drugs, to wounds, ulcers, injuries or surgical sites  
XX  
SQ Sequence 965 AA;

Query Match 87.9%; Score 4490.5; DB 3; Length 965;  
Best Local Similarity 86.7%; Pred. No. 0;  
Matches 843; Conservative 62; Mismatches 60; Indels 7; Gaps 2;

Qy 1 MNTLSQAIKAYNSNDYQALALFKPKSAEYGRKIVEFQITCKEKLKSAHPSVNSAHLNVN 60  
Db 1 MNTLSQAIKAYNSNDYQALALFKPKSAEYGRKIVEFQITCKEKLKSAHPSVNSAHLNVN 53  
Qy 61 KEEKVNVCSDPLDIATQLLSNVKLVLSSEKNTLKNKWLTKKSENAEVRVALVP 120  
Db 54 EDKNSVCDSLDIATQLLSNVKLVLSSEKNTLKNKWLTKKSENAEVRVALVP 113  
Qy 121 KDFPKDLVLAFLPDHVDFTYKGRKGLGKPEHQVGLSIIVTNRPAILSITLACL 180  
Db 114 KDFPKDLVLAFLPDHVDFTYKGRKGLGKPKVKNKIGLSIIPTNRSRILDTLACL 173  
Qy 181 VNQKTHYFVIVTDDSGOEDLPIIROYENKLDIRYVRQKNGFQASAAARMGLRLAKY 240  
Db 174 VNQKTHYFVIVTDDSGOEDLPIIROYENKLDIRYVRQKNGFQASAAARMGLRLAKY 233  
Qy 241 DFIGLLDCMAPLWVHSYVAELLEDLLTIIGPKYIDTOHIDPKDFLNNASLLSLP 300  
Db 234 DFVSLDCMAPLWVHSYVAELLEDLLTIIGPKYIDTOHIDPKDFLNNASLLSLP 293  
Qy 301 EVKTNNSVAAGBGTSLDWLEQPEKTENIRLSDSPRFAAGNVAFAKKWLKNSGFPD 360  
Db 294 ETATNNPISITSGNISLWLEHFKPTDNLRLCDSPPRYFVAGNVAFAKKWLKNSGFPD 353  
Qy 361 EEFNHGGEDEFGVRLFRYGFPTIDIGIMAYHQEPGKNETDREAGKNTIDIREK 420  
Db 354 EEFNHGGEDEFGVRLFRYGFPTIDIGIMAYHQEPGKNETDREAGKNTIDIREK 413  
Qy 421 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRVDSALNQTVVDLEVCICNDGST 480  
Db 414 VPYIYRKLPIEDSHIHRIPLVSIYIPAYNCANYIQRVDSALNQTVVDLEVCICNDGST 473  
Qy 481 DNTLEVINKLYGNPRVRIMSKPNGGIIASASNAAVSPAKGYIIGQLSDDDYLEDPAVELC 540  
Db 474 DNTLEVINKLYGNPRVRIMSKPNGGIIASASNAAVSPAKGYIIGQLSDDDYLEDPAVELC 533  
Qy 541 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
Db 534 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 593  
Qy 601 TDGFNEKIENAVDYDMFLKSEVGKFKHLNKICYNRVLHGDNTSIKLGIOKQNHFFVVN 660  
Db 594 TDGFNEKIENAVDYDMFLKSEVGKFKHLNKICYNRVLHGDNTSIKLGIOKQNHFFVVN 653  
Qy 661 QSLNRQGITVYDFDLDDESKYIFNKTAQYQSEIDLKDIKIQNDKAKIAYSIFYP 720  
Db 654 QSLNRQGITVYDFDLDDESKYIFNKTAQYQSEIDLKDIKIQNDKAKIAYSIFYP 713  
Qy 721 NTGLGVKKLNNIIEYNNKIIFVILVHDKNHLTPDIKKEILAFYHKKHVNILLNNDISY 780  
Db 714 NTGLGVKKLNNIIEYNNKIIFVILVHDKNHLTPDIKKEILAFYHKKHVNILLNNDISY 773  
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMMNFSALTH 840  
Db 774 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMMNFSALTH 833

Qy 841 DWIEKINAHPPFKKLIKTYFNDNDLSKSMNVKGASQGMFTYALAHELLTTIKKEVITSQCS 900  
Db 834 DWIEKINAHPPFKKLIKTYFNDNDLSKSMNVKGASQGMFTYALAHELLTTIKKEVITSQCS 893  
Qy 901 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKTSLTLYMPWERKLOWTNEQIESAKRGNI 960  
Db 894 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKTSLTLYMPWERKLOWTNEQIESAKRGNI 953  
Qy 961 PVNKFIIINSITL 972  
Db 954 PVNKFIIINSITL 965

RESULT 10  
AAM47335  
ID AAM47335 standard; protein; 965 AA.  
XX AAM47335;  
AC  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Pasteurella multocida chondroitin synthase #1.  
XX  
XX Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer;  
KW eye application; joint application; moisturiser; drug delivery;  
KW wound dressing; biocompatible film.  
XX  
OS Pasteurella multocida.  
XX  
FN WO200180810-A2.  
XX  
PD 01-NOV-2001.  
XX  
PF 25-APR-2001; 2001WO-US013395.  
XX  
PR 25-APR-2000; 2000US-0199538P.  
XX  
XX (DANG/) DE ANGELIS P L.  
XX  
XX De Angelis PL;  
FI WPI; 2002-049237/06.  
XX N-PSDB; ABA05097.  
XX  
PT New chondroitin synthase gene obtained from Pasteurella multocida, useful  
PT as hyaluronan polysaccharide substitute in medial or cosmetic  
PT applications, e.g. for eye or joint applications, for moisturizer or  
PT wound dressings.  
XX  
PS Claim 3; Page 119; 125pp; English.  
XX  
CC The present invention relates to the coding sequence of the Pasteurella  
CC multocida chondroitin synthase. A chondroitin polysaccharide may be used  
CC as a hyaluronan polysaccharide substitute in medial or cosmetic  
CC applications, for example in eye or joint applications, for moisturiser  
CC or wound dressings. The enzyme may be used in covalently coupling  
CC specific drugs, proteins or toxins to the structurally modified  
CC chondroitin for general or targeted drug delivery or radiological  
CC procedures, covalently cross linking the hyaluronic acid itself or to  
CC other supports to achieve a gel or other three dimensional biomaterial  
CC with stronger physical properties, and covalently linking hyaluronic acid  
CC to a surface to create a biocompatible film or monolayer. The present  
CC sequence is one version of the protein of the invention  
XX  
SQ Sequence 965 AA;

Query Match 87.9%; Score 4490.5; DB 5; Length 965;  
Best Local Similarity 86.7%; Pred. No. 0;  
Matches 843; Conservative 62; Mismatches 60; Indels 7; Gaps 2;

Qy 1 MNTLSQAIKAYNSNDYQALALFKPKSAEYGRKIVEFQITCKEKLKSAHPSVNSAHLNVN 60  
Db 1 MNTLSQAIKAYNSNDYQALALFKPKSAEYGRKIVEFQITCKEKLKSAHPSVNSAHLNVN 53



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Db 354 EEFNHWGGEVEFGYRLFAGKCFPRVDGGMAHQEPGKENEREAGKSITLKVKEK 413
Qy 421 VPIYIRKLLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCINDGST 480
Db 414 VPIYIRKLLPIEDSHIHRIPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCINDGST 473
Qy 481 DNTLEVNKLNGNPRVIRMSKPNGGTASASNAVSPAKGYIGQLSDDDYLEPDAVELC 540
Db 474 DNTLEVNKLNGNPRVIRMSKPNGGTASASNAVSPAKGYIGQLSDDDYLEPDAVELC 533
Qy 541 LKEFLKDKTLACVYTTNRNVNPDGSLJANGYNWPEFSREKLTAMIAHHFRMFTIRAWHL 600
Db 534 LKEFLKDKTLACVYTTNRNVNPDGSLJANGYNWPEFSREKLTAMIAHHFRMFTIRAWHL 593
Qy 601 TDGNEKIENAVDYMFLKSEVGKFKHLNKKIYNRVLHGDNTSIKKLGICQKHFFVNVN 660
Db 594 TDGFENIENAVDYMFLKSEVGKFKHLNKKIYNRVLHGDNTSIKKLGICQKHFFVNVN 653
Qy 661 QSLNRQGITVYNYDEFDLDESRYIFNKTAEOEEIDILKDIIQNKDAKIAVSIFYP 720
Db 654 QSLNRQGINVYNYDKFDLDESRYIFNKTAEOEEIDILKDIIQNKDAKIAVSIFYP 713
Qy 721 NTLNGLVKLNIIIEYKNKIIFVILVHDKNHLPDIKKEILAFYKHQVNIILLNDISYY 780
Db 714 NTLNGLVKLNIIIEYKNKIIFVILVHDKNHLPDIKKEILAFYKHQVNIILLNDISYY 773
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHSLFVNDSYAYMKYDVGWNFSAETH 840
Db 774 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHSLFVNDSYAYMKYDVGWNFSAETH 833
Qy 841 DWIEKINAHPPFKLITKYTFNDNDLKSNNVKGASQGMFTYALAEHLITTIKEVITSQS 900
Db 834 DWIEKINAHPPFKLITKYTFNDNDLKSNNVKGASQGMFTYALAEHLITTIKEVITSQS 893
Qy 901 IDSVPYNTEDIWQFALLILEKKTGHVFNKTSITLTYMPWPKLQWNTNEQIESAKRGNI 960
Db 894 IDSVPYNTEDIWQFALLILEKKTGHVFNKTSITLTYMPWPKLQWNTNEQIESAKRGNI 953
Qy 961 PVNKFINSITL 972
Db 954 PVNKFINSITL 965

RESULT 12
ID ADN40555
XX ADN40555 standard; protein; 965 AA.
AC ADN40555;
XX ADN40555;
DT 15-JUL-2004 (first entry)
DE Glycosaminoglycan (GAG) polymer production-related pmCS protein #1.
XX enzymatic production; glycosaminoglycan; GAG; functional acceptor;
XX uronic acid; hexosamine; GAG transferase; UDP-sugar; cytoostatic;
KW anticoagulant; immunosuppressive; antiallergic; cell growth;
KW behaviour modulator; blood vessel formation; dendritic cell maturation;
KW polysaccharide biomaterial; bioadhesive sealant; tissue engineering aid;
KW cell matrix mimetic; cell behaviour; growth modulator;
KW drug delivery agent; wound; ulcer; injury; surgical site; cytokine;
KW angiogenic; bFGF; heparin-binding growth factor; blood coagulation;
KW cancer metastasis; cell growth; infection; allograft reaction; allergy;
KW cancer; autoimmune disease.
XX
OS Pasteurella multocida.
XX
XX WO2004032830-A2.
XX
XX 22-APR-2004.
XX
XX 14-AUG-2003; 2003WO-US025750.
XX
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PR 16-AUG-2002; 2002US-0404356P.
PR 18-JUN-2003; 2003US-0479432P.
PR 31-JUL-2003; 2003US-00479432.
XX (DEAN/) DEANGELIS P L.
XX Deangelis PL, Jing W;
XX WPI; 2004-375496/35.
XX
XX Enzymatically producing defined glycosaminoglycan (GAG) polymers, by
XX providing functional acceptor, recombinant GAG transferase and UDP-sugar
XX to elongate functional acceptor to provide GAG polymers having desired
XX size distribution.
XX
XX Disclosure; SEQ ID NO 4; 163pp; English.
XX
XX This invention relates to a novel method of enzymatically producing
XX defined glycosaminoglycan (GAG) polymers, by providing functional
XX acceptor chosen from uronic acid and hexosamine, providing recombinant
XX GAG transferase capable of elongating functional acceptor in controlled
XX or repetitive fashion to form extended GAG, providing UDP-sugar to
XX functional acceptor such that GAG transferase elongates functional
XX acceptor to provide GAG polymers having desired size distribution. The
XX method may be useful for the production of compounds with a cyostatic,
XX anticogulant, immunosuppressive or antiallergic activity acting as cell
XX growth and/or behaviour modulators or blood vessel formation and
XX dendritic cell maturation stimulators. The invention is useful for
XX enzymatically producing defined glycosaminoglycan polymers or for
XX producing a polysaccharide biomaterial. The polysaccharide biomaterial
XX produced is useful as a bioadhesive sealant, a tissue engineering aid a
XX cell matrix mimetic, a cell behaviour or growth modulator, a drug
XX delivery agent. The invention is also useful for producing a
XX polysaccharide biomaterial containing a medicament delivery assembly for
XX administration at a wound, ulcer, injury or surgical site. The
XX glycosaminoglycan polymers produced by the method of the invention are
XX capable of interacting, triggering or binding a variety of molecules
XX including cytokines, receptors and growth factors and hence useful for
XX modulating cell behaviour and/or growth through numerous natural pathways
XX in mammals. The glycosaminoglycan polymers are useful for promoting
XX growth and angiogenic activities of bFGF and other heparin-binding growth
XX factors. The glycosaminoglycan polymers are also useful as potential non-
XX toxic to therapeutic agents to modulate blood coagulation, cancer
XX metastasis or cell growth and stimulating blood vessel formation and
XX stimulating dendritic cell maturation and hence for prophylaxis and/or
XX treatment of infections, allograft reaction, allergy, cancer and
XX autoimmune disease. The method enables efficient production of
XX glycosaminoglycan polymers with very narrow, substantially monodisperse
XX size distributions. The present sequence is that of a protein which is
XX related to the invention.
XX
XX Sequence 965 AA;
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```
Query Match 87.6%; Score 4475.5; DB 8; Length 965;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 841; Conservative 62; Mismatches 62; Indels 7; Gaps 2;

Qy 1 MNTLSQAIKAYNSNDYQALALFKESAIEYGRKIVEFOITCKEKLSAHPSVNSAHLVSN 60
Db 1 MNTLSQAIKAYNSNDYQALALFKESAIEYGRKIVEFOITCKEKL---STNS---YVS 53
Qy 61 KEEKVNVCDSPDLIATQILLNSNVKLVLSDSSEKNTLKNKWLTKKSENAEVRVALVLP 120
Db 54 EDKNSVCDSSLDIATQILLNSNVKLVLSSEKNSKNKWSITCKKSENAEIRKVELVP 113
Qy 121 KDFPKDLVLAPLPHVNDFTWYKRRKGLGKPBHQHVGLSIIIVTFNRPAILSTLACL 180
Db 114 KDFPKDLVLAPLPHVNDFTWYKRRKGLGKPBHQHVGLSIIIVTFNRSRLDITLACL 173
Qy 181 VNQKTHYPEVIVTDDGSEDLSPITROYENKLDIRYVRQKNDGFOASARNMGLRLAKY 240
Db 174 VNQKTHYPEVIVVADGSKENLLTIVQYKQLDIDIKYVRQKNDYQOLCAVRNGLURTAKY 233
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Db 541 LKEFLDKTKLACVYTTNRNVPDGLSIANGYNNPFSREKLTAMIAHHFPMFTIRAWHL 600
Qy 601 TDGFNEKIENAVDYDMFLKLSVCGKFKHLNKKICYNRVLHGDNTSIIKKGIOKKHFFVYVN 660
Db 601 TDGFNEKIENAVDYDMFLKLSVCGKFKHLNKKICYNRVLHGDNTSIIKKGIOKKHFFVYVN 660
Qy 661 QSLNRQGITTYNYDEFDLDESRYIIFNKTAEQEEIDILKDI 703
Db 661 QSLNRQGITTYNYDEFDLDESRYIIFNKTAEQEEIDILKDI 703

RESULT 14
ADP75656
ID ADP75656 standard; protein; 703 AA.
XX AC
XX ADP75656;
XX 12-AUG-2004 (first entry)
XX Pasteurella multocida hyaluronidic acid synthase #2.
XX polymer production; hyaluronidic acid polymer; chondroitin polymer;
XX hyaluronidic acid synthase; enzyme.
XX Pasteurella multocida.
XX WO2003029261-A2.
XX 10-APR-2003.
XX 12-JUL-2002; 2002WO-US022386.
XX 13-JUL-2001; 2001US-0305263P.
XX 22-JAN-2002; 2002US-0350642P.
XX 08-MAY-2002; 2002US-00142143.
XX (DEAN/) DEANGELIS P L.
XX Deangelis PL;
XX WPI; 2003-532558/50.

Producing polymer, e.g. hyaluronidic acid or chondroitin polymer, by
providing a functional acceptor, a synthase capable of elongating the
acceptor and sugars such that the synthase elongates the acceptor to provide
polymer.
Disclosure; SEQ ID NO 9; 538pp; English.

The invention comprises a method for producing a polymer, especially a
hyaluronidic acid (HA) or chondroitin (CD) polymer composed of less than
150 sugars. The method involves providing a functional acceptor,
providing a synthase capable of elongating the functional acceptor, and
providing sugars such that the synthase elongates the functional acceptor
to provide the polymer. The method of the invention is useful for
producing a hyaluronidic acid or chondroitin polymer composed of 1-150
sugars. The present amino acid sequence represents a Pasteurella
multocida hyaluronidic acid synthase of the invention.
XX Sequence 703 AA;

Query Match 72.3%; Score 3693; DB 7; Length 703;
Best Local Similarity 99.9%; Pred. No. 1.9e-287;
Matches 702; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQALALFEKSAEYIGRKIVFQITKCKEKLSAHPSVNSAHLNVN 60
Db 1 MNTLSQAIKAYNSNDYQALALFEKSAEYIGRKIVFQITKCKEKLSAHPSVNSAHLNVN 60
Qy 61 KEEKNVCDSPDIATQALLSNVKKLVLSDESKNTLNKKWKLITKKSSENAEVRVALVP 120
Db 61 KEEKNVCDSPDIATQALLSNVKKLVLSDESKNTLNKKWKLITKKSSENAEVRVALVP 120

121 KDFPKDLVLAFLPDHVNDFTWYKKRKRKLGIKPEHQHVGLSIIIVTTNRRPAILSITLACL 180
121 KDFPKDLVLAFLPDHVNDFTWYKKRKRKLGIKPEHQHVGLSIIIVTTNRRPAILSITLACL 180
181 VNOKTHYPFVIVTDDGSQEDLSPIITROYENKLDIRVYVROKNGFQASAAARNMGLRLAKY 240
181 VNOKTHYPFVIVTDDGSQEDLSPIITROYENKLDIRVYVROKNGFQASAAARNMGLRLAKY 240
241 DFTGLLDCDMPNPLVHVSVAELLEDLDTIIGPRKYIDTQHIDPKDFLNASLLESPL 300
241 DFTGLLDCDMPNPLVHVSVAELLEDLDTIIGPRKYIDTQHIDPKDFLNASLLESPL 300
301 EVKTNNSVAAKGEVTSVLDWRLEQFEKTEMLRLSDSPFRFAAGNVAFAKWLKNSGFFD 360
301 EVKTNNSVAAKGEVTSVLDWRLEQFEKTEMLRLSDSPFRFAAGNVAFAKWLKNSGFFD 360
361 EEFNHGGEDEVFGYRLFRYGSFPKTIIDGIMAYHQBPGEKNETDREAGKNITLIDIMREK 420
361 EEFNHGGEDEVFGYRLFRYGSFPKTIIDGIMAYHQBPGEKNETDREAGKNITLIDIMREK 420
421 VPYIYRKLLPIEDSHINRVPLVSIIPAYNCANYIQRVDSALNQTVVDLEVCIKNDGST 480
421 VPYIYRKLLPIEDSHINRVPLVSIIPAYNCANYIQRVDSALNQTVVDLEVCIKNDGST 480
481 DNTLEVINKLYGNPNRVRIMSKPNGGIASASNAASPAKGYIIGQLSDDDYLEDPVBLCL 540
481 DNTLEVINKLYGNPNRVRIMSKPNGGIASASNAASPAKGYIIGQLSDDDYLEDPVBLCL 540
541 LKEFLDKTKLACVYTTNRNVPDGLSIANGYNNPFSREKLTAMIAHHFPMFTIRAWHL 600
541 LKEFLDKTKLACVYTTNRNVPDGLSIANGYNNPFSREKLTAMIAHHFPMFTIRAWHL 600
601 TDGFNEKIENAVDYDMFLKLSVCGKFKHLNKKICYNRVLHGDNTSIIKKGIOKKHFFVYVN 660
601 TDGFNEKIENAVDYDMFLKLSVCGKFKHLNKKICYNRVLHGDNTSIIKKGIOKKHFFVYVN 660
661 QSLNRQGITTYNYDEFDLDESRYIIFNKTAEQEEIDILKDI 703
661 QSLNRQGITTYNYDEFDLDESRYIIFNKTAEQEEIDILKDI 703

RESULT 15
ADP75758
ID ADP75758 standard; protein; 703 AA.
XX AC
XX ADP75758;
XX 12-AUG-2004 (first entry)
XX Pasteurella multocida mutant hyaluronidic acid synthase.
XX polymer production; hyaluronidic acid polymer; chondroitin polymer;
XX hyaluronidic acid synthase; enzyme; mutant; mutagen.
XX Pasteurella multocida.
XX Synthetic.
XX WO2003029261-A2.
XX 10-APR-2003.
XX 12-JUL-2002; 2002WO-US022386.
XX 13-JUL-2001; 2001US-0305263P.
XX 22-JAN-2002; 2002US-0350642P.
XX 08-MAY-2002; 2002US-00142143.
XX (DEAN/) DEANGELIS P L.
XX Deangelis PL;
XX WPI; 2003-532558/50.
XX
```

Job time : 143 secs

PT Producing polymer, e.g. hyaluronic acid or chondroitin polymer, by  
PT providing a functional acceptor, a synthase capable of elongating the  
PT acceptor and sugars such that synthase elongates the acceptor to provide  
PT polymer.

XX Disclosure; SEQ ID NO 111; 538pp; English.

XX  
CC The invention comprises a method for producing a polymer, especially a  
CC hyaluronic acid (HA) or chondroitin (CD) polymer composed of less than  
CC 150 sugars. The method involves providing a functional acceptor,  
CC providing a synthase capable of elongating the functional acceptor, and  
CC providing sugars such that the synthase elongates the functional acceptor  
CC to provide the polymer. The method of the invention is useful for  
CC producing a hyaluronic acid or chondroitin polymer composed of 1-150  
CC sugars. The present amino acid sequence represents a mutant Pasteurella  
CC multocida hyaluronic acid synthase of the invention.

XX  
SQ Sequence 703 AA;

Query Match	72.2%;	Score 3690;	DB 7;	Length 703;
Best Local Similarity	99.7%;	Pred. No. 3.4e-287;		
Matches 701;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNTLSQAIKAYNSNDYQALALKEKSAEIIYGRKIVEFOITKCKEKL	SAHPSVNSAHL	SVN 60
DB	1	MNTLSQAIKAYNSNDYQALALKEKSAEIIYGRKIVEFOITKCKEKL	SAHPSVNSAHL	SVN 60
QY	61	KEEKVNVCDSPDLATQLLLSNVKLVLSDSEKNTLKNWKLLTEKSENAEVR	AVALVP	120
DB	61	KEEKVNVCDSPDLATQLLLSNVKLVLSDSEKNTLKNWKLLTEKSENAEVR	AVALVP	120
QY	121	KDPKDLVLAPLDHVNDFTWYKKRKRKLGIKPEHQHVGLSIIVTNRPAIL	SITLACL	180
DB	121	KDPKDLVLAPLDHVNDFTWYKKRKRKLGIKPEHQHVGLSIIVTNRPAIL	SITLACL	180
QY	181	VNQKTHYPPEVIVTDDGSQEDLSPIIROYENKLDIRYVROKNGFO	ASAAARNMGL	RLAKY 240
DB	181	VNQKTHYPPEVIVTDDGSQEDLSPIIROYENKLDIRYVROKNGFO	ASAAARNMGL	RLAKY 240
QY	241	DFIQLLDCMAPNPLMVHYSVABELLEDDDLTIIGPRKYIDTOHIDPK	FLNNASL	LESPL 300
DB	241	DFIQLLDCMAPNPLMVHYSVABELLEDDDLTIIGPRKYIDTOHIDPK	FLNNASL	LESPL 300
QY	301	EVKTNNSVAAKGGTYSLDWRLRQFEKTEENLRISDSPFRFAAGN	VAFAKKWLNK	SGFFD 360
DB	301	EVKTNNSVAAKGGTYSLDWRLRQFEKTEENLRISDSPFRFAAGN	VAFAKKWLNK	SGFFD 360
QY	361	EEFNHWGGEDVEFGYRLFYVGSFPKTIDGIMAYHQBP	PGKENETDRE	AGKNITLDMREK 420
DB	361	EEFNHWGGEDVEFGYRLFYVGSFPKTIDGIMAYHQBP	PGKENETDRE	AGKNITLDMREK 420
QY	421	VPYIYRKLPIEDSHINRVLPSIYIPAYNCANYIQR	CVDSALNQ	TVDLEVCINDGST 480
DB	421	VPYIYRKLPIEDSHINRVLPSIYIPAYNCANYIQR	CVDSALNQ	TVDLEVCINDGST 480
QY	481	DNTLEVINKLYGNPRVIMSKNGGIASASNAAVSFAKGYIYG	QLDSD	DYLEDPAVELC 540
DB	481	DNTLEVINKLYGNPRVIMSKNGGIASASNAAVSFAKGYIYG	QLDSD	DYLEDPAVELC 540
QY	541	LKEFLDKDTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLT	TAMIAHFRMFTIRAWHL	600
DB	541	LKEFLDKDTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLT	TAMIAHFRMFTIRAWHL	600
QY	601	TGDFNEKIENAVDYMFLKLSVKGFKHLNKI	CYNRVLHGDNTSIKKLGIQKKNHFVVVN	660
DB	601	TGDFNEKIENAVDYMFLKLSVKGFKHLNKI	CYNRVLHGDNTSIKKLGIQKKNHFVVVN	660
QY	661	QSLNRQGITYYNDEFDDLDES	KYIFNKTAEYQEEIDIL	KDI 703
DB	661	QSLNRQGITYYNDEFDDLDES	KYIFNKTAEYQEEIDIL	KDI 703

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 6, 2006, 15:56:36 ; Search time 40 Seconds  
(without alignments)  
2338.067 Million cell updates/sec

Title: US-10-642-248-2  
Perfect score: 5108  
Sequence: 1 MNTLSQAIKAYNSNDYQLAL.....SAKRGENIPVKFIINSITL 972

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No... is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5104	99.9	972	T09595	Glucuronosyltransf
2	298.5	5.8	327	A31211	glycosyltransferas
3	293	5.7	604	E37757	hypothetical prote
4	276.5	5.4	696	D95206	hypothetical prote
5	263.5	5.2	323	A02189	hypothetical prote
6	260.5	5.1	324	A82190	hypothetical prote
7	259.5	5.1	303	A84114	glycosyltransferas
8	257	5.0	298	B75096	glycosyl transfera
9	251	4.9	321	A02188	hypothetical prote
10	248.5	4.9	333	B97168	glycosyltransferas
11	247	4.8	333	H97167	glycosyltransferas
12	242	4.7	318	E71690	minor teichoic aci
13	238.5	4.7	333	AH2026	hypothetical prote
14	238	4.7	306	T50038	beta-1,3-N-acetyl
15	238	4.7	318	AH2189	hypothetical prote
16	236.5	4.6	257	B84107	teichuronic acid b
17	236.5	4.6	336	A97168	glycosyltransferas
18	235	4.6	344	A70037	capsular polysacch
19	234.5	4.6	1013	AE1876	hypothetical prote
20	232.5	4.6	776	F81289	probable sugar tra
21	231.5	4.5	322	T44647	glycosyl transfera
22	231.5	4.5	323	H64130	glycosyl transfera
23	230	4.5	316	AE2189	hypothetical prote
24	229	4.5	318	T50039	beta-1,4-galactosy
25	229	4.5	389	E81318	probable galactosy
26	227	4.4	334	G71153	hypothetical prote
27	227	4.4	340	T44330	glycosyl transfera
28	226.5	4.4	445	B81289	probable sugar tra
29	225	4.4	349	D81027	lacto-N-neotetraos

ALIGNMENTS

RESULT 1

T09595

Glucuronosyltransferase (EC 2.4.1.17) - Pasteurella multocida

N;Alternate names: hyaluronan synthase

C;Species: Pasteurella multocida

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: T09595

R;DeAngelis, P.L.; Jing, W.; Drake, R.R.; Achyuthan, A.M.

J. Biol. Chem. 273, 8454-8458, 1998

A;Title: Identification and molecular cloning of a unique hyaluronan synthase from Paste

A;Reference number: Z16757; MUID:98192645; PMID:9525958

A;Accession: T09595

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-972 <DEA>

A;Cross-references: UNIPROT:O68389; UNIPARC:UPI000000B47B2; EMBL:AF036004; NID:g3043922;

A;Experimental source: strain P-1059; ATCC 15742

C;Genetics:

A;Gene: HAS

C;Function:

A;Description: polymerizes hyaluronan (HA, hyaluronate, hyaluronic acid) polysaccharide

C;Keywords: capsule synthesis; glycosyltransferase; hexosyltransferase; hyalurononic acid

Query Match	Best Local Similarity	Score	DB 2	Length	972;
Matches 971;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	MNTLSQAIKAYNSNDYQLALPKESABIIYGRKIVEFOITKCKEKLSDHPSVNSAHLNVN	60		
Db	1	MNTLSQAIKAYNSNDYQLALPKESABIIYGRKIVEFOITKCKEKLSDHPSVNSAHLNVN	60		
Qy	61	KEEKVNCDSPLDITATQLLLSNVKKLVLSDEKNTLKNKKLLTEKKSENAEVRAVALVP	120		
Db	61	KEEKVNCDSPLDITATQLLLSNVKKLVLSDEKNTLKNKKLLTEKKSENAEVRAVALVP	120		
Qy	121	KDFPKDLVLAFLPDHVNDFTWYKKRKKLGKIGKPEHQHVGLSIIVTTFNRPAILSTLACL	180		
Db	121	KDFPKDLVLAFLPDHVNDFTWYKKRKKLGKIGKPEHQHVGLSIIVTTFNRPAILSTLACL	180		
Qy	181	VNQKTHYPFEVITDDGSQEDLSPIIROYENKLDIRYVRQKNGFQAARNGRLAKY	240		
Db	181	VNQKTHYPFEVITDDGSQEDLSPIIROYENKLDIRYVRQKNGFQAARNGRLAKY	240		
Qy	241	DFIGLLDCDMAPNLVWHSYVAELLEDDDLTIIGPRKYIDTQHIIDPKDPLNNASLESPL	300		
Db	241	DFIGLLDCDMAPNLVWHSYVAELLEDDDLTIIGPRKYIDTQHIIDPKDPLNNASLESPL	300		
Qy	301	EVKTTNSVAAKGEVTVSLDWLEQPEKTENLRSLSPFRFFAAGNVAFKKWLKNSGPGFD	360		
Db	301	EVKTTNSVAAKGEVTVSLDWLEQPEKTENLRSLSPFRFFAAGNVAFKKWLKNSGPGFD	360		
Qy	361	EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQEPGKENETDREAGNITLIDIMREK	420		

glycosyl transfera  
hypothetical prote  
probable regulator  
probable glycosyl  
hypothetical prote  
glycosyl transfera  
hypothetical prote  
glycosyltransferas  
hypothetical 40.5K  
lacto-N-neotetraos  
probable galactosy  
glycosyl transfera  
spore coat polysac  
hypothetical prote  
probable glycosylt



QY 819 KND5YAMKYYVGMNFSALTDWIEKINAHPPFKLIKITYFNDNDLKSMNVKASQCMF 878  
Db 386 K-DKIBIQLFMEBNF-IFSHTSYHKINE-----KGKVISSVHGLF 426  
QY 879 MTYALAHELLTIKEVITSC 898  
Db 427 SG-----NVFPQVQTC 438

RESULT 4  
D95206  
hypothetical protein SPI771 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: D95206  
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: D95206  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-696 <KUR>  
A:Cross-references: UNIPROT:Q97P72; UNIPARC:UPI00000519A1; GB:AE005672; PIDN:AAK75845.1;  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SPI771

Query Match 5.4%; Score 276.5; DB 2; Length 696;  
Best Local Similarity 21.3%; Pred. No. 1.9e-07;  
Matches 107; Conservative 86; Mismatches 175; Indels 135; Gaps 17;  
QY 442 VSIYIPAYNCANYIQCVCDSALNQTVDLEVCICNDGSTNTLVINKLYGNPRVRIMS 501  
Db 7 ITVIVPVYVNYLRKCLDSITQYKRIEIVVNDGSTDASGEICKREFSMDHILYIE 66  
QY 502 KPNGGIAASNAASNAFAGYIGQSDSDYDLEPAVELCLK---EFLKDKTLACVYTNR 558  
Db 67 QENAGLSAARTGLNNSGNVTFVDSDDWIEQDYVELYKKIVEYQADIAGVNYSPNE 126  
QY 559 N-----VNPDSLIANGYNWPEFSREKLTAMIAHHPMTTIRAWHL-- 600  
Db 127 SEGMPYFHLGDSYYEKVDNVSIPENLYE---TQEMKSFALISAWGLYKARLFEQLR 182  
QY 601 -----TDGF-NEKIENAVDYDMFLKLVSEVCKPKHLANKICY-NRVLHGD----- 641  
Db 183 FDIGKLGEDGYLNQKV-----YLLSE--KVYLNKSLYAYRIRKGSLSRVWTEKWM 231  
QY 642 -----NTSIKKLGITQKNHFVWVQNQL-----NRQG-----ITYNYD----- 674  
Db 232 HALVDAMSERITLLANMGYPLEKHLAVYRQMLEVSLANGQASGLSDTATYKEFEMKQRLL 291  
QY 675 -EFDLDESRRKYIFNKTAYOBEIDILDKIKIQNKDAKIAVISIYPNTLNGLVKLLNI 733  
Db 292 NQLSRQESSEKKAIVLAANYGVVDQVLTIKSICYHNRSIRFYLIHSDFFNEWIKQLNKR 351  
QY 734 IRYNKNIFVVLVHVDKNHLTPDKKEILAFYHKHQVNNILLNNDISYNTSLRIKTEAHL 793  
Db 352 LE-----KFDSEIINCRVTSEQISCY-----KSDISYTVFLRYFIADF--- 389  
QY 794 NINKLSQLNLNCEYIIFDNHDSLFVKN-DSY-----A 824  
Db 390 -VQEDKALYLDCLVLTQKLDLDPATDLDQDYPLAAVRDGGRAYFGQEIFNAGVLLVNA 448  
QY 825 YMKKYDVGMNFSALTDWIEKIN 847  
Db 449 FWKKENMTQKLDVINEWHDKVD 471

## RESULT 5

AD2189  
hypothetical protein alr3067 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AD2189  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AD2189  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-323 <KUR>  
A:Cross-references: UNIPROT:Q8YSL7; UNIPARC:UPI000000CE669; GB:BA000019; PIDN:BAB74766.1;  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr3067  
C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 5.2%; Score 263.5; DB 2; Length 323;  
Best Local Similarity 25.0%; Pred. No. 3.4e-07;  
Matches 90; Conservative 67; Mismatches 114; Indels 89; Gaps 16;  
QY 436 INRVPLVSIYIPAYNCANYIQCVCDSALNQTVDLEVCICNDGSTNTLVINKLYGNRP 495  
Db 7 LNFVPIISVIVPYNGEKTIETIASVQHQTFLDIEIIVNDGSTNTLFLVRNIQDN-- 64  
QY 496 RVRIMSPKNGGIAASNAASNAFAGYIGQSDSDYDLEPAVEL---CLKEFLKDKTLAC 552  
Db 65 RLKIFSYENGGLPVARNRGITHAVGQFIAPFDADDLTWTDKLEQFAALOQY-PEAGLAY 123  
QY 553 VYTNRNVPDGS-----LIANGYNWPEFSREKLTAMIAHHPRM 592  
Db 124 SWTYKPFANEADSYADESNSFAGDVYAEILLKFNFLQNSN-PLTRRAIDSVGL----- 176  
QY 593 FTIRAWHLTDGFNEKIENAVDYDMFLKLVSEVCKPKHLNK--ICYNRVLHGDNTSICKLGI 650  
Db 177 -----FDPTLKSCEWDVFLRLAAKQWQALVKQAIIYRQ---SPTMTSKLDV 222  
QY 651 QKQNHFFVVVN-----QSLNRQGITV--YNYDEFDDLDSESKYIFNKTAYEQEETDI 699  
Db 223 MEKYSSIVIERAFNAAPPQLHKKQSLAWYKE---TAQCCLKYNSHK----- 268  
QY 700 LKDIKIQNKDAKIAVISIYPNTL-----NGLVKLLNIIEYNKIFVILVHV----DKNH 751  
Db 269 LADIKLAA-KRLKMAITLYPKNLLEDYTHGLIRKL-----IKSWILLQFHMVYIPKSH 321

## RESULT 6

AB2190  
hypothetical protein alr3073 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AB2190  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AB2190  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-324 <KUR>  
A:Cross-references: UNIPROT:Q8YSL1; UNIPARC:UPI000000CE66F; GB:BA000019; PIDN:BAB74772.1;  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr3073  
C:Superfamily: Neisseria meningitidis glycosyl transferase A

```

Query Match          5.1%; Score 260.5; DB 2; Length 324;
Best Local Similarity 25.9%; Pred. No. 4.9e-07;
Matches 101; Conservative 63; Mismatches 123; Indels 103; Gaps 16;

QY 439 VPLYSIYPAYNCANYIQRCDVSALNQTIVDVLEVCINCDSGTDNTLEVINKLYGNPNRVR 498
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MPKISVIIIPAYNABRTTLETINSVLNQTFSDLEIIVINDGSTDRTEVLQNV--DDARLK 58

QY 499 IMSKPNGGIASASNAAVSFAGKYIIGQDSDDYLEPDAVELCLKEFLDKDTLACVYTTNR 558
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 VYSYENSRSAGARNHGISHAVGDFISFLDADDLTPDKLEQLSALNNHPAGVAYSWTY 118

QY 559 NVNPDGSLIANGYNWPFSPREKLTTAMIAHHFRMFTIRAMHLTDGFNEKIEINAVDYDMFL 618
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 TIDKGBELLKPF--PLYEGNVYTDLLIAN-----FLTNGSNPLIRKAA----- 160

QY 619 KLSVGVGFKLKLNKICYNRVLHGDNTSIKK-----LGIQKNHFVVV--NOSLNROGIT 669
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 -IASIGF-----DTTURSGBDWYLRLAYKVPFVVVKHQHILYRRSVT 204

QY 670 YNNYDEPDLDESRYIFNKTAEQEETIDLKDIKI-IONKDAKIAVSIFYPNTLGLVKK 728
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 205 SKSP-----KLQIIREASLALDKAMKV-----LPLELOYLKK 237

QY 729 -KLNIIYEYKNIPIVILHVD--KNHLTPDPIK-----KEILAFYHKHQ 768
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 HSLSNIIYRYN-----VELYDLSINNNTVDIKYVIGNLLSYIRSRPOTLKEI--YTVKLI 290

QY 769 VNILNNDISYVTSNRL--IKTEAHLNLI 795
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 IKILLVIVLSPKLSRLLQFIKKSKQMKNL 320

RESULT 7
glycosyltransferase BH3713 [imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: A84114
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujita,
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: A84114
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-303 <STO>
A/Cross-references: UNIPROT:Q9K6L6; UNIPARC:UPI00000C429F; GB:AP001519; GB:BA00
A/Experimental source: strain C-125
C/Genetics:
A/Gene: BH3713
C/Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match          5.1%; Score 259.5; DB 2; Length 303;
Best Local Similarity 26.2%; Pred. No. 5.1e-07;
Matches 89; Conservative 60; Mismatches 96; Indels 95; Gaps 14;

QY 442 VSYIYPAYNCANYIQRCDVSALNQTIVDVLEVCINCDSGTDNTLEVINKLYGNPNRVRIMS 501
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 VSIIPHTNRKLLKRALESTNQTNYKNIEVIVVSDGSTONT-DIVMDYKRDGRVNFIS 61

QY 502 -KPNGGIASASNAAVSFAGKYIIGQDSDDYLEPDAVELCLKEFLDKDTLACVYTT-- 555
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 YHPAKGNYARNTGINKAKGEFI AFLDDDDDEWMPDKLEQLKEFNQANVGLVYTVGVEII 121

QY 556 ---TNRNVNPDGSLIANGYNWPF-----FSREKL-----TTAMIAHHFRMFTIRAWHLTD 602
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 YNFKNRI-----KYISLPKKTGNLSKEILVANCIGITSSV-----MYRKNLITE 166

QY 603 --GFNEKIEINAVDYDMFLKLSVEGKFKHLNKKICYNRVLHGDNTSIEKKLGIOKQKHFVVVN 660
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 167 CGMFDEKFKARQDYDLWI-----RVC-----QKTLVGVVN 196

```

Qy 661 QSLNRQGITYNY-----DFDDLDESKYIFNKTAE-----YQEIDILK 701  
Db 197 KPL----VRYNYYTTNKIQSDDIKKYSAIEYIDNKYVDLYSKVSEIRKRHSMTMLI 252  
Qy 702 DIKIIONDKAKIA-----VSYPYNTLNGLVKKLNNIIYEY 736  
Db 253 VNKALRNQSPKVARYALKNSFLKRPTLTALTAIMYMLSFLKY 292

RESULT 8  
B75096  
glycosyl transferase PAB0772 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: B75096  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure  
A:Reference number: A75001  
A:Accession: B75096  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-298 <KAW>  
A:CROSS-references: UNIPROT:Q9UZI6; UNIPARC:UPI0000034510; GB:AJ248286; GB:AL096836; NID  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB0772  
C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match	5.0%;	Score 257;	DB 2;	Length 298;
Best Local Similarity	24.9%;	Pred. No. 6.7e-07;		
Matches	83;	Conservative 65;	Mismatches 135;	Indels 50; Gaps 8;

Qy 440 PLVSIYPAYNCANVIQRCDVSALNQTVVDLEVCINCDSGTDNTLEVINKLYGNPNVR-- 498  
|:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|  
Db 4 PIVSVIPTYNRANLLRRRAIASVLNKFDPFELVVDDASTDNTPEVESI--EDGRIRY 61

Qy 499 IMSPKNGSIGASNAAVSFAGYVIGQLSDSDVLEPDVAVELCLKEFLK-DKTLCACVVTN 557  
|:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|  
Db 62 IRLKNSSGPTARNIGIKAKGRFTALLDDDEWLPHRIEVQVRKENLKCFGVVYGGP 121

Qy 558 RNVNPDGSLIANGYNWPFESREKLTAMTAAHF-----RMFTIRAWHLTDGFNEKIENAV 612  
|:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|  
Db 122 YVVSQDGRIL--GKELPK-HRGDIYSHLLENKFNFIGSPTLLIRRECCKAGLFDPRLSSQ 178

Qy 613 DYDMFLKLSVEGKFKHLNKCYNRVLHGDNSTISKLGIOKKHFFVNVVQSLNRQGIITYN 672  
|:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|  
Db 179 DWDWMRLARIYYKFDYVDEIIAKYVHVKGQISF----- 211

Qy 673 YDEPDFDLDESRYIFNKTAEQEEIDILKOIKIIONKDAKIAVSIFYPNTLNGLVKLN- 731  
|:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|  
Db 212 -----NMKKYIPGRERLRKHLDIDWNKPILSIHLSQLMGILLLSNNTGKGLKILT 263

Qy 732 --NIIEYNKNFIIVLHVHDKNHLPDPIKKEILA 762  
|:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|  
Db 264 SIATAPLNLNEMILLKALDSRTVEYIKRILS 296

RESULT 9  
AG2188  
hypothetical protein alr3062 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AG2188  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 9, 205-213, 2001  
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana-  
baena sp. PCC 7120  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AG2188  
A>Status: preliminary  
A:Molecule type: DNA

A; Cross-references: UNIPROT: Q9ZDI9; UNIPARC: UPI00000D37A5; GB: AJ235271; GB:

QY 670 YNYDEFDLDESRYIFNKTAEQEEIDILDKII--QNKDAKIA---VSIFYPNT- 722

C;Genetics:  
A;Gene: ggab; RP339  
C;Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 4.7%; Score 242; DB 1; Length 318;  
Best Local Similarity 24.8%; Pred. No. 4.9e-06;  
Matches 86; Conservative 47; Mismatches 122; Indels 92; Gaps 12;

Qy 440 PLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGSDTNTLEVINKLYGNPRVR I 499  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 8 PLVSIILPVNGANYMREADISALAQTQKIEIIIVNDSKDET-ETIALSYGD--KICY 64  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Qy 500 MSPXNGGIASNAAVSFAKYIYGQLDSDDYILEPDAVE-----LCLKE S43  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 65 LYXENGCGSALNCGIKMKRGKYPFSLSHDDVVYPNKIEHQINILNKLNDKDVIVYCGYE 124  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Qy 544 FL-KOKTLACVYTNRNVNPDGSLIANGYNWPEFSREKLTAM-----IAHFRMFTI 595  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 125 LIDQKSHLYC-----VKPD-----QRYSEKELDI SLFPLLHLHGCTLLIP 167  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Qy 596 RAWHLTGT-FNEKIENAVDMFLKSEVGKFHNLKICYNRVLRHGDNSTIKKLGIOKKN 654  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 168 SILFQKIGLFDESLSKYTHDYLDFKFPVRSIIYFDHEVLKSRIHAQTT----- 217  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Qy 655 HFVVVNOSLNROGITYYNYDEPDFDL-----DESKYIFNKTAHYQBEIDI----- 699  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 218 ----NTALNQ-----LBEYEDLWSGFLKLTKEEMIMIKGSTHOFLSDIAVFLKKG 265  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Qy 700 -----LKDKIITONKDAIVSIFYPNTINGLVKKLNII EY 736  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 266 YIKSYQALAMTDQKIIGFYTSIITEIYSLRRHGINTTITKIYKW 312  
| | | | | : | | | | : | | | | : | | | | : | | | | :

RESULT 13  
AH2026  
hypothetical protein all1766 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AH2026  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AH2026  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-333 <KUR>  
A;Cross-references: UNIPROT:Q8YW50; UNIPARC:UPI00000CE1D8; GB:BAO00019; PIDN:BAB73465.1;  
A;Experimental source: Strain PCC 7120  
C;Genetics:  
A;Gene: all1766  
C;Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 4.7%; Score 238.5; DB 2; Length 333;  
Best Local Similarity 27.4%; Pred. No. 7.9e-06;  
Matches 64; Conservative 50; Mismatches 83; Indels 37; Gaps 6;

Qy 439 VPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGSDTNTLEVINKLYGNPRVR 498  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 8 LPISVIIPAYNCEKTIKKTIDSVLDSQSFDTBELIVINDGSQDATLDIVSQI--EDSR IK 65  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Qy 499 IMSPXNGGIASNAAVSFAKYIYGQLDSDDYILEPDAVELCLKEFKDKTLACVYTTNR 558  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 66 IFSEFNAGGVNVRNGLNLA VGKFI SFGLDADDITWTPNKLESQLEALHNPNPGHFVAYSWT 125  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Qy 559 NVNPDGSLIANG-----YNNWPEFSREKLT-----TTAMIAHHFRMFTIRAWHLT 601  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Db 126 YIEDGNFLISRGRVTINGVDYKFLFNNFLENGSNPLICKEALIA-----L 172  
| | | | | : | | | | : | | | | : | | | | : | | | | :  
Qy 602 DGFNEKIENAVDMFLKSEVGKFHNLKICYNRVLRH--GDNSTIKKLGIOKK 653  
| | | | | : | | | | : | | | | : | | | | : | | | | :

Db 173 GGFDESLKAAQDWMWMLANKYSFV---AVPYVQILYRVSSNSLSNLVRQEK 223

RESULT 14

T50038

beta-1,3-N-acetylglucosaminyltransferase [validated] - Streptococcus pneumoniae

C:Species: Streptococcus pneumoniae

C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004

C:Accession: T50038

R:Kolkman, M.A.B.; Wakarchuk, W.; Nuijten, P.J.M.; van der Zeijst, B.A.M.

Mol. Microbiol. 26, 197-208, 1997

A:Title: Capsular polysaccharide synthesis in Streptococcus pneumoniae serotype 14: molecular biology of the tetrasaccharide subunit.

A:Reference number: 225028; MUID:98043549; PMID:9383201

A:Accession: T50038

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-306 <COL>

A:Cross-references: UNIPROT:O07339; UNIPARC:UPI0000B0E9F; EMBL:X85787; PIDN:CAAS9781.1

A:Experimental source: isolate NCTC 11902; serotype 14

C:Genetics:

A:Gene: cpsA14

C:Function:

A:Description: necessary for the addition of the third sugar in the synthesis of the type 14 capsular polysaccharide biosynthesis

A:Pathway: capsular polysaccharide biosynthesis

C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match	4.7%;	Score 238;	DB 2;	Length 306;
Best Local Similarity	25.2%;	Pred. No. 7.5e-06;		
Matches	83;	Conservative	53;	Mismatches 97;
			Indels	96;
			Gaps	14;

Qy 442 VSIYIPAYNCANYTORCVDSALNQTVLDVLCVINGDSTDTNLEVINKLYGNNPRVRIMS 501

Db 4 VSIITPIYNAEKTIKNCVDSALKQNLSEVLVNDGNSDSTKILEQ-YGDNPPQVMIFH 62

Qy 502 KPNGSIASANAASFAGYIYGQDSDPYLDPDAVELCLKEFLKDK---TLACVY--- 554

Db 63 QVNVGVSAAARNGLUSYAGSEVFFLDSDIDLEGLMSK-MYQFAKSNKTLDLLSCWHKEPS 121

Qy 555 TT--NRNVNPDGSLIANGYNWPEFSREKLTTAMIAHF-----RMFTIRAWHLTD 602

Db 122 TTYGGNDNSSASFIAR-----TKEEIGNHFVDIPRSACAKFLRRRIE--- 166

Qy 603 GFNEKIENAVDYDFELKSLSEVGKFKHLNKICVNRVLHGDNTSIKKLGIOKKHFFVNVQS 662

Db 167 -----ENNIAFSTMSLGEDMSF-----VC-----QYLMVSR 194

Qy 663 LNRQGITVYNDPEDDLDESKEYFNKTAEQEEIDILKDIKIQNK--DAKIAVSIFYP 720

Db 195 IAVDGLYTTQNVNPQSLSKRYVSN-----TENSLLMQNLWDQLLEV---YP 240

Qy 721 NTLNGLVKK-----LNNIIENY 737

Db 241 KIEENYKQHMDFRYLASLYVNNLFKFD 269

RESULT 15

AH2189

hypothetical protein alr3071 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C:Accession: AH2189

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AH2189

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-318 <KUR>

A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alx3071  
C;Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 4.7%; Score 238; DB 2; Length 318;  
Best Local Similarity 23.7%; Pred. No. 7.9e-06;  
Matches 82; Conservative 55; Mismatches 123; Indels 86; Gaps 13;

Qy 439 VPLVSIYIPAYNCANYIQRCDNALNQTVVDLEVCICNDGSTDNTLEVINKLYGNRPVR 498  
Db 1 MPKSVVPIPAYNAKYLPAATVESVLQSFDTIEIILINDGSSDIIIAWTAQI--TDPRVQ 58  
Qy 499 IMSPKNGGIASASNAAVSFAKGYIIGQLDSDDYLEPDPAVELCLKEFLKDKTLACVYT--- 555  
Db 59 VISQOQGLSGARNTGIHHASGEYIAFIDADDLWLP TKLEKQVKCLDNSPOAGLVYTWTA 118  
Qy 556 -TNRNVNPDGSLIAN--GYNWPEFSREKLTMTAMIAHFRMFTIRAWHLTDGFNEKIENA 611  
Db 119 WTDETGKPTGVIVASHVEGYWEO-----MVV-----NDKISN- 151  
Qy 612 VDYDMFLKLEVGKFKHLNKICYNRV-----LHGDNTSINKLGIQKKNHFVVVNQSLNR 665  
Db 152 -----GSSAMVRRICFDKVLFDTELTSSEDRDMWIRLAAHYHFVAVVKEPL-- 197  
Qy 666 QGITYYNYDEPDDLDEGRKYIFNKTAEYQEBEIDLKDI-KIIQNKDAKIAVSIFY-PNTL 723  
Db 198 ---TLYRRHS-QSMSEKRP-----KMLKNIRRVFEKTFATVPTTELLYLRNR 240  
Qy 724 NGLVKLNNIIEYNKNIFVIVLHVDKNHLTPDIKKEILAFYHKQV 769  
Db 241 YGWI-----NLYTAWTCMDERNYQEAIKTRQALLHYPOI 275

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 15:58:46 ; Search time 46 Seconds  
(without alignments)  
1746.973 Million cell updates/sec

Title: US-10-642-248-2  
Perfect score: 5108  
Sequence: 1 MNTLSQAIKAYNSDYQLAL.....SAKGENIPVKNFIINSITL 972

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues  
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgm2\_6/ptodata/1/iaa/6 COMB.pep.\*  
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4: /cgm2\_6/ptodata/1/iaa/PCTRUS COMB.pep.\*  
5: /cgm2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5108	100.0	972	2	US-09-469-200E-9
2	5104	99.9	972	2	US-10-172-527A-10
3	4490.5	87.9	965	2	US-09-437-277-3
4	3673.5	71.9	702	2	US-09-437-277-1
5	301.5	5.9	721	2	US-09-107-532A-6889
6	300	5.9	331	2	US-09-634-238-247
7	287.5	5.6	842	2	US-09-134-000C-5749
8	264.5	5.2	333	2	US-09-107-532A-5123
9	250.5	4.9	534	2	US-09-134-000C-5087
10	244.5	4.8	327	2	US-09-107-532A-6181
11	241.5	4.7	330	2	US-09-134-000C-6392
12	238.5	4.7	324	1	US-08-597-236-10
13	238.5	4.7	324	1	US-08-746-682A-10
14	236.5	4.6	1056	2	US-09-134-000C-5086
15	231.5	4.5	674	2	US-08-961-083-200
16	231.5	4.5	674	2	US-09-536-784-200
17	231.5	4.5	674	2	US-09-765-272A-200
18	231.5	4.5	674	2	US-09-765-272A-200
19	228.5	4.5	727	2	US-09-134-001C-4067
20	212	4.2	270	2	US-09-495-406-25
21	212	4.2	270	2	US-09-816-028A-39
22	212	4.2	270	2	US-10-303-162-39
23	212	4.2	270	2	US-10-303-134-39
24	212	4.2	270	2	US-10-303-118-39
25	212	4.2	270	2	US-10-303-128-39
26	210	4.1	301	2	US-09-495-406-15
27	210	4.1	301	2	US-09-816-028A-27

ALIGNMENTS

RESULT 1

US-09-469-200E-9  
; Sequence 9, Application US/09469200E  
; Patent No. 6833264  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Kumari, Kshama  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/09/469,200E  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: Pastuerella Multocida  
US-09-469-200E-9

Query Match	100.0%;	Score 5108;	DB 2;	Length 972;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 972;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNTLSQAIKAYNSDYQLALFKESABYGRKIVEFOITCKEKLKLSAHPVNSAHLVSN	60	
DB	1	MNTLSQAIKAYNSDYQLALFKESABYGRKIVEFOITCKEKLKLSAHPVNSAHLVSN	60	
QY	61	KEEKVNVCDSPDLATQLLLSNVKLVLSDEKNTLKNKWLTKKSENAEVRVALVP	120	
DB	61	KEEKVNVCDSPDLATQLLLSNVKLVLSDEKNTLKNKWLTKKSENAEVRVALVP	120	
QY	121	KDFPKDLVLAFLPDHVNDFTWYKKRKGRLGKPEHQHVGLSIIVTFNRPAILSLTACL	180	
DB	121	KDFPKDLVLAFLPDHVNDFTWYKKRKGRLGKPEHQHVGLSIIVTFNRPAILSLTACL	180	
QY	181	VNOKTHYFEVITVDDGSQEDLSPIIROYENKLDIRYVRQKNGFQASARNMGLRLAKY	240	
DB	181	VNOKTHYFEVITVDDGSQEDLSPIIROYENKLDIRYVRQKNGFQASARNMGLRLAKY	240	
QY	241	DFIGLLDCMAPNPLVHSHYVAELLEDLTLIIIPRKYIDTQHDIDPKDFLNNASLESPL	300	
DB	241	DFIGLLDCMAPNPLVHSHYVAELLEDLTLIIIPRKYIDTQHDIDPKDFLNNASLESPL	300	
QY	301	EYKTNNSVAAKGEGTVSLDWRLEQFETENLRLSDSPRFFPAAGNVAFKKWLKSGFPD	360	

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Db 301 EVKTNNSVAAKGBGTVSLDWRLEQFEKTEENLRSLSDSPFRFFAAGNVAFAKWLKNSGFFD 360
Qy 361 EEFNHWGGEDVFGYRLFRYGSFETIDGIMAYHQBPQKQENETDREAGNIIITLDMREK 420
Db 361 EEFNHWGGEDVFGYRLFRYGSFETIDGIMAYHQBPQKQENETDREAGNIIITLDMREK 420
Qy 421 VPIYIRKLLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Db 421 VPIYIRKLLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Qy 481 DNTLEVINLKYGNPRVRIMSKPNGGIIASASNAVSAKGYIIGQLSDDDYLDPELVC 540
Db 481 DNTLEVINLKYGNPRVRIMSKPNGGIIASASNAVSAKGYIIGQLSDDDYLDPELVC 540
Qy 541 LKEFLKDKTLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIEANVDYDMFLKLSVGFKPHLKI CYNRVLHGDNTSIKKLGIQKKNHFWVNV 660
Db 601 TDGFNEKIEANVDYDMFLKLSVGFKPHLKI CYNRVLHGDNTSIKKLGIQKKNHFWVNV 660
Qy 661 QSLNRQGITYYNYDEFDLDESRYIFNKTAEYQEEIDILKDIKIIQNKDAKIAVSIFYP 720
Db 661 QSLNRQGITYYNYDEFDLDESRYIFNKTAEYQEEIDILKDIKIIQNKDAKIAVSIFYP 720
Qy 721 NTNLGLVKKLNNIIEYNKNI FVIVLHVDKXHLTPDIKKEILAFYHKHQVNIILNNDISYY 780
Db 721 NTNLGLVKKLNNIIEYNKNI FVIVLHVDKXHLTPDIKKEILAFYHKHQVNIILNNDISYY 780
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYII FDNHDSL FVKND SYAYMKKYDVGWNFSA LTH 840
Db 781 TSNRLIKTEAHLNINKLSQNLNCEYII FDNHDSL FVKND SYAYMKKYDVGWNFSA LTH 840
Qy 841 DWIEKINAHPPPKKLIKTYPNDNDLKS MNVKGASQGMFTYALAHELLTIIKEVITSCQS 900
Db 841 DWIEKINAHPPPKKLIKTYPNDNDLKS MNVKGASQGMFTYALAHELLTIIKEVITSCQS 900
Qy 901 IDSVPEYNTEDIWFQALLILEKKTGHVFNKTSITLTYMPWERKLOWTNEQIESAKRGENI 960
Db 901 IDSVPEYNTEDIWFQALLILEKKTGHVFNKTSITLTYMPWERKLOWTNEQIESAKRGENI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
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## RESULT 2

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US-10-172-527A-10
; Sequence 10, Application US/10172527A
; Patent No. 6951743
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H
; APPLICANT: Kumari, Kshama
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: HYALURONAN SYNTHASE GENES AND EXPRESSION THEREOF IN BACILLUS HOST
; FILE REFERENCE: 3554,048
; CURRENT APPLICATION NUMBER: US/10/172,527A
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/297,788
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/297,744
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 09/469,200
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Pasteurella multocida
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RESULT 3
US-09-437-277-3
; Sequence 3, Application US/09437277
; Patent No. 644447
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
; FILE REFERENCE: 5820.551
; CURRENT APPLICATION NUMBER: US/09/437,277
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
; SEQ ID NO 3
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-09-437-277-3

Query Match      87.9%; Score 4490.5; DB 2; Length 965;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 843; Conservative 62; Mismatches 60; Indels 7; Gaps 2;

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DB      1 MNTLSQAIKAYNSNDYQALALFKESAEIYGRKIVEFOITCKEKLSAHPSVNSAHLN 60
QY      61 KEEKVNVCDSPDLATQALLSNVKKLVLSDESKNTLKNKWKLLTEKKSENAEVRALVLP 120
DB      54 EDKKNVCDSPDLATQALLSNVKKLVLSDESKNTLKNKWKLLTEKKSENAEVRALVLP 113
QY      121 KDFPKDLVLAPLPHVNDFTYKRRKRLGKIKPEHQHVGLSIIIVTTFNRPAILSLTACL 180
DB      114 KDFPKDLVLAPLPHVNDFTYKRRKRLGKIKPEHQHVGLSIIIVTTFNRPAILSLTACL 173
QY      181 VNQKTHYFEVIVTDDGSEDLSPITROYENKLDIYRQKNGFQASARNMGLRLAKY 240
DB      174 VNQKTHYFEVIVTDDGSEDLSPITROYENKLDIYRQKNGFQASARNMGLRLAKY 233
QY      241 DFIGLLDCMAPNPLVHSHYVAELLEDLTIIGPRKYIDTQHDIDPKDPLNNASLESPL 300
DB      234 DFIGLLDCMAPNPLVHSHYVAELLEDLTIIGPRKYIDTQHDIDPKDPLNNASLESPL 293
QY      301 EVKTNNSVAAGGEGTVSDWRLQPEKTEKNTLKNKWKLLTEKKSENAEVRALVLP 360
DB      294 ETATNNPSITSGKNSLDWRLQPEKTEKNTLKNKWKLLTEKKSENAEVRALVLP 353
QY      361 EEFNHWGGEDVEFGYRLFRYGSFFKTIDGIMAYHOEPGKNETDREAGKNTLIMREK 420
DB      354 EEFNHWGGEDVEFGYRLFRYGSFFKTIDGIMAYHOEPGKNETDREAGKNTLIMREK 413
QY      421 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRQVDSALNTQVVDLEVCINCDSGT 480
DB      414 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRQVDSALNTQVVDLEVCINCDSGT 473
QY      481 DNTLEVINKLYGNRPVIMSKPNGIGIASASNAVSPAKGYIIGQLDSDDYLEPDAVELC 540
DB      474 DNTLEVINKLYGNRPVIMSKPNGIGIASASNAVSPAKGYIIGQLDSDDYLEPDAVELC 533
QY      541 LKEFLKDKTACVYTTNRNVNPDGSLIANGYNWBPFSREKLTAMAHFRMFTTIRAWHL 600
DB      534 LKEFLKDKTACVYTTNRNVNPDGSLIANGYNWBPFSREKLTAMAHFRMFTTIRAWHL 593
QY      601 TDFNFKENIENAVDYDMFLKSEVGKPKHLNKKIYNRVLHGDNTSISIKLGIQKKNHVVVN 660
DB      594 TDFNFKENIENAVDYDMFLKSEVGKPKHLNKKIYNRVLHGDNTSISIKLGIQKKNHVVVN 653
QY      661 QSLNRQGIYNNYDFDDDESRRKIFNKTAEYQBEIDLKDIKIQNDKAKIANSIFYP 720
DB      654 QSLNRQGIYNNYDFDDDESRRKIFNKTAEYQBEIDLKDIKIQNDKAKIANSIFYP 713
QY      721 NTLNGLVKKLNNIIEYNKQIFVILHVDKNHLPDIDKKEILAFYHKHQVNILLNDISYY 780
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DB      714 NTLNGLVKKLNNIIEYNKQIFVILHVDKNHLPDIDKKEILAFYHKHQVNILLNDISYY 773
QY      781 TSNRLIKTEAHLNINKNLSQNLNCEYIIFDNHDSLFVKNDISYAYMKKYDVGWNFSAETH 840
DB      774 TSNRLIKTEAHLNINKNLSQNLNCEYIIFDNHDSLFVKNDISYAYMKKYDVGWNFSAETH 833
QY      841 DWIEKINAHPPFKKLKIKTYFNDNDLKSMMNVKGASQGMFYALAHALLTIIKEVITSQCS 900
DB      834 DWIEKINAHPPFKKLKIKTYFNDNDLKSMMNVKGASQGMFYALAHALLTIIKEVITSQCS 893
QY      901 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEOIESAKRGNI 960
DB      894 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEOIESAKRGNI 953
QY      961 PVNKFIINSITL 972
DB      954 PVNKFIINSITL 965

RESULT 4
US-09-437-277-1
; Sequence 1, Application US/09437277
; Patent No. 644447
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
; FILE REFERENCE: 5820.551
; CURRENT APPLICATION NUMBER: US/09/437,277
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
; SEQ ID NO 1
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-09-437-277-1

Query Match      71.9%; Score 3673.5; DB 2; Length 702;
Best Local Similarity 99.7%; Pred. No. 4.6e-313;
Matches 701; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY      1 MNTLSQAIKAYNSNDYQALALFKESAEIYGRKIVEFOITCKEKLSAHPSVNSAHLN 60
DB      1 MNTLSQAIKAYNSNDYQALALFKESAEIYGRKIVEFOITCKEKLSAHPSVNSAHLN 60
QY      61 KEEKVNVCDSPDLATQALLSNVKKLVLSDESKNTLKNKWKLLTEKKSENAEVRALVLP 120
DB      61 KEEKVNVCDSPDLATQALLSNVKKLVLSDESKNTLKNKWKLLTEKKSENAEVRALVLP 120
QY      121 KDFPKDLVLAPLPHVNDFTYKRRKRLGKIKPEHQHVGLSIIIVTTFNRPAILSLTACL 180
DB      121 KDFPKDLVLAPLPHVNDFTYKRRKRLGKIKPEHQHVGLSIIIVTTFNRPAILSLTACL 180
QY      181 VNQKTHYFEVIVTDDGSEDLSPITROYENKLDIYRQKNGFQASARNMGLRLAKY 240
DB      181 VNQKTHYFEVIVTDDGSEDLSPITROYENKLDIYRQKNGFQASARNMGLRLAKY 240
QY      241 DFIGLLDCMAPNPLVHSHYVAELLEDLTIIGPRKYIDTQHDIDPKDPLNNASLESPL 300
DB      241 DFIGLLDCMAPNPLVHSHYVAELLEDLTIIGPRKYIDTQHDIDPKDPLNNASLESPL 300
QY      301 EVKTNNSVAAGGEGTVSDWRLQPEKTEKNTLKNKWKLLTEKKSENAEVRALVLP 360
DB      301 EVKTNNSVAAGGEGTVSDWRLQPEKTEKNTLKNKWKLLTEKKSENAEVRALVLP 360
QY      361 EEFNHWGGEDVEFGYRLFRYGSFFKTIDGIMAYHOEPGKNETDREAGKNTLIMREK 420
DB      361 EEFNHWGGEDVEFGYRLFRYGSFFKTIDGIMAYHOEPGKNETDREAGKNTLIMREK 420
QY      421 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRQVDSALNTQVVDLEVCINCDSGT 480
DB      421 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRQVDSALNTQVVDLEVCINCDSGT 479
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QY 481 DNTLEVKLNKYNPRVRIMSKNGGKTASNAVSPAKGYIIGOLDSDDYLEPDAVELC 540
Db 480 DNTLEVKLNKYNPRVRIMSKNGGKTASNAVSPAKGYIIGOLDSDDYLEPDAVELC 539
QY 541 LKEFLKDKTLACVYTTNRNVPDGLSIANGYNWPEFSREKLTMTAMIAHFRMFTIRAWHL 600
Db 540 LKEFLKDKTLACVYTTNRNVPDGLSIANGYNWPEFSREKLTMTAMIAHFRMFTIRAWHL 599
QY 601 TDGFNEKIENAVDYDMFLKSEVGKFKHLNKCYNRVLHGDNTSIKKLGIOKKNHFFVFN 660
Db 600 TDGFNEKIENAVDYDMFLKSEVGKFKHLNKCYNRVLHGDNTSIKKLGIOKKNHFFVFN 659
QY 661 QSLNRQGITVYNYDEPDLDSESRKYIFNKTAEQEIEDILKDI 703
Db 660 QSLNRQGITVYNYDEPDLDSESRKYIFNKTAEQEIEDILKDI 702

RESULT 5
US-09-107-532A-6889
; Sequence 6889, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6889:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (B) LOCATION 1...721
; SEQUENCE DESCRIPTION: SEQ ID NO: 6889:
US-09-107-532A-6889
Query Match 5.9%; Score 301.5; DB 2; Length 721;
Best Local Similarity 21.2%; Pred. No. 3.1e-17;
Matches 153; Conservative 121; Mismatches 259; Indels 187; Gaps 28;
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QY 269 DLTIIG-----PRKYIDTQHIDPKDFLNNSLLESLP-----EVTNNS-----VAAKG 312
Db 30 DLLIVGWAIDEVTKELPTIKVEKNVIAEATHVRLDINHLYNLDVKTOSGFKVRUSGKM 89
QY 313 EGTVSJLDMRLEQPEKTENLRLSDS-PPREFFAAGNAVAFKAKKWLNKSQFFPDEEFNHGGEDV 371
Db 90 RGKAILDFQTARHONGIAVLKNGKYPY-----DDGISSWERKKRLLKKGINVARTHG 143
QY 372 EGYRLFRYSGFFKTIIDGI--MAYHQEPGPKENETDREAGKNITLDMREKVPYIIRKLL 429
Db 144 KKAIRRVKLELPGSIDIYAEWISRHEKPDLKEQR-----REVQGFAYR--- 186
QY 430 PIEDSHINRVPLVSIYIPAYNC-ANYIORCVDSALMOTVVQDLEVCICNDGSTONTL-EVI 487
Db 187 -----PLISILMPYVVEIKLEKCIISVLDQTYDHWELCISDASTDPARKCL 236
QY 488 NKLYGNNPRVRIM-SKPNGGIASASNAVSPAKGYIIGOLDSDDYLEPDAVELCLKEFLK 546
Db 237 ESYQAKDDRIKVVFRQENGHISLATNSALEMAEGEFIALDNDDELPPFALYEVAKVLNV 296
QY 547 DKTILACVYTTNRNVPDGLSIANGYNWPEFSREKLTMTAMIAHFRMFTIRAWHLTDGFNE 606
Db 297 HPELDLYSDEDKIDADGNRFPDFHK-ADWSPDTLMGNNYISHLGVYRTSIVKELGGRK 355
QY 607 KIENAVDYDMFLKSEVGKFKHLNKCYNRVLHGDNTSIKKLGIOKKNHFFVFNQSLNRQ 666
Db 356 GYEGSQDYDLVURVTEQIPAEHIYHI--DRVLY-----HWRTIPGSTASN 398
QY 667 GITVYNYDEPDLDSESRKYIFNKTAEQEIEDILKDIKIIONKDAKI---AVSIFYPNTL 723
Db 399 G-----EAKSYI-----YDSGVKALTDALSRNIIKGSVHPGRISGFYEITY 439
QY 724 NGLVKLNNIIEYNKNIF-----VI-----VLHVDKNHLLTDPDKKEILAFYH 765
Db 440 DVLQEDLVSVIIPTKNGYEDLTKCVDSIIETKTSYPNYEIIADNGSTDPKM-QELFAEY- 497
QY 766 KHQVN---ILLNNDISYTSNRLIKTEAHLNINKLSQNLNCEYIIFNHDLSLFVKND- 821
Db 498 KHQLKDRFIV-----ELIDIPFNYSRINNLAEEKANGKYFLFLNNDTEVIEPDW 546
QY 822 -----SYAY-----MKKYD-----V 831
Db 547 MTAMVSYAQFDRIGCVGAKLFYPPDDTTOHAGVLLGIGGVAGHALNNYDRTHCGYFGRLLVI 606
QY 832 GNFPSALTHDWI-----EKINAHPPPKKLIKTYFNDNLDKSMNVKSGASQGMFTYALAH 887
Db 607 DYNILAVTAAACMMVKAAADFNNAVNGFDBILEVAFNDVDL---CLKVVELGRYNYIAHQAEL 663

RESULT 6
US-09-634-238-247
; Sequence 247, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 247
; LENGTH: 331
```

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; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-247

Query Match      5.9%; Score 300; DB 2; Length 331;
Best Local Similarity 28.6%; Pred. No. 1.2e-17;
Matches 90; Conservative 53; Mismatches 130; Indels 42; Gaps 11;

Qy 439 VPLSVIIPAYNCANYIQCVDNALQTVVDLEVICNDGSDTNTLEVINLKYNNPRVR 498
Db 6 MPLSVIIPVYNVEKYLQRCIDSLFAQTYNIEIIVLVDGSDRSLICKNAQQDRVR 65
Qy 499 IMSKPNGGIASANAAYSFRAKGYIGOLSDDDLEPAVELCLKEFLKDKTLACVYITNR 558
Db 66 VFSKNGGVADTRNFGVSVARGQWISFVDPDDYVDPDYIEYLGILVKSNAWTSI-CQHR 124
Qy 559 NVNPDGSLIANGYNWPE-----FSREKLTTAMIAHFRMFTIRAWHLTDG-FNE 606
Db 125 NVYKNGKIQTNLYEGPAVLDSHTAVKLLYDDQIDTSVWAKLYPAWVFKKIHPKGRLE 184
Qy 607 KIENAVDYDFLKLSEV---GKFKHLNKICYNVHLHGDNTSIKKLGI-----QKK 653
Db 185 DI--AATYKTFPLASDSIAGSEAKYSYPRYSIVN-DQFSLHKLDLIDMTQMAQCEVKK 241
Qy 654 NHFVVNQSLNRQGITVNY-----DEPDLDSESKYIFNKTAAYQOEIDILKDIKI- 705
Db 242 ---VYPDLQIASQRRVLYAYISTLNQMNQVQGYQIEIREQLISKIKELRK--PVLEDHKAP 296
Qy 706 IQNKDAKIAVSIFYP 720
Db 297 IRDKVAICLIGFSYP 311

RESULT 7
US-09-134-000C-5749
; Sequence 5749, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5749
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5749

Query Match      5.6%; Score 287.5; DB 2; Length 842;
Best Local Similarity 19.5%; Pred. No. 6.9e-16;
Matches 191; Conservative 147; Mismatches 315; Indels 327; Gaps 42;

Qy 156 OHVGLSIITVFNRPAILSIITLACLVNQKTHYPFEVIVTDGSDQSDLSPIIQVYENKLDI 215
Db 8 ENVKSVIVPVYVNVETYLEEALMSLKQ-TLKEIEFLINDGSDTNSQKIIIE-----59
Qy 216 RYVRQKNGFQSAARNGLRLAKYDFTLGLDCDAPNPLVHVSIVVAELLEDLDTIIGP 275
Db 60 --IAQDDPRFRVFNKNGG--IGKAPNLGVSEAK-----GEYIAEFSDSDYVALHAY 107
Qy 276 RXYIUT---QHIDPKDFLNASLLESLEPVKTNNSVAAKGETVSLD--WRL-EQFEXTE 329
Db 108 ERLYNTAKSHHAD-----VRCNNWFESSEEEVERDILMQIPDKYNQI 151
Qy 330 NLRSDSPRPFAAGNAPFAKKWLKSGF-FDEEFNHMGGEDVDFGYRLFRYGSFFK---385
Db 152 DLKTTDLIVQVY-PWNAIYKSMIEKENVTWDEEIKSYGDT-----GLFWKINS 199

386 -----TIDGIMAYHQEPPEKGENETDRBAGKNITLDMREKVPYIYR-----426
200 ASQNVIFIKDCLVYRQDNP-----NSTVNVATKVPFQFQKLIIRSNLIEQ 247
427 -----KLLPIED-----433
248 NKPERYKGYFYKQMFKEYFAIEKLTHLRDESVEYIQKAVDPROALETDQDNDIDFEY 307
434 -----SHINRVPLSVIIPAYNCANYIQCVDNALQTVVDLEVICND 477
308 IKQFYQIANDPAAYEDYLNLYKVSVMPIHNASKYLRTLETVCESQSLREIILVEN 367
478 GSTDNTLEVINLKYNNPRVRIMSKPNGGIASANAAYSFRAKGYIGOLSDDDYLE-----533
368 GSTDNTMDIINEFAVKDPRIITGISIGKSNPGHARNVIGISMARGRYLQFLDADDDHFEANLL 427
534 -----PAVELCLKEFLKDKTLACVYITNRNVNPDGSLIANG--YNNPEFSEK 580
428 QDAYYRAYDSATDILLFGMKELPNGEVHVH-----NP-----LLTNGGRMSGEEISLDE 478
581 LTTAMIAHFRMFTIRAWHLTDGTFNEKIEANAVDYDMFL---KLSEVGKFKHLNKICYNRV 637
479 VTPYLYDKLFLLEYIKENNLVN-----LEQFVGEDAYFTYTALLGTEKIVALNKYLLTRI 533
638 LHGDNTSIKKLGIQKKNHVVVNQSL-----NR-----QCITYNYNDEPD--DLDE 681
534 VRQDGL-MSTYGMNRYRDEFNLHDKMLEYLKQHAPNRTEAYRLKIINTLNMFIPDMNRVDQ 592
682 SRKYIFNKTAAYQOEIDILKDIKIQNKDAKIAVSIFYPNTLNGL--VKLNNIIEYNKN 739
593 AFKERF-----YQE-----LKE-KYIQLGLDLVKKEKYSNDPEQVERITRIQILQNL 642
740 IFVIV---LHVQDNHLPDIK---KEILAFYHKHGVN-----ILNNDISYVTS 782
643 IYQNIYKDFGKKTPIIPNVHIOBGRGKVIFGQKTOGTAIEMFSIIADND-----TS 698
783 NRLIKTEAHLNSINKLSQNLNCEYIIFDNHDSLFVKNDSYAYNMKKYDVGNFNSALTHDW 842
699 N-----ASGVDFVYMGDNTKII---HDSLLVS---LLJKKGGTLLKSIVLQAEW 742
843 IEKINAHPPFKLIKTYFNNDNLKSMNVKGSQGMFTYALAHELL--TIKEVITSCQS 900
743 -----EKG-----YTLQENMYVTFVDNVFT-----763
901 IDSVPYNTEDIW-----FOFALLILEKKTGHVENKTSITLYMPWERKQWNEQI 951
764 -----IWAGYTKYAAFDYVNRILTSREGE-----THFSVVRQNGYIQDT 804
952 ESAKRGENIPVNFINSIT 971
805 MTSIGNELTPINKIEGNEPT 824

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
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; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/107.532A
;   FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/085,598
;   FILING DATE: 14 May 1998
;   APPLICATION NUMBER: 60/051571
;   FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ariniello, Pamela Deneke
;   REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781)893-5007
;   TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5123:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 333 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
;   ORGANISM: Enterococcus faecium
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (B) LOCATION 1...333
; SEQUENCE DESCRIPTION: SEQ ID NO: 5123:
US-09-107-532A-5123

Query Match      5.2%; Score 264.5; DB 2; Length 333;
Best Local Similarity 23.3%; Pred. No. 1.5e-14;
Matches 85; Conservative 66; Mismatches 129; Indels 85; Gaps 12;

QY 442 VSIYIPAYNCANYIQCVCDSALNQTVVDLVCIQNDGSTDTNTLEVINKLYGNNPRVRIMS 501
Db 13 ISIIVPVYVVEKYLKCVDSILQGTFTDFELLIDGSTDNGSSICDELAKTNRIKVIH 72

QY 502 KPGNGIASNAAVSFAGKYIYQGLSDDDYLEPDVAVELCLKEFLK---DKTLACVYTYNR 558
Db 73 KENGGLSDARNIGIEVAKGDFIGFIDSDVDYDEDMVAFYNNILKYDAELSMGCIYDVHK 132

QY 559 N-----VNPDCSLIANGYNWPFESREKLITTA-MIAHHFRMFTIRAWHLTDGPFNEKEN-- 610
Db 133 NKEIKLTPFSQLVTKSEATIELVDGLKVYVANAVSKLYK-----KELFENVR 179

QY 611 -----AVDYDMFLKSEVGKFKHLNKCYNRVVLHGDNSTSIKLGIGQKNHFVVVQSLN 664
Db 180 YPKGKIAEDAAVILKI-----INQCKI-----HVDTS-----QKYYVHRGDSIT 220

QY 665 RQGITVYNYVDEFDLDESRYIFNKTAEYQSEID-----ILKDIKIQNKDAKIAV 715
Db 221 SKKFTKKDFDIIDVWNEKEMWIKNYPQMDYKVTVCWAYFVVLKLVLTBEK----- 274

QY 716 SIPYPNTLGLVKLANIIEYKNIFVILVHDNHLTPDIKEIILAFYHKHQVNILLNN 775
Db 275 -----GLYQEKQVREYLDIDNFFI-----IKNRLTFQKISM-LLLTFF 313

QY 776 DISYY 780
Db 314 GIAAY 318

RESULT 9
US-09-134-000C-5087
; Sequence 5087, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5087
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-5087

Query Match      4.9%; Score 250.5; DB 2; Length 534;
Best Local Similarity 21.2%; Pred. No. 5.7e-13;
Matches 114; Conservative 91; Mismatches 189; Indels 145; Gaps 21;

QY 295 LLESPEVKTNNNSVAAKGEGTVSLDWRLEQFQFTEKNTLRSLSDSPFRFFAAAGNVAFKAKWLN 354
Db 21 IFDSIYRDKTNNLTITG-----WALDTIYK-----ESP--TFTINNENQVSAY-N 63

QY 355 KSGFFDEEPN--HWGGEDVEFGYRLFRYGSFPKTTIDGI-----MAYHQB----- 397
Db 64 IORVLREDVNOIYQTEPAIEAG-----FVVTLEGIKQKKVLPFPFQSSAHVITVDFP 115

QY 398 -----PKENETDR-----EAGKNIITLIDIMEKVPYI-----YRK 427
Db 116 LNKKYPVIFGTEDKVTRLMIKAKGKYMAKNGISHTIORAKIEKLNRQAQSYPNWLARNE 175

QY 428 LLPIED-----SHINRVLVSIYIPAYNC-ANYIQCVCDSALNQTVVDLVCIQNDGSTD 481
Db 176 VLDIEAMTQEIATFHYQPKISIAMPVYVVEKWLRLCIDSILNQVYTNWELCWADDASTD 235

QY 482 -NTLEVINKLYGNNPRVRIM-SKPNGGIASNAAVSFAGKYIYQGLSDDDYLEPDVAVEL 539
Db 236 PNWKILTEYQQLDERIRVVFREQNGHISEATNSALAIATGSEFVALLDNDDELAINAFYE 295

QY 540 CLKEFLKDKTLACVYTYNENVPDGLSIANGYNWPFESREKLITTA-MIAHHFRMFTIRAWH 599
Db 296 VVKLVNENPELDLITSDDEKIDMDGNRSDPAFK-PDWSDDLGLGTNYIISHLGVYRRSILE 354

QY 600 LTDGFEKLENAVDYDMFLKSE---VGKFKHLNKCYNRVVLHGDNSTSIK--LGIQKN 654
Db 355 EIGGRKYGEGSDYDLVLRFTTEKTERIKHIPKLYVYWRMLPTSTAVDQSGKYAPEA 414

QY 655 HFVVNQSLNRQGI-----TYNYDE-----PDDLDESRYIF 687
Db 415 GLRAVQDALVRRINGHATHGAANGLYDVYDIESEKLVSIIPTKNGYKDVQRCVSSII 474

QY 688 NKT-----AEYQ-----EEDILKDIKIQNKDAKIA 714
Db 475 EKTYYQNYEIIWADNGSTDPKMHLYAEFEQQLPGRFFVESIDIPFNFTINNRAAKA 533

RESULT 10
US-09-107-532A-6181
; Sequence 6181, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;   STREET: 100 Beaver Street
;   CITY: Waltham
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02354
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: CD/ROM ISO9660
;   COMPUTER: PC
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; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107.532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...327
; SEQUENCE DESCRIPTION: SEQ ID NO: 6181:
US-09-107-532A-6181

Query Match 4.8%; Score 244.5; DB 2; Length 327;
Best Local Similarity 26.0%; Pred. No. 8.4e-13;
Matches 85; Conservative 59; Mismatches 100; Indels 83; Gaps 15;

Qy 442 VSIYIPAYNCANYIQRCDVSALNQTVDLEVCINCDSGTNTLEVINLGNPRVRIMS 501
Db 10 ISIIVPVYKYLKCKVDSILAQTFTDFEILVDDGSPDMSGKICDEYAEKDNVRVH 69
Qy 502 KPNGGIASANAASVAFKGYIGQLSDSDYLDPAVELCLKEFLK--DKTLACVY---- 554
Db 70 KENGGLSARAGIDVARGKYLGFVDSDDYIDEDMYEI-LYENLKIHDADISSVELIPFY 128
Qy 555 -TTNRNVNPDGSLIA-----NGYNWPEFSREKLTMTAMIAHHFRMFTIRA 597
Db 129 GDYKKANKKKVILNKKEAIKSVLEGTQFYAYAWNKLYRKEL-----FKD 175
Qy 598 WHLTDFGNEKIENA-VDYDMFLK----LSEVGKFKHLKICYNRVLHGDNTSIKLGIIQ 651
Db 176 NRYLDG--KTFEDAVIILDLFQTEKIVVSNEEKFYIQR-----NDSIMGKFS 223
Qy 652 KKNHFVWVQSLNRQIGIYYNDEPDDLDES--RK-----YIFNK---TAYQOE---EI 697
Db 224 MNFVIVAEAWYNKEKI-----LDAPDLHDSYRCLWCWAYFVLDKMWLSSSYQIIPRK 279
Qy 698 DILDKIKIION-----KDAKIAV 715
Db 280 TWIEFLKKNRNPIFYKGTGTSRKIAI 306

RESULT 11
US-09-134-000C-6392
; Sequence 6392, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
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; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6392
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6392

Query Match 4.7%; Score 241.5; DB 2; Length 330;
Best Local Similarity 23.9%; Pred. No. 1.6e-12;
Matches 84; Conservative 64; Mismatches 116; Indels 87; Gaps 14;

Qy 439 VPLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCINCDSGTNTLEVINLGNPRVR 498
Db 7 MPKISIIIPVYVYKYLEKCVRSILAQTFTDFEILVDDGSPDSSGAMCQFAEQDQVRK 66
Qy 499 IMSPKNGGIASANAASVAFKGYIGQLSDSDYLDPAVELCLKEFLK--DKTLACVYT 555
Db 67 VIHKEGGLSDARNAGIEIATGYLGFVDSDDYIADDMYELLYTNIVKREDADLSICGIYD 126
Qy 556 TNRNVNPDGSLIANGYNWPEFSREKLTMTAMIAHHFRMFTIRAHLTDGFNEKIENAVDYD 615
Db 127 VYEGKEPIVKSIIQG-----TFSREALLLLIQGN--IISVHA----- 162
Qy 616 MFLKLSSEVGKFKHLKICYNRVLHGDNTSIKLGIIQKKNHFVWVQSLNRQIGIYYNDE 675
Db 163 -----VNKL-YKKLFADLRYPK--GKYHEDSFIIIVDLLSECCQKVS----- 200
Qy 676 FDDLDESRKYIF-----NKTABYQE--EIDILKDKIIONKDAKIAVS----- 716
Db 201 ---IDSTQKYVYHRMGSIINTETFSKQFEFIEAWKXNELK-----LKGKGAIVIEAAHQ 253
Qy 717 IFYPNTI-----NGLVKK-LNNIIEYNKNIFVILVHVDKQHLTPDIKK 758
Db 254 VCFANFLVDLKILISNAPKKRQIVRYLRENFIFIM---KXKVFTYSRK 301

RESULT 12
US-08-597-236-10
; Sequence 10, Application US/08597236
; Patent No. 5733765
; GENERAL INFORMATION:
; APPLICANT: STINGELE, Francesca
; APPLICANT: MOLLET, Beat
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
; TITLE OF INVENTION: EXOPOLYSACCHARIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americans
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/597,236
; FILING DATE:
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95201669.9
; FILING DATE: 20-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci A. Allan
; REGISTRATION NUMBER: 30256
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-597-236-10

Query Match 4.7%; Score 238.5; DB 1; Length 324;
Best Local Similarity 23.1%; Pred. No. 2.8e-12;
Matches 87; Conservative 64; Mismatches 136; Indels 89; Gaps 12;

QY 441 LVSIIYPAYNCANYIQRCDVSALNQTVDVLEVCINCDSGTNTLTLEVINKLYGNPRVRIM 500
Db 6 LISIIVPVNVEKLEKCLQSQVQNTYNNFEVILVNDGSTSSLSICEKFNQDKRPSVF 65
QY 501 SKPNGIASASNAAVSFAGYVIGQLSDSDYLEPDAVE-----LCLKEFLKDK 548
Db 66 SKENGGMSSARNFGIKKAGSFITFVDSDDYIVKDYLSHLVAGIKSETSVCSKFFLVD 125
QY 549 TLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTMTAMIAHFRMTIRAWHLTDGPFNEKI 608
Db 126 -----KGSLLTK-----KEAPKKKSEVVSIEESIKILLQ----- 155
QY 609 ENAVDYDFMLKSEVGKFKHLNKCYNRVLHGDNTSIKKLGIOKKNHVVVQNSLNQGI 668
Db 156 QNGYDLAVWGKLYPVSPFFETIS-FPEGKLYEDMGITTYKLLKLASEVWFL----- 203
QY 669 TYNYDEFPDDLDESRYIFNKTAEQEEDILKDIKIIQNCKDAKIAVSIFYPNTLGLVK 728
Db 204 -----DAYDAYVQVRPNSSIMNSSFNLLKKLDIEMVHEM-----NDILA 242
QY 729 KLNIIIEYNKN-IFV-----IVLHVDKNHLTPDIKEILAFYHKHQVNILLNDISYTSN 783
Db 243 QFPNLALYVKNRAFAAEVVKIFLEIPKEKEFEQAOKL---WH-----DIKKNRKAPFMTKG 295
QY 784 RLIKTE--AHLNSINK 797
Db 296 ARLKNRLGASLSFLGK 311

RESULT 13
US-08-746-682A-10
; Sequence 10, Application US/08746682A
; Patent No. 5786184
; GENERAL INFORMATION:
; APPLICANT: STINGBLE, Francesca
; APPLICANT: MOLLET, Beat
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
; TITLE OF INVENTION: EXOPOLYSACCHARIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americans
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,682A
; FILING DATE: 14-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/597,236
; FILING DATE: 20-JUN-1995
; APPLICATION NUMBER: EP 95201669.9
; FILING DATE: 20-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci A., Allan
; REGISTRATION NUMBER: 30256
; INFORMATION FOR SEQ ID NO: 10:

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QY 557 NRNVNPGSLIANGYNWPEFSREKLTTAMIAHFRMTTIRAWHLTDGFNEKIENAVDYDM 616  
Db 683 EDKITENRRFP-NAFYKSDWNPBLIILNHNVIITHFVVVKRDLLEKVGGLNSAYNGAODYDF 741  
QY 617 FLKLSE-VGFKHLNLCYIN-RVLHGDNITSIKKLGHQKNHFVVVQVQ-----SLNRQGI- 668  
Db 742 VLRAEQATKIKHPCGMVYHRAIE---SSTALNPESKGYAVVAGQKAVQAATERGLK 797  
QY 669 -----TY-----YNYD-----EFDDLDESRYIKFNT-----ASYQ 694  
Db 798 AQVEIAEFYSGYKINLYLDHVPVMSLIITNDTENMSSYLRQLLEKTAYTAYTNYEILLPARFE 857  
QY 695 EEDILKQ-----IKIQNKDAKIAVSIFYPNTLGLVKVKKLNNI----- 733  
Db 858 NQINQIDRLRYVSTETRHGMIOAAKEGYVALLNAGLVP-TKNDWLKELMNIQOQETSGL 916  
QY 734 -----IEYNKNI FIVLHVDKNHL-----TPDIKKEILAFYHKHQVNILLNNDISYY 780  
Db 917 VTGRVVDARYRVETVGVSDTKRLLYPEKGTGP-----KSLGYVYR-----IALPRNIQAA 969  
QY 781 TSNRLIKTEAHLNKNKLSQNLNCEYIIIFDNHDSLFVKNDS-----YAYMK 827  
Db 970 TEDCLL-----FNK--QLYLNLEGI-----NESLGKEMMGVDSLQFASAG 1008  
QY 828 KYDVGMNFSALTHDWIEKINAHF-----PFFKKLIKTY 859  
Db 1009 KRNVYVYAILKAD--ERMQNHDKGYSYKSLAEKW 1041

RESULT 15  
US-08-961-083-200  
; Sequence 200, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961.083  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 200:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 674 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-961-083-200

Query Match 4.5%; Score 231.5; DB 2; Length 674;

Best Local Similarity 20.9%; Pred. No. 3.9e-11;  
Matches 102; Conservative 79; Mismatches 171; Indels 135; Gaps 17;  
QY 458 CVDLSALNQTVDLEVCICNDGSGTNTLEVINKLYGNPRVIMSKPENGIGIASASNAVSF 517  
Db 1 CUDSIITQYKNIEIVVNDGSDTASGEICKFSEMDHRLIYIEQENAGLSAARTNGLNN 60  
QY 518 AKGYIIGQLDSDYLEPDAVELCLK---BFLKDKTKLACVYTTNRN----- 559  
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QY 560 -VNPDSGLIANGYNWPEFSREKLTTAMIAHFRMTTIRAWHL-----TDGP-NEKI 608  
Db 121 KYVDNVSIFENLYE---TQEMKSFALISAWGKLYKARLFEQLRFDIGKLGEDGYLNQKV 176  
QY 609 ENAVDYMFLKLSVKGFKHLNKICY-NRVLHGD-----NTSIKK 647  
Db 177 -----YLLSE--KVYLNKSLYAIRKGSLSRVWTEKWMHALVDMASERITLLAN 225  
QY 648 LGIQKKNHFVVVQSL-----NRQG-----ITYNYD-----BFDDLDESRYIKF 689  
Db 226 MGYPLEKHLAVYRQMLEVSLANGQASGLSDTATYKEFEMKQRLNQLNSROESEKKAIVL 285  
QY 690 TABYQBEIDILDKIKIIONKDAKIAVSIFYPNTLGLVKVKKLNNIIEYNKNI FIVLHVDK 749  
Db 286 AANYGYVDQVLTITKISICYHNRSIRFYLIHSDPPEMIKQLNKRL-----KFDS 335  
QY 750 NHLTPDIKKEILAFYHKHQVNILLNNDISYVTSNRLIKTEAHLNKNKLSQNLNCEYII 809  
Db 336 EIINCRVTSEQISCY-----KSDISYTVFLRYFIADP-----VQEDKALYLDCLVV 382  
QY 810 FDNHDSLFVKN-DSY-----AYMKYDVGMNFSALTH 840  
Db 383 TKNLDDLFAFDLQDYPLAAVRDFGGRAYFGQEIFNAGVLLVNNAFWKKNMTOKLIDVTN 442  
QY 841 DWIEKIN 847  
Db 443 EWHDKVD 449

Search completed: January 6, 2006, 16:06:20  
Job time : 48 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 8, 2006, 23:00:16 : Search time 1157 Seconds  
(without alignments)  
612.490 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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10: /cgn2\_6/prodata/1/pubpna/US60 NEW PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5108	100.0	2920	7	US-11-172-145-1
2	5104	99.9	2937	7	US-11-124-215-2
3	5104	99.9	2937	7	US-11-120-422-9
4	4502.5	88.1	2979	7	US-11-172-145-3
5	3697	72.4	2112	7	US-11-172-145-11
6	3692	72.3	2112	7	US-11-172-145-17
7	3692	72.3	2112	7	US-11-172-145-18
8	3692	72.3	2112	7	US-11-172-145-19
					Sequence 1, Appli
					Sequence 2, Appli
					Sequence 3, Appli
					Sequence 11, Appl
					Sequence 17, Appl
					Sequence 18, Appl
					Sequence 19, Appl

9	3692	72.3	2112	7	US-11-172-145-20
10	3471	68.0	1980	7	US-11-172-145-13
11	3336	65.3	1902	7	US-11-172-145-14
12	3225	63.1	1830	7	US-11-172-145-15
13	3116	61.0	1764	7	US-11-172-145-16
14	235	4.6	2736	7	US-11-194-246-190
15	211.5	4.1	37500	6	US-10-522-037-1
16	210.5	4.1	5859	7	US-11-102-497-1
17	210.5	4.1	5859	7	US-11-102-497-7
18	202	4.0	1774	6	US-10-510-386-103
19	139.5	3.9	1851	7	US-11-172-145-5
20	133.5	3.8	1854	7	US-11-172-145-7
21	182	3.6	2990	6	US-10-793-626-3899
22	169	3.2	6507	6	US-10-485-517-75
23	161.5	3.2	918	6	US-10-467-657-1317
24	156	3.1	3202	6	US-10-793-626-3774
25	150.5	2.9	3021	6	US-10-793-626-153
26	149.5	2.9	2475	6	US-10-131-826A-195
27	148.5	2.9	981	6	US-10-467-657-2407
28	142.5	2.8	8503	7	US-11-124-368A-45
29	142	2.8	3504	7	US-11-052-554A-505
30	141.5	2.8	3167	6	US-10-793-626-4117
31	141	2.8	8512	7	US-11-124-368A-46
32	140.5	2.8	1767	7	US-11-052-554A-718
33	139.5	2.7	3285	6	US-10-793-626-3448
34	139	2.7	12732	6	US-10-802-796-1
35	136.5	2.7	6014	7	US-11-102-476-45
36	135.5	2.7	5925	6	US-10-615-668-4
37	132.5	2.6	15071	6	US-10-793-626-2963
38	132	2.6	3438	6	US-10-793-626-1431
39	130.5	2.6	540	6	US-10-873-528-299
40	130.5	2.6	3549	6	US-10-793-626-3796
41	129.5	2.5	3204	6	US-10-793-626-3940
42	129	2.5	3344	6	US-10-793-626-4102
43	129	2.5	4605	7	US-11-102-476-3
44	127	2.5	3068	6	US-10-793-626-3824
45	126.5	2.5	14991	6	US-10-346-706B-18

ALIGNMENTS

RESULT 1

US-11-172-145-1  
; Sequence 1, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DEATGELLIS, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.

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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-1

Alignment Scores:
Pred. No.: 0 Length: 2920
Score: 5108.00 Matches: 972
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-642-248-2 (1-972) x US-11-172-145-1 (1-2920)

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Db 1 ATGAATACATATATCACAGCAATAAAGCATATACAGCAATAGCATATCAATTAGCACTC 60

Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AAATTATTTGAAAGTCGGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAAATTACC 120

Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 121 AAATGCAAGAAAAAATCTCAGCACATCCTTCTGTTAAATTCAGCACATCTTTCTGTAAT 180

Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 181 AAGAGAGAAAGTCAATGTTTGGATAGTCGCTTAGATATTTGCAACACAACTGTTACTT 240

Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100
Db 241 TCCAAACGTAAATAAATTTAGTACTTTCTGACTCGGAAAAAACACGTTAAAAAATAATGG 300

Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValAlaArgAlaValAlaLeuValPro 120
Db 301 AAATTGCTCACTGAGAGAAATCTGAAATCGGAGGTAAGAGCGGTGCGCCTTTGTACCA 360

Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 361 AAGATTTTCCAAAGATCTGGTTTTAGCGCCTTTTACTGATCATGTTTAATGATTTTACA 420

Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160
Db 421 TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACTGAACTGAACATCAACATGTTGGTCTT 480

Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 481 TCTATTATCGTTACAACATTCATCGACCAACAAATTTTATCGATTACATTAGCCCTGTTTA 540

Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAACCAAAAACACATATACCCGTTTGAAGTTTATCGTACAGATGATGTTAGTGCAGAA 600

Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 601 GATCTATCACCGATCATTCGCCAATATGAAATAAATTTGGATATTCGCTAGCTCAGACAA 660

Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 661 AAAGATAACGGTTTTCAGCCAGTGCCTCGGAATATGGGATTACGGATTAGCAAAAATAT 720

Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260
Db 721 GACTTTTATGGCTTACTCGACTGTGATATGCGCCAAATCCATTTATGCGTTTCATCTTAT 780

Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db 781 GTTGCAGAGCTATTAGAAGATGATGATTTTAACAATCATTTGTTCCAGAAAAATACATCGAT 840

Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro 300
Db 841 ACACAAATATTGACCCAAAGACTTCTTAAATAACGCGAGTTTGCCTTGAATCATTACCA 900

Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGlyThrValSerLeuAspTyr 320
Db 901 GAAGTGAAACCAATATAGTGTTCGCCAAAAGGGGAAGAACAGTCTTCTCTGGATTGG 960

Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 961 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCGCTTATCCGATTCGCCTTTCGCTTTT 1020

Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPhePheAsp 360
Db 1021 TTTGCGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAATTCGCTTTCTTTGAT 1080

Qy 361 GluGluPheAsnHisTyrGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1081 GAGGAATTTAATCACTGGGTCGAGAGATGTCGAAATTTGATATCGCTTATTCGCTTAC 1140

Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1141 GGTAGTTTCTTTAAAACTATTGATGTCATTTATGGCTTACCATTCAAGAGCCACCAGGTAAA 1200

Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db 1201 GAAAAAGAAACCCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAG 1260

Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGATACCT 1320

Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1321 TTAGTTTCAATTTATATCCAGCTTATACGTGTGCAAACTATATTCAACGCTGCGTAGAT 1380

Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1381 AGTGCACTGAATCAGACTGTTGTGATCTCGAGGTTTGTATTGTTAACGATGGTTCAACA 1440

Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1441 GATAATACCTTAGAGTGATCAATAGCTTTATGGTAATAATCTTAGGGTAGCATCATG 1500

Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 1501 TCTAAACCAAAATGCGGAATAGCTCAGCATCAAAATGCGAGCGGTTCTTTTGTCTAAAGGT 1560

Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540
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Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560
Db 1621 TTTAAAGAAATTTTAAAGATATAACCGTAGCTTGTGTTTATACCACATAATAGAAACGTC 1680

Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580
Db 1681 AATCCGAGTGGTAGCTTAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTCCAGCAGAAAA 1740

Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrHisLeu 600
Db 1741 CTCAACCGCTATGATTGCTCCACACTTTAGAAATGTTTCAGGATTAGAGCTTGGCATTTA 1800

Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1801 ACTGATGGATTCAATGAAAAAATTTGAAATTTGCGGTAGACTATGACATGTTCTTCAAACTC 1860

Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
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Qy 641 AspAsnThrSerIleLysValLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660
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Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 1981 CAGTCATTAATAGACAAGGCATAACTATTATTAATATGACGAATTTGATGATTTAGAT 2040
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2041 GAAAGTAGAAAGTATATTTCATAAACCCGCTGAATATCAAGAGAGATGATATCTTTA 2100
Qy 701 LysAspIleLysIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2101 AAGATATTAATATCATCCAGATTAAGATGCCAAATCCGAGTCAGTATTTTATATCCC 2160
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnHisPheGluTyrAsnLysAsnIle 740
Db 2161 AATACATTAACGGCTTAGTGAATAAACTAAACAATATTATTGAATATAATAAAATATA 2220
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2221 TTCGTTATTGTTTACATGTTGATAAGAAATCATCTTACACCCAGATATCAAAAAAGAAATA 2280
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780
Db 2281 CTAGCCCTTCTATCATAAACATCAAGTGAATATTTTACTTAATATGATATCTCATATTTAC 2340
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
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Qy 801 LeuAsnLeuAsnCysGluTyrIleLysPheAspAsnHisAspSerIlePheValLysAsn 820
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Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2461 GACAGCTATGCTTATGAAAAATATGATGTCGCATGAAATTTCTCAGCATTAAACAT 2520
Qy 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
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Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSer 900
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Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 2701 ATTGATAGTGTCCAGATAATAACACTGAGGATATTGGTTCCAAATTTGACCTTTTAAATC 2760
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db 2761 TTAGAAAAGAAAAACCGCCCATGTTTAAATAAAACATCCAGCCCTGACTTATATATGCGCTGG 2820
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2821 GAACGAAATTAACAATGGCAATTAAGCAAAATTTGAAGTGCAGAAAGAGAGAGAAATATA 2880
Qy 961 ProValAsnLysPheIleLeuAsnSerIleThrLeu 972
Db 2881 CCTGTTAACAGTTTCATTTAATAGTATTAACCTTA 2916
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RESULT 2

US-11-124-215-2

; Sequence 2, Application US/11124215

; Publication No. US20050266460A1

; GENERAL INFORMATION:

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; APPLICANT: DEANGELIS, PAUL
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTEURRELLA MULTOCIDA AND
; FILE REFERENCE: 35541.101
; CURRENT APPLICATION NUMBER: US/11/124.215
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: 10/217,613
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-124-215-2
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Alignment Scores:
Pred. No.: 0 Length: 2937
Score: 5104.00 Matches: 971
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.92% Indels: 0
DB: 7 Gaps: 0
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US-10-642-248-2 (1-972) x US-11-124-215-2 (1-2937)

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Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 79 AAATTTATTTGAAAGTCGCGGAAATCTATGACGCGAAATTTGTTGAAATTTTCAAAATTACC 138
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 139 AAATGCCAAGAAATACTCTCAGCACATCTTCTGTTAAATTCAGCACATCTTCTGTTAAAT 198
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 199 AAAGAAGAAAGAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 258
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db 259 TCCAAACGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACACGCTTAAAAAATAAATGG 318
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 319 AAATTTGCTCACTGAGAAGAAATCTGANAATTCGGAGGTAAAGAGCGGTCCGCTTTGTACCA 378
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 379 AAAGATTTTCCCAAGATCTGGTTTTAGCGCCCTTTTACCTGATCATGTTAATGATTTTACA 438
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 439 TGGTACAAAAACGGAAGAAAAAGACTTGGCATAAAAACCTGAAACATCAACATGTTGCTCTT 498
Qy 161 SerIleLeuValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 499 TCTATTATCGTTTACAACATTTCAATCGACAGCAATTTTATCATGATTACATTAGCCTGTTTA 558
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 559 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATTCGTGACAGATGATCGTAGTCAGGAA 618
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
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Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
Db 739 GACTTTTATGGCTTACTCGACTGTGATATGCGCAAAATCCATTTATGGGTTTCATTTCTTAT 798  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 799 GTTGCAGAGCTATTAGAAAGATGATGATTTAAACATCAATGGTCCAGAAATACATCGAT 858  
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Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
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Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
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Qy 361 GluGluPheAsnHisIleTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1099 GAGGAATTTAATCACTGGGGTGGAGAAGATGTGAAATTTGGATATCGCTTATTCCGGTAC 1158  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
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Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1219 GAAATGAACCGATCGTGAAGCGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1278  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1279 GTCCCTTATATCTATAGAAACTTTTACCATAGAAATTCGCATATCAATAGAGTACCT 1338  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
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Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
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Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1459 GATAAATACCTTTAGAAGTGATCAATTAAGCTTTATGGTAAATTAATCTCAGGTCAGCATGT 1518  
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Db 1519 TCTAACAACAAATGGCGAATAGCTCAGCATCAATGCAAGCGGTTTCTTTTGGCTAAAGGT 1578  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1579 TATTACATTGGCCAGTTTAGATTTCAGATGATTATCTTGAGCCTGATGCAAGTTGAACCTGTG 1638  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560  
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Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580  
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Db 1699 AATCCGGATGGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTTCACGAGAAAAA 1758  
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Db 1759 CTCACAACCGCTATGATGCTCACCACCTTTAGAAATGTTACGATTAGAGCTTGGCATTTA 1818  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1819 ACTGATGGATTCATGAAAAAATGAAATGCGCGTAGCATGTGACATGTTCTCTCAAACTC 1878  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
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Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
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Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
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RESULT 3
US-11-120-422-9
; Sequence 9, Application US/11120422
; Publication No. US20050287646A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H
; APPLICANT: Kumari, Kshama
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HVALUONAN SYNTHASE GENE AND EXPRESSION
; TITLE OF INVENTION: IN BACILLUS SUBTILIS
; FILE REFERENCE: 3554.049
; CURRENT APPLICATION NUMBER: US/11/120,422
; CURRENT FILING DATE: 2005-05-02
; PRIOR APPLICATION NUMBER: US/09/879,959
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/469,200
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 05/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: pasteurrella multocida
US-11-120-422-9

Alignment Scores:
Pred. No.: 0 Length: 2937
Score: 5104.00 Matches: 971
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.92% Indels: 0
DB: 7 Gaps: 0

US-10-642-248-2 (1-972) x US-11-120-422-9 (1-2937)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 19 ATGAATACATTTATCACAAGCAATAAAGCATATATAACAGCAATGACTATCAATTAGCACTC 78

Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 79 AAATTTATTTGAAAGTCGCGGAAATCTATGAGCGGAAATTTGTTGAATTTCAAATTACC 138

Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
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Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeu 80
Db 199 AAAGAAGGAAAGTCAATGTTTGGATAGTCGTTAGATATTGCAACACAACTGTTACTT 258

Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
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Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 319 AAATTTGCTCAGTGAAGAAATCTGAAATGCGAGGTAAGACCGGTGCGCCCTGTACCA 378

Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 379 AAAGATTTTCCCAAGATCTGGTTTGTAGCGCCTTTTACCTGATCATGTTAATGATTTTACA 438
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Qy 141 TrpTyrLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 439 TGGTACAAAAAGCGAAAGAAAGACATTGGCATAAAAACCTGAAACATCAACATGTTGGTCTT 498

Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 499 TCTATTATCGTTTACAACATTCAATCGACCAGCAATTTTATCGATTACATTAGCTGCTTTA 558

Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 559 GTAAACCAAAAAACACATTACCCTTTGAAGTTATCGTGACAGATGATGTTAGTACAGAA 618

Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 619 GATCTATCACCGATCATTCGCCAATATGAAATAAATTTGGATATTTCCTACGTCAGCAAA 678

Qy 221 LysAspAsnGlyPheGlnAlaSerAlaLeuAsnMetGlyLeuArgGluAlaLysTyr 240
Db 679 AAAGATAACCGTTTCAAGCCAGTCGCGCTCGGAATATGGGATTACGCTTAGCAAAATAT 738

Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260
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Qy 261 ValAlaGluLeuLeuGluAspAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db 799 GTTCGACAGAGCTATTAGAAGATGATGATTTAAACAATCATTCGTCCAGAAAAATACATG 858

Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 859 ACACAACATATTGACCCAAAAGACTTCTTAAATAACGCGAGTTTGTCTTGAATCAATTACA 918

Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320
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Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 979 CGCTTTAGAACAAATTCGAAAAAACAAGAAATCTCGCTTATCCGATTCGCTTTCCGTTT 1038

Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPheAsp 360
Db 1039 TTTGCGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATAATCCGGTTTCTTTGAT 1098

Qy 361 GluGluPheAsnHisTrpGlyGlyValGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1099 GAGGAATTTTATCACTCGGGTGGAGAGAGATGGGAATTTGGATATCGCTTATTCGTTTAC 1158

Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
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Qy 401 GluAsnGluThrAspArgGluAlaGlyAsnIleThrLeuAspIleMetArgGluLys 420
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Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
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Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1339 TTAGTTTCAATTTATATCCAGCTTATAAATCTGCAAACTATATTCAACAGTTGCGTAGAT 1398

Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
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DB 1579 TATTACATTGGCGNGTTAGATTTCAGATTGATTAATCTTGAGCTGATGAGTTCAGTGTGT 1638
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QY 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
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RESULT 4
US-11-172-145-3
; Sequence 3, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-3

Alignment Scores:
Pred. No.: 0 Length: 2979
Score: 4502.50 Matches: 845
Percent Similarity: 93.21% Conservative: 61
Best Local Similarity: 86.93% Mismatches: 59
Query Match: 88.15% Indels: 7
DB: 7 Gaps: 2

US-10-642-248-2 (1-972) x US-11-172-145-3 (1-2979)
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QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
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DB 181 AAATGTAAGAAAAACCTC-----TCGACCAATCT-----TATGTAAGT 219  
QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
DB 220 GAAGATAAAAAACACAGTGTTCGATAGCTCATTAGATATCGCAACACAGCTCTTACTT 279  
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QY 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
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DB 580 GTCAATCGAAAAACAACTACCCATTTCGAAGTCGTTGTTGCAGATGATGGTAGTAAGGAA 639  
QY 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
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Qy  
2101 AAAGATATT 2109  
Db

## RESULT 6

US-11-172-145-17  
; Sequence 17, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:

; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145

; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 17  
; LENGTH: 2112  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-172-145-17

## Alignment Scores:

Pred. No.: 1,45e-313 Length: 2112  
Score: 3692.00 Matches: 702  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.86% Mismatches: 0  
Query Match: 72.28% Indels: 0  
DB: 7 Gaps: 0

US-10-642-248-2 (1-972) x US-11-172-145-17 (1-2112)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 1 ATGAATACATTATCACAGCAATATAAGCATATATACAGCAATGACTATCAATTAGCACTC 60  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 61 AAATTATTGAAAGTCGGCGGAANTCTATGGACGGAAATTTGTTGAATTTCAAAATACC 120  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 121 AAATGCAAGAAAGAACTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTCTGTTAAT 180  
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 181 AAAGAAGAAAGAAAGTATGTTGCGATAGTCGGTTAGATATTGCAACACAACTGTTACTT 240  
Qy 81 SerAsnValLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
Db 241 TCCAAACGTAAAGAAATTTAGTACTTTCTGACTCGGAAAGAAACACGTTAAAGAAATAAATGG 300  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 301 AAATTGCTCACTGAGAGAAATCTGAAATGCGGAGGTAAGAGCGGTCGCCCTTGTACCA 360  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 361 AAAGATTTCCTCAAGATCTGGTTTATGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
Qy 141 TrpTyrLysLysArgLysLeuArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160  
Db 421 TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAAACATCAACATGTTGGTCTT 480  
Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 481 TCTATTATCGTTACACATTCATCGACCAGCAATTTATCGATTACATTAGCCTGTTTA 540  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 541 GTAAACCAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Qy 201 AspLeuSerProIleLeuArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 601 GATCTATCACCAGTCACTTCGCGCAATATGAAATTAATTTGGATATTCGCTACGTGACAGAA 660  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 661 AAAGATAACGGTTTCAAGCCAGTCCGCTCGGAATATGGGATTCGCTTAGCAAAATAT 720  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
Db 721 GACTTTTATGGCTTACTCAACTGTGATATGCGCGCAAAATCCATTTATGGGTTTCATCTTAT 780  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 781 GTTCGAGAGCTATTAGAGATGATGATTAAACAATCATTTGTTGCCAGAAATAATCATCGAT 840  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 841 ACACAACATATTGACCCAAAGACTTCTTAAATAACGCGAGTTTGTCTTGAATCATTACCA 900  
Qy 301 GluValLysThrAsnAsnSerValAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 901 GAAGTGAAGAAACCAATAATAGTGTTCGCCCAAAAGGGGAAGAACAGTTTCTCTCGATTGG 960  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 961 CGCTTTAGAACCAATTCGAAAAAACAGAAATCTCCGCTTATCCGATTCGCCCTTTCCGTTT 1020  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
Db 1021 TTTGCGGGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTAAATAATCCGGTTTCTTTGAT 1080

Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1081 GAGAAATTTAATCACCTGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 1140  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1141 GGTAGTTTCTTTAAACTATTGATGCAATTATGCGCTACCATCAAGAGCCACCAGGTAAA 1200  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1201 GAAAATGAACCCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1260  
Qy 421 ValProTyrIleTyrArgLysLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1261 GTCCCTTATATCTATAGAAAACTTTTACCCAATAGAAGATTCGCATATCAATAGATACCT 1320  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1321 TTAGTTTCAATTTATATCCAGCTTATNACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1381 AGTGCACTGAATCAGACTGTGTTGATCTCGAGGTTGTATTTGTAAACGATGGTTCAACA 1440  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1441 GATAATACCTTAGAAGTGATCAATAGCTTTTATGGTAATAANTCTAGGGTACGCATCATG 1500  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1501 TCTAAACCAATCGCGGAATAGCTCAGCATCAATGCAAGCCGCTTCTTTTGTAAAGGT 1560  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLysGluProAspAlaValGluLeuCys 540  
Db 1561 TATTACATTGGCGAGTTAGATTGATGATGATCTTGAGCCTGATGCACTGTAACCTGTGT 1620  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
Db 1621 TTAAGAAGAAATTTTAAAGATAAAACGCTAGCTGTGTGTTATATACCACTAATAGAAACGTC 1680  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
Db 1681 AATCCGGATGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTCACGAGAAAA 1740  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1741 CTCACAACGGCTATGATTGCTCACCACTTTAGAAATGTTACGATTTAGAGCTTGGCATTTA 1800  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1801 ACTGATGGATTCAATGAAAAAATTTGAAAAATGGCGTAGACTATGACATGTTCCCTCAAACTC 1860  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1861 AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1920  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660  
Db 1921 GATAACACATCAATTAAGAAACTTGGCAATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Db 1981 CAGTCATTAATAGCAAGGCATAACTATTATAATTTATGACCAATTTGTATGATTTAGAT 2040  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
Db 2041 GAAAGTAGAAAGTATATTTTCAATAAAAACCGCTGAATATCAAGAGAGATTGATATCTTA 2100  
Qy 701 LysAspIle 703  
Db 2101 AAAGATATT 2109

## RESULT 7

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US-11-172-145-18
; Sequence 18, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-18

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Qy	121	LyAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAppPheThr	140
Db	361	AAAGATTTTCCCAAGATCTGGTTTTAGCGCTTTTACCTGATCATGTGTAATGATTTACA	420
Qy	141	TrpTyrLysLysArgLysValLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu	160
Db	421	TGGTACAAAAGCGAAGAAAGACITGGCATAAACCTGAACATCAACATGTTGGTCTT	480
Qy	161	SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu	180
Db	481	TCTATTATCTGTACAAACATTCATTCAGCAGCAATTTTATCGATTACATTTAGCCCTGTTA	540
Qy	181	ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu	200
Db	541	GTAACCAAAAAACACATTACCGCTTTGAAGTTATCTGTACAGATGATGGTAGTCAGAA	600
Qy	201	AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln	220
Db	601	GATCTATCACCGATCATTCGCCAATATGAAATATAATTCGATATTCGTACGTCAGACAA	660
Qy	221	LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgIleuAlaTyrTyr	240
Db	661	AAAGATAACGGTTTTTCAAGCCAGCTGGCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT	720
Qy	241	AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr	260
Db	721	GACTTTTATGGCTTACTCGACTGTATATATGGCCCAATCCATTATGGGTTTCATTCTTAT	780
Qy	261	ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp	280
Db	781	GTTGCAGAGCTATTAGAAGATGATGATTTTAAACAATCATTTGGTCCAAGAAAATACATCGAT	840
Qy	281	ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro	300
Db	841	ACACAACATATTGACCCAAAAGACTTCTTAAATTAACGCGAGTTTGTCTTGAAATCATTTACCA	900
Qy	301	GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp	320
Db	901	GAAGTGAACCAATAATAGTGTTCGCGCAAAAGGGAGGAACAGTTTCTCTGGATTGG	960
Qy	321	ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerPropheArgPhe	340
Db	961	CGCTTAGACAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCGTTTCCGTTTT	1020
Qy	341	PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp	360
Db	1021	TTTCGCGGGGTAAATGTGTCTTCGCTTAAAAAATGGCTAAATAAATCCGGTTTCTTTGAT	1080
Qy	361	GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr	380
Db	1081	GAGAAATTAATCACTGGGTGGAGAGATGTGGAAATTTGGATATCGCTTATTCGGTTAC	1140
Qy	381	GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys	400
Db	1141	GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCCTTACCATCAAGAGCCACCAGGTAAA	1200
Qy	401	GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys	420
Db	1201	GAATAATGAACCCGATCTGTAAGCGGGAATAAATATTACGCTCGATATTATGAGAGAAAG	1260
Qy	421	ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro	440
Db	1261	GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAGATTCGCATATCAATAGATGACCT	1320
Qy	441	LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp	460
Db	1321	TTAGTTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTTCAACGTTCGCTAGAT	1380
Qy	461	SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr	480
Db	1381	AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTGTTGTAATTTGTAAACGATGGTTCACAA	1440

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Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProAsqValArgIleWet 500
Db 1441 GATATATACCTTAGAAGTGATCAATAGCTTTATGGTAATATCTTAGGGTAGCATCATG 1500
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGly 520
Db 1501 TCTAAACCAATGCGGAATAGCCTCAGCATCAATGCGAGCGTTCTCTTTGCTAAAGGT 1560
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrIleGluProAspAlaValGluLeuCys 540
Db 1561 TATTACATGGCGAGTTAGATTTCAGATTATCTTGAGCGCTGATGCGAGTTGAACCTGTG 1620
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1621 TTAAGAAGATTTTAAAGATATAAAGCGCTAGCTTGTTTATACCATTAATAGAAACGTC 1680
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580
Db 1681 AATCCGGATGGTAGCTTAATCGCTAAATGGTTTACAATTTGGCCAGAAATTTTCACGAGAAAAA 1740
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1741 CTCACAACGGCTATGATGTGCTCACCACTTTTAGAATGTTACGATTAGAGCTTGCGCATTTA 1800
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1801 ACTGATGATTCATAGAAAAAATTTGAAAATGCCGTAGACTAGCATGCTTCTCCTCAAACTC 1860
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1861 AGTCAAGTTGGAAAAATTAACACATCTTAATAAATCTGTATAAACCGTGTATTACATGGT 1920
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660
Db 1921 GATAACACATCAATTAAGAAACTTGGCATTCAAAAGAAAAACCACTTTTGTGTAGTCAAT 1980
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 1981 CAGTCATTAATAGACAGGCTAACTTATTATTAATATGACGAATTTGATGATTTAGAT 2040
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2041 GAAAGTAGAAGATATATTTTCAATAAACCCTGAATATCAAGAAGAGATTGATATCTTA 2100
Qy 701 LysAspIle 703
Db 2101 AAAGATATT 2109

RESULT 8
US-11-172-145-19
; Sequence 19, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; FILE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172.145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
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; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
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; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-19

Alignment Scores:
Pred. No.: 1,45e-313 Length: 2112
Score: 3692.00 Matches: 702
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.86% Mismatches: 0
Query Match: 72.28% Indels: 0
DB: 7 Gaps: 0
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US-10-642-248-2 (1-972) x US-11-172-145-19 (1-2112)

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Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 1 ATGAATACATTATCAACAGCAATAAAGCATATAACAGCAATGACTATCAATATAGCACTC 60
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AAATTATTGAAAAGTCGGCGGAAATCTATGAGCGGAAATTTGTGAATTTCAAATTTACC 120
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 121 AAATGCAAGAAAAAATCTCAGCACATCTCTCTGTTAAATTCAGCACATCTTCTGTAAAT 180
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 181 AAAGAGAAAAAAGTCAATGTTTCGGATAGTCCGTAGATATATGCAACACAACTGTGTACTT 240
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db 241 TCCACGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACACGTTTAAAAAATAAATGG 300
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 301 AAATTGCTCACTGAGAAGAAATCTGAAAAATCGGAGGTAAGAGCGGTGCGCCTTGTACCA 360
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 361 AAAGATTTTCCCAAGATCTGGTTTTAGCCGCTTTACTGATCATGTATATGATTTTACA 420
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 421 TGGTACAAAAAGCGAAAGAAAGACTTGGCATATAAACCTCAACATCAACATGTTGTCTT 480
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 481 TCTATTATCGTTTCAACATTTCAATCGACCAGCAATTTTATCGATTATACATTAGCCTGTTTA 540
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAAACCAAAAAACACATTAACCCGTTTGAAGTTATCTGTGACAGATGATGTAGTCAGAA 600
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 601 GATCTATCACCAGTCAATTCGCCAATATGAAAAATAAATTTGATATTCGCTACGTACAGAA 660
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 661 AAAGATAACGGTTTTCAGGCCAGTGGCGCTCGGAATATATGGATTACGCTTAGCAAAATAT 720
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Qy	241	AspPheileGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr	260	Db	1801	ACTGATGATTCATGAAATAATTTGAAATGCGGTAGCATGACATGTTCTCTCAAACTC	1860
Db	721	GACITTTATGGCTTACTCGACTGTGATATGGCGCAATCCATATATGGTTCAITCTTAT	780	Qy	621	SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly	640
Qy	261	ValalaGluLeuLeuGluAspAspLeuThrIleleGlyProArgLysTyrIleAsp	280	Db	1861	AGTGAAGTTGGAAATTTAAACATCTTATAAATCTGCTATAACCGTGTATTACATGGT	1920
Db	781	GTTGCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT	840	Qy	641	AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn	660
Qy	281	ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro	300	Db	1921	GATAACACATCAATTAAGAACTTGGCATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT	1980
Db	841	ACACAACATATTTGACCCAAAAGACTTCTTAATAACCGAGTTTGCCTTGAATCAATTACCA	900	Qy	661	GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp	680
Qy	301	GluValLysThrAsnAsnSerValalaLysGlyGluGlyThrValSerLeuAspTrp	320	Db	1981	CAGTCATTAATAAGACAGCAATCTTATAAATATGACGAATTTGATGATTTAGAT	2040
Db	901	GAAGTGAACCAATATAGTTTGGCGCAAAAGGGAGAAACAGTTTCTCTGATGG	960	Qy	681	GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu	700
Qy	321	ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe	340	Db	2041	GAAGTGAACCAATATATTTCAATTAACCGCTGAATATCAAGAAGAGATTGATATCTTA	2100
Db	961	CGCTTAGAACCAATTCGAAAAACAGMAAATCTCCGCTTATCCGATTCGCCCTTTCGGTTTT	1020	Qy	701	LysAspIle 703	
Qy	341	PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp	360	Db	2101	AAAGATATT 2109	
Db	1021	TTTGGCGGGGTAAATGTTGCTTTCGCTAAAAAATGGCTAAATAATCCGGTTTCTTTGAT	1080	RESULT 9			
Qy	361	GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr	380	US-11-172-145-20			
Db	1081	GAGGAATTTAATCACTGGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTAC	1140	; Sequence 20, Application US/11172145			
Qy	381	GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys	400	; Publication No. US20050272696A1			
Db	1141	GGTAGTTTCTTTAAACATATTGATGGCATTTATGGCTTACCATTCAAGACCCACAGGTAAA	1200	; GENERAL INFORMATION:			
Qy	401	GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys	420	; APPLICANT: DeAngelis, Paul			
Db	1201	GAATAATGAACCGATCGTGAACGCGGAAAAAATATTACGCTCGATATTATCAGAGAAAAAG	1260	; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC			
Qy	421	ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro	440	; FILE REFERENCE: 3554.104			
Db	1261	GTCCCTTATATCTATAGAAAACTTTTCAATAGAAAGATTGCAATATCAATAGAGTACT	1320	; CURRENT APPLICATION NUMBER: US/11/172.145			
Qy	441	LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp	460	; CURRENT FILING DATE: 2005-06-30			
Db	1321	TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT	1380	; PRIOR APPLICATION NUMBER: 60/584,442			
Qy	461	SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr	480	; PRIOR FILING DATE: 2004-06-30			
Db	1381	AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTGTAACGATGTTTCAACA	1440	; PRIOR FILING DATE: 2003-08-15			
Qy	481	AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet	500	; PRIOR APPLICATION NUMBER: 10/642,248			
Db	1441	GATAATACCTTAGAAGTGATCAATTAAGCTTTTATGGTAAATATCTTAGGGTACGCATCATG	1500	; PRIOR FILING DATE: 2003-07-31			
Qy	501	SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly	520	; PRIOR APPLICATION NUMBER: 60/404,356			
Db	1501	TCTAAACCAATGGCGGATACCTCAGCATCAATGCGAGCGTTCTTTTGTCTAAAGGT	1560	; PRIOR FILING DATE: 2002-08-16			
Qy	521	TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys	540	; PRIOR APPLICATION NUMBER: 60/479,432			
Db	1561	TATTACATTTGGCAGTTAAATTCAGATGATTTATCTTTGAGCTGTATGCGATGTTGACTGTGT	1620	; PRIOR FILING DATE: 2003-06-18			
Qy	541	LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal	560	; PRIOR APPLICATION NUMBER: 60/491,362			
Db	1621	TTAAAGAAATTTTAAAGATAAACCGCTAGCTGTGTTTATACCACCTAATAGAACGTC	1680	; PRIOR FILING DATE: 1998-11-11			
Qy	561	AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys	580	; PRIOR APPLICATION NUMBER: 09/283,402			
Db	1681	AATCCGATGGTAGCTTAATCCCTAATGGTTACATTTGCCAGAAATTTTACAGAGAAAA	1740	; PRIOR FILING DATE: 1999-04-01			
Qy	581	LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu	600	; PRIOR APPLICATION NUMBER: 60/080,414			
Db	1741	CTCACACGGCTATGATTTGCTCACCACCTTTAGAAATGTTTCCAGATTAGAGCTTGGCATTTA	1800	; PRIOR FILING DATE: 1998-04-02			
Qy	601	ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu	620	; Remaining Prior Application data removed - See File Wrapper or PALM.			
				; NUMBER OF SEQ ID NOS: 25			
				; SOFTWARE: PatentIn version 3.3			
				; SEQ ID NO 20			
				; LENGTH: 2112			
				; TYPE: DNA			
				; ORGANISM: Pasteurella multocida			
				US-11-172-145-20			
Alignment Scores:				1.45e-313	Length:	2112	
Pred. No.:				3692.00	Matches:	702	
Score:				100.00%	Conservative:	1	
Percent Similarity:				99.86%	Mismatches:	0	
Best Local Similarity:				72.28%	Indels:	0	
Query Match:				7	Gaps:	0	
DB:							
US-10-642-248-2 (1-972) x US-11-172-145-20 (1-2112)							

QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
DB 1 ATGAATACATTTATCACAGCAATTAAGCAATATAACAGCAATGACATATCAATTAGCACTC 60  
QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
DB 61 AAATTTATTTGAAAGTCGGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAATATACC 120  
QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
DB 121 AAATGCAAGAAAAAATCTCTCAGCACATCTCTCTGTTAAATTCAGCACATCTTCTGTAAAT 180  
QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
DB 181 AAAGAAGAAAGTCAATGTTTGGCATAGTCCGTGTAGATATTGCAACACAACTGTACTTT 240  
QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
DB 241 TCCAACGTAAAAAATTAGTACTTTCTGACTCGGMAAAAAACACGTGTAAAAAATAATGG 300  
QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
DB 301 AAATTTGCTCACTGAGAAGAAATCTGAAAAATCGGAGGTAAGAGCGGTGCGCCTGTACCA 360  
QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
DB 361 AAAGATTTTCCCAAGAGATCTGGTTTTAGCCGCTTTACCTGATCATGTTAATGATTTTACA 420  
QY 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160  
DB 421 TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAAACCTGCAACATCAACATGTTGGTCTT 480  
QY 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
DB 481 TCTATTATCGTTTCAACATTTCAATCGACCACGAATTTTATCGATTACATTTAGCGCTGTTA 540  
QY 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
DB 541 GTAAACAAAAACACATTAACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
QY 201 AspLeuSerProIleLysArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
DB 601 GATCTATACCGATCATCTCCCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA 660  
QY 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
DB 661 AAAGATAACGGTTTTCAGGCCAGTCGCGCTCGGAATATGGGATATACGCTTAGCAAAATAT 720  
QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
DB 721 GACTTTTATGGCTTACTCGACTGTGATATGGCGCAAAATCCATATATGGGTTCAATCTTAT 780  
QY 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
DB 781 GTTTCAGAGCTATTAGAGATGATGATTTAACCAATCATTTGGTCCAGAAAAATACATCGAT 840  
QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro 300  
DB 841 ACACAAACATATTGACCCAAAAGACTTCTTAAATAAACCGCAGTTTGGCTTGAATCAATACCA 900  
QY 301 GluValLysThrAsnAsnSerValAlaLysGlyGluLysThrValSerLeuAspTrp 320  
DB 901 GAAAGTAAAAACCAATTAATAGTGTGGCGAAAAGGGGAAGGAACAGTTTCTCTGGATGG 960  
QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
DB 961 CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGCTTTCGCCCTTT 1020  
QY 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPheAsp 360  
DB 1021 TTTGCGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAATCAATCCCGTTTCTTTGAT 1080  
QY 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380

DB 1081 GAGGAATTTAATCACTGGGTCGAGNAGATGTGGAATTTGGATATCGCTTATTCGCTTAC 1140  
QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
DB 1141 GGTAGTTTTCTTTAAAAATATTGATGGCATTTATGGCTACCATCAAGAGCCACCAGGTAAA 1200  
QY 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
DB 1201 GAAAAATGAACCGATCGTGAAGCGGAAAAAATATTACCGCTGATATTATGAGAGAAAAAG 1260  
QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
DB 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320  
QY 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
DB 1321 TTAGTTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTTCAACGTTGCGTAGAT 1380  
QY 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
DB 1381 AGTGCACTCAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAAACGATGGTTCAACA 1440  
QY 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
DB 1441 GATNATACCTTAGAGTGATCAATAAGCTTTATGGTAAATAAATCTTAGGGTACGCATCATG 1500  
QY 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
DB 1501 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCAGCGGTTTCTTTTGTAAAGGT 1560  
QY 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540  
DB 1561 TATTACATTTGGCAGTTAGATTCAAAATGATTTATCTTGAGCCGTGATGCAGTTGAACGTGT 1620  
QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
DB 1621 TTAAAAAGATTTTAAAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAAACGTC 1680  
QY 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
DB 1681 AATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTTGGCCAGAAATTTTTCAGAGAAAAA 1740  
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
DB 1741 CTCACAAACGGCTATGATTGCTCACCACCTTTAGAAATGTTCCAGATTAGAGCTTGGCAATTA 1800  
QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
DB 1801 ACTGATGGATTCATGAAGAAAAAATTTGNAATGCGGTAGACTATGACATGTTCTCCAAACTC 1860  
QY 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
DB 1861 AGTGAAGTTTGGAAAAATTTTAAACATCTTAATAAAATCTGCTATAACCGTGTATTACATGGT 1920  
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
DB 1921 GATAACACATCAATTAAGAAACTTGGCATTCAAAAGAAAAAACCATTTCTTGTGTAGTCAAT 1980  
QY 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680  
DB 1981 CAGTCATTAATATAGACAGGCATTAATTTATTAATATATGACGAATTTGATGATTTAGAT 2040  
QY 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeu 700  
DB 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGAGATTGATATCTTA 2100  
QY 701 LysAspIle 703  
DB 2101 AAAGATATT 2109

RESULT 10

US-11-172-145-13

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; Sequence 13, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-13

Alignment Scores:
Pred. No.: 3,2e-294 Length: 1980
Score: 3471.00 Matches: 658
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.95% Indels: 0
DB: 7 Gaps: 0

US-10-642-248-2 (1-972) x US-11-172-145-13 (1-1980)
QY 46 LeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsnLysGluGluLysVal 65
DB 4 CTCTCAGCACATCCTTCTGTTTAATTCAGCACATCTTTCTGTAAATTAAGAGAAAAAGTC 63
QY 66 AsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeuSerAsnValLysLys 85
DB 64 AATGTTGCGATAGTCGTTAGATATTGCAACACAACTGTTACTTTTCAACGTAATAAAAA 123
QY 86 LeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysThrLysLeuLeuThrGlu 105
DB 124 TTAGTACTTCTGACTCGGAAAAAACACGTTAAAAATAAATGAAATGCTCACTGAG 183
QY 106 LysLysSerGluAsnAlaGluValAlaAlaLeuValProLysAspPheProLys 125
DB 184 AAGAATCTGAAATGCGGAGGTAGAGCGGTGCGCCCTTGTACCAAAAGATTTTCCCAA 243
QY 126 AspLeuValLeuAlaProLeuProAspHisValAsnAspPheThrTrpTrpLysLysArg 145
DB 244 GATCTGTTTATAGCCCTTACTCATGATGTTAATGATTTTACATGGTACAAAAGCGA 303
QY 146 LysLysArgLeuGlyLysProGluHisGlnHisValGlyLeuSerIleIleValThr 165
DB 304 AAGAAAAGACTTGGCATAAACCTGAACATCAACATGTTGGTCTTTCTATTATTCGTACA 363
QY 166 ThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeuValAsnGlnLysThr 185

364 ACATTCAATCGACAGCAATTTTATCGATTACATTAGCCCTGTTTAGTAAACCAAAAAACA 423
186 HisTy-ProPheGluValIleValThrAspAspGlySerGlnGluAspLeuSerProIle 205
424 CATACCCGTTGAGTTATCGTCAGACATGATGGTAGTCAGGAAGATCTATCACCAGTC 483
206 IleArgGlnTyArgLysLeuAsnLysLeuAspIleArgTyValArgGlnLysAspAsnGlyPhe 225
484 ATTCGCCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAAAAAGATAACGGTTTT 543
226 GluAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyArgPheIleGlyLeu 245
544 CAAGCCAGTCGCCCTCGGAATATGGGATATCGCTTAGCAAAATATGACTTTATTTGGCTTA 603
246 LeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyValAlaGluLeuLeu 265
604 CTGACTGTGATATGGCCCAATCCATATATGGGTTCACTTCTTATGTTGCAGAGCTATTA 663
266 GluAspAspLeuThrIleIleGlyProArgLysTyIleAspThrGlnHisIleAsp 285
664 GAAGATGATGATTTAAACAATCATTTGGTCCAAGAAAAATACATCGATACACAACTATTGAC 723
286 ProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuProGluValLysThrAsn 305
724 CCAAAAGACTTCTTAAATAACGCGAGTTTCTTGAATCATTTACCAGAGTGAAACCAAT 783
306 AsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrpArgLeuGluGlnPhe 325
784 AATAGTGTTCGCCCAAAAGGGAGAACAGATTTCTCTGGATGGCGCTTAGAACAAATTC 843
326 GluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhePheAlaAlaGlyAsn 345
844 GAAAAACACAGAAATCTCCGCTTATCCGATTCGCTTTTCCGTTTTTTTTCGCGCGGTAAT 903
346 ValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAspGluGluPheAsnHis 365
904 GTTCTTTTCGCTAAAAAATGGCTAAATAATCCGGTTCTTTTGAATGAGGAATTAATCAC 963
366 TrpGlyGlyGluAspValGluPheGlyTyArgLeuPheArgTyGlySerPhePheLys 385
964 TGGGTGGAGAGATGGAATTTGGATATCGCTTATTCGTTACGGTAGTTCTTTCTTAAA 1023
386 ThrIleAspGlyIleMetAlaTyHisGlnGluProProGlyLysGluAsnGluThrAsp 405
1024 ACTATTGATGCAATTTATGGCTACCATCAAGAGCCACAGGTAAAGAAAAATGAACCGAT 1083
406 ArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLysValProTyIleTy 425
1084 CGTGAAGCGGAAAAAATATTTACGCTCGATATTAAGAGAAAAAGGTCCCTTATATCTAT 1143
426 ArgLysLeuLeuProIleGluAspSerHisIleAsnArgValProLeuValSerIleTy 445
1144 AGAAACATTTTACCATAAGAGATTCGCATATCAATAGATGACCTTTAGTTTCAATTTAT 1203
446 IleProAlaTyArgAsnCysAlaAsnTyIleGlnArgCysValAspSerAlaLeuAsnGln 465
1204 ATCCAGCTTATACTGTGCAAACTATATTTCAACGTTGCGTAGATAGTGCCTGAATCAG 1263
466 ThrValValAspLeuGluValCysIleCysAsnAspGlySerThrAspAsnThrLeuGlu 485
1264 ACTGTGTTGATCTCGAGGTTTGTATTTGTAAACATGTTTCAACAGATTAATACCTTAGAA 1323
486 ValIleAsnLysLeuTyGlyAsnAsnProArgValArgIleMetSerLysProAsnGly 505
1324 GTGATCAATAAGCTTTATGGTAATAATCTTAGGTCAGCATCATGCTCTAAACCAANTGCG 1383
506 GlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGlyTyTyIleGlyGln 525
1384 GGAATAGCTCAGCATCAATGACCGCTTTCTTTTGTAAAGGTTATTTACATGGCGAG 1443
526 LeuAspSerAspAspTyLeuGluProAspAlaValGluLeuCysLeuLysGluPheLeu 545
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Db 1444 TTAGATTTCAGATGATTATCTTGAGCCTGATGTCAGTTGAACTGTGTTTAAAGAAATTTTAA 1503  
Qy LysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnValLeuValLeuSerGlySer 565  
Db 1504 AAAGATAAAACGCTAGCTGTGTTTATACCACTAATAAGAACGTCATCCGGATGGTAGC 1563  
Qy LeuLeuAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLysLeuThrThrAlaMet 585  
Db 1564 TTATTCCTANTGTTTCAATTTGCCAGAAATTTTCAGAGAAAACCTCACACGGCTATG 1623  
Qy IleAlaHisPheArgMetPheThrIleArgAlaTyrHisLeuThrAspGlyPheAsn 605  
Db 1624 ATTGCTCACCATTTAGAAATGTTCAAGATTAGAGCTTGGCATTTAACTGATGATTCAT 1683  
Qy GluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeuSerGluValGlyLys 625  
Db 1684 GAAAAAATTGAAATGCGTAGACATATGACATGTTCCTCAAACTCAGTGAAGTTGAAAA 1743  
Qy PheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGlyAspAsnThrSerIle 645  
Db 1744 TTTAAACATCTTAAATAAATCTGCTATAACCGTGATTATACATGTTGATGATAACATCATT 1803  
Qy LysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsnGlnSerLeuAsnArg 665  
Db 1804 AAGAACTTGGCATTTCAAAAGAAAAACCATTTTGTCTAGTCAATCAGTCAATTAATAGA 1863  
Qy GlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAspGluSerArgLysTyr 685  
Db 1864 CAAGGCATAACTTATTATAATTATGACGAATTTGATGATTTAGATGAAGTAGAAGTAT 1923  
Qy IlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeuLysAspIle 703  
Db 1924 ATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTAAAGATATT 1977

## RESULT 11

US-11-172-145-14  
; Sequence 14, Application US/11172145  
; Publication No. US2005027696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 14  
; LENGTH: 1902  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
; US-11-172-145-14

## Alignment Scores:

Pred. No.:	2,09e-282	Length:	1902
Score:	3336.00	Matches:	632
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	65.31%	Indels:	0
DB:	7	Gaps:	0

US-10-642-248-2 (1-972) x US-11-172-145-14 (1-1902)

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Db	64	GAAAAAACACGTTAAAAAATAAATGGAATTTGCTCACTGAGAGAAATCTGAAAAATGCG	123
Qy	112	GluValArgAlaValAlaLeuValProLysAspPheProLysAspLeuValLeuAlaPro	131
Db	124	GAGGTAAAGAGCGGTGCGCCCTTGACCAAAAGATTTTCCCAAGATCTGGTTTTAGGCGCT	183
Qy	132	LeuProAspHisValAsnAspPheThrTyrTyrLysLysArgLysLysArgLeuGlyIle	151
Db	184	TTACCTGATCATGTTTAATGATTTTACATCGTACAAAAAGCGAAAGAAAGACTTGGCATA	243
Qy	152	LysProGluHisGlnHisValGlyLeuSerIleValThrThrPheAsnArgProAla	171
Db	244	AAACCTGAAACATCAACATGTTGCTCTTTCTATTATCGTTACAACATTCATTCGACCGCA	303
Qy	172	IleLeuSerIleThrLeuAlaCysLeuValAsnGlnLysThrHisTyrProPheGluVal	191
Db	304	ATTTTATCATTTACATTTAGCCTGTTTAGTAAACCAAAAAACACATTTACCGTTTGAAGTT	363
Qy	192	IleValThrAspAspGlySerGlnGluAspLeuSerProIleArgGlnTyrGluAsn	211
Db	364	ATCGTGACAGATGATGTTAGTCAGGAAGATCTATCACCGCATCTTCGCCCAATATGAANA	423
Qy	212	LysLeuAspIleArgTyrValArgGlnLysAspAsnGlyPheGlnAlaSerAlaArg	231
Db	424	AAATTGGATATTGCTTACGTCAGACAAAAAAGATAACGGTTTTCAAGCCAGTTCGCTCGG	483
Qy	232	AsnMetGlyLeuArgLeuAlaLysTyrAspPheIleGlyLeuLeuAspCysAspMetAla	251
Db	484	AATATGGGATTACGCTTAGCAAAATATGACTTTATTGGCTTACTCGACTGTGATATGGCG	543
Qy	252	ProAsnProLeuTyrValHisSerTyrValAlaGluLeuLeuAspAspLeuThr	271
Db	544	CCAAATCCATTATGGGTTTCATTTATGTTGCAGACCTATTAGAAGATGATGATTTAACA	603
Qy	272	IleIleGlyProArgLysTyrIleAspThrGlnHisIleAspProLysAspPheLeuAsn	291
Db	604	ATCATTTGGTCCAGAAAAATACATCGATACACACATATTGACCCCAAAAGACTTCTTAAAT	663
Qy	292	AsnAlaSerLeuLeuGluSerLeuProGluValLysThrAsnAsnSerValAlaLys	311
Db	664	AACGCGAGTTTGGTCTGAATCATTTACCAGAAAGTGAACCAATATATAGTTTGGCGGAAA	723
Qy	312	GlyGluGlyThrValSerLeuAspTyrArgLeuGluGlnPheGluLysThrGluAsnLeu	331
Db	724	GGGGAAGGAACAGTTTCTCTGGATTGCGCTTAGAACAAATTCGAAAAACAGAAAAATCTC	783
Qy	332	ArgLeuSerAspSerProPheArgPhePheAlaAlaGlyAsnValAlaPheAlaLysLys	351
Db	784	CGCTTATCCGATTTCGCTTTTCCGTTTTTTTGGCGGGTAAATGTTGCTTTCGCTAAAAA	843
Qy	352	TyrLeuAsnLysSerGlyPheAspGluGluPheAsnHisTyrGlyGlyGluAspVal	371
Db	844	TGCTTAAATAAATCCGGTTCTTTGATGAGGAATTTAATCACCCTGGGGTGGAGAGATGTG	903
Qy	372	GluPheGlyTyrArgLeuPheArgTyrGlySerPhePheLysThrIleAspGlyIleMet	391

Db 904 GAATTTGGATATCGCTTATTCCGTACGGTAGTGTCTTTTAAACATATTGATGGCATTTATG 963  
Qy 392 AlaTyrHisGlnGluProGlyLysGluAsnGluThrAspArgGluAlaGlyLysAsn 411  
Db 964 GCCTACCATCAAGAGCCACCGGTTAAGAAATGAAACCGATCGTGAAGCGGGAAAAAT 1023  
Qy 412 IleThrLeuAspIleMetArgGluValProTyrIleTyrArgLysLeuLeuProIle 431  
Db 1024 ATTACGTCGATATTATGAGAGAAAGCTCCCTATTATCTATAGAAAACTTTTACCAATA 1083  
Qy 432 GluAspSerHisIleAsnArgValProLeuValSerIleTyrIleProAlaTyrAsnCys 451  
Db 1084 GAAGATTCCGATATCAATAGAGTACCTTTAGTTTCAATTATATATCCAGCTTAACTGT 1143  
Qy 452 AlaAsnTyrIleGlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGlu 471  
Db 1144 GCAAACTATATTCAACGTTGGGTAGATAGTGCATGAACTGAACTGTTTGTATCTGAG 1203  
Qy 472 ValCysIleCysAsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyr 491  
Db 1204 GTTTGTATTGTACGATGGTTCAACAGATAATACCTTTAGAAGTGATCAATAAGCTTTAT 1263  
Qy 492 GlyAsnAsnProArgValArgIleMetSerLysProAsnGlyGlyIleAlaSerAlaSer 511  
Db 1264 GGTAAATATCTAGGTACGCATCATGCTTAAACCAAAATGGCGGAATAGCTCTACGATCA 1323  
Qy 512 AsnAlaValSerPheAlaLysGlyTyrIleGlyGlnLeuAspSerAspAspTyr 531  
Db 1324 AATGACGCGCTTCTTTGCTTAAAGGTTATTACATTTGGCGAGTTAGATTTCAGATGATTAT 1383  
Qy 532 LeuGluProAspAlaValGluLeuCysLeuLysGluPheLeuLysAspLysThrLeuAla 551  
Db 1384 CTTGAGCCTGATGAGTGGTGAATGCTGTGTTTAAAGAAATTTTAAAGATAAAGCTAGCT 1443  
Qy 552 CysValTyrThrThrAsnArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyr 571  
Db 1444 TGTGTTTATACCACTAATAGAAAGCTCAATCCGGATGGTAGCTTAAATCGCTTAATGGTTAC 1503  
Qy 572 AsnTyrProGluPheSerArgGluLysLeuThrThrAlaMetIleAlaHisPheArg 591  
Db 1504 AATTGGCCAGAAATTTTCACGAGAAAACTCAACGGCTATGATTGCTCACCATTTAGA 1563  
Qy 592 MetPheThrIleArgAlaTyrHisLeuThrAspGlyPheAsnGluLysIleGluAsnAla 611  
Db 1564 ATGTTACAGATTAGAGCTTGCAATTAATCTGATGATTCATGAAAAAATTTGAAAAATGCC 1623  
Qy 612 ValAspTyrAspMetPheLeuLysLeuSerGluValGlyLysPheLysHisLeuAsnLys 631  
Db 1624 GTAGACTATGACATGTTCTCAAACTCAGTGAAGTTGGAAAAATTTAAACATCTTAAATAA 1683  
Qy 632 IleCysTyrAsnArgValLeuHisGlyAspAsnThrSerIleLysLeuLysGlyIleGln 651  
Db 1684 ATCTGCTATAACCGGTGATTATCATGGTGATTAACACATCAATTAAGAAACTTTGGCAATCAA 1743  
Qy 652 LysLysAsnHisPheValValValAsnGlnSerLeuAsnArgGlnGlyIleThrTyrTyr 671  
Db 1744 AAGAAAAACCAATTTGTTGTAGTCAATCAGTCATTAATAGACAGGATCAATATTAT 1803  
Qy 672 AsnTyrAspGluPheAspLeuAspGluSerArgLysTyrIlePheAsnLysThrAla 691  
Db 1804 AATTATGCAATTTTATGATGATTAGATGAAGTAGAAAGTATATTTTCAATAAAACCGCT 1863  
Qy 692 GluTyrGlnGluIleAspIleLeuLysAspIle 703  
Db 1864 GAATATCAAGAGAGATTGATATCTTAAAGATATT 1899

## RESULT 12

US-11-172-145-15  
; Sequence 15, Application US/11172145  
; Publication No. US2005027269A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC

; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104

; CURRENT APPLICATION NUMBER: US/11/172,145

; PRIOR FILING DATE: 2005-06-30

; PRIOR APPLICATION NUMBER: 60/584,442

; PRIOR FILING DATE: 2004-06-30

; PRIOR APPLICATION NUMBER: 10/642,248

; PRIOR FILING DATE: 2003-08-15

; PRIOR APPLICATION NUMBER: 60/404,356

; PRIOR FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: 60/479,432

; PRIOR FILING DATE: 2003-06-18

; PRIOR APPLICATION NUMBER: 60/491,362

; PRIOR FILING DATE: 2003-07-31

; PRIOR APPLICATION NUMBER: 10/195,908

; PRIOR FILING DATE: 2002-07-15

; PRIOR APPLICATION NUMBER: 09/437,277

; PRIOR FILING DATE: 1999-11-01

; PRIOR APPLICATION NUMBER: 60/107,929

; PRIOR FILING DATE: 1998-11-11

; PRIOR APPLICATION NUMBER: 09/283,402

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 60/080,414

; PRIOR FILING DATE: 1998-04-02

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 15

; LENGTH: 1830

; TYPE: DNA

; ORGANISM: Pasteurella multocida

; US-11-172-145-15

## Alignment Scores:

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	63.14%	Indels:	0
DB:	7	Gaps:	0

US-10-642-248-2 (1-972) x US-11-172-145-15 (1-1830)

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Db	4	TTAAAAAATAAATCGAAATTCCTCACTGAGAAGAAATCTGAAAAATGCGGAGTAAAGCG	63
Qy	116	ValAlaLeuValProLysAspPheProLysAspLeuValLeuAlaProLeuProAspHis	135
Db	64	GTCCGCTTGTACCAAAAGATTTTCCCAAGATCTGGTTTACCGCCTTTTACCTGATCAT	123
Qy	136	ValAsnAspPheThrTyrTyrLysArgLysLysArgLeuGlyIleLysProGluHis	155
Db	124	GTTAATGATTTTATGTTACAAAGCAAGAAAGACCTGGCATAAAAACCTGAACAT	183
Qy	156	GlnHisValGlyLeuSerIleValThrThrPheAsnArgProAlaIleLeuSerIle	175
Db	184	CAACATGTGCTTCTTCTATTATTCGTTACAACTTCAATCGACCAGCAATTTTATCGATT	243
Qy	176	ThrLeuAlaCysLeuValAsnGlnLysThrHisTyrProPheGluValIleValThrAsp	195
Db	244	ACATTAGCCTGTTTAGTAAACCAAAACACATTTACCGCTTTGAAGTTTATCGTGACAT	303
Qy	196	AspGlySerGlnGluAspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIle	215
Db	304	GATGGTAGTCAGGAAGATCTATCCGATCATTCGCCATATGAANAATAAATTTGATATT	363
Qy	216	ArgTyrValArgGlnLysAspAsnGlyPheGlnAlaSerAlaIaArgAsnMetGlyLeu	235
Db	364	CGCTACGTCAGCAAAAAGATAACGGTTTTCAAGCCAGTCGCGCTCGGAATATGGGATTA	423
Qy	236	ArgLeuAlaLysTyrAspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeu	255



Db 4 CTTGTACCAAAAGATTTTCCAAAGATCTGGTTTTAGCGCTTTTACCTGATCATGTTAAT 63  
Qy 138 AspPheThrTpyrLysLysArgLysLeuGlyLysProGluHisGlnHis 157  
Db 64 GATTTTTACATGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAAACATCAACAT 123  
Qy 158 ValGlyLeuSerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeu 177  
Db 124 GTTGGTCTTCTATATATCGTTACCAACATTCATCGACCAGCAATTTTATCGATTACATTA 183  
Qy 178 AlaCysLeuValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGly 197  
Db 184 GCCTGTTTAGTAAACCAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGT 243  
Qy 198 SerGlnGluAspLeuSerProIleArgGlnTyrGluAsnLysLeuAspIleArgTyr 217  
Db 244 AGTCAGGAAGATCTATCACCGCATCTTCGCCCAATATGAAATAAATTTGGATATTTCGGTAC 303  
Qy 218 ValArgGlnLysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeu 237  
Db 304 GTCAGACAAAAGATACGGTTTTTCAGCCAGTCCGCTCGAATATGGGATTACGCTTA 363  
Qy 238 AlaLysTyrAspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrVal 257  
Db 364 GCAAAATATGACTTTATTGGCTTACTCGACTGTGATATGGCGCCAAATCCATTATGGGTT 423  
Qy 258 HisSerTyrValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLys 277  
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Qy 278 TyrIleAspThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGlu 297  
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Qy 298 SerLeuProGluValLysThrAsnAsnSerValAlaLysGlyGluGlyThrValSer 317  
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Qy 318 LeuAspTyrArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerPro 337  
Db 604 CTGGATTGGCGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCGCT 663  
Qy 338 PheArgPhePheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGly 357  
Db 664 TTCCGCTTTTTCGCGCGGGTAAATGTTGCTTCGCTAAAAAATGCTTAATTAATCCGGT 723  
Qy 358 PheAspGluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeu 377  
Db 724 TTCCTTGTATGAGGAATTTAATCACCTGGGTGGAGAAGATGTGGAATTTGGATATCGCTTA 783  
Qy 378 PheArgTyrGlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluPro 397  
Db 784 TTCCTGTTACCGTAGTCTTTTAAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCA 843  
Qy 398 ProGlyLysGluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMet 417  
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Qy 418 ArgGluLysValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsn 437  
Db 904 AGAGAAAGGTCCTTATATCTATAGAAAACCTTTTACCAATAGAGAATTCGCATATCAAT 963  
Qy 438 ArgValProLeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArg 457  
Db 964 AGAGTACCTTTAGTTTCAATTTATATCCAGCTTATTAATCTGTGCAAACTATATTTCAAGCT 1023  
Qy 458 CysValAspSerAlaIleAsnGlnThrValValAspLeuGluValCysIleCysAsnAsp 477  
Db 1024 TCGCTAGATAGTGCACACTGAATCAGACTGTTGTGTATCTCGAGGTTGTATTGTGAACCAT 1083  
Qy 478 GlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgVal 497  
Db 1084 GGTTCACACAGATAATACCTTAGAAGTGATCAATAGCTTTATGTTAATAATCTTAGGGTA 1143

Qy 498 ArgIleMetSerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaValSerPhe 517  
Db 1144 CGCATCATGTCTAAACCAAAATGCGGAATAGCCTCAGCATCAATGCGCGTTCTTTT 1203  
Qy 518 AlaLysGlyTyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaVal 537  
Db 1204 GCTAAAGGTTATTACATTTGGCAGTTAGATTTCAGATGATTATCTTGAGCCTGATCGAGTT 1263  
Qy 538 GluLeuCysLeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsn 557  
Db 1264 GAATCTGTTTAAAGAAATTTTAAAGATAAACCGCTAGCTTGTGTGTATACCACTAAT 1323  
Qy 558 ArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSer 577  
Db 1324 AGAAACGTCAATCCGGATGGTAGCTTAATCGCTAAATGGTTACAAATTCGCCAGAAATTTTCA 1383  
Qy 578 ArgGluLysLeuThrThrAlaMetIleAlaHisIlePheArgMetPheThrIleArgAla 597  
Db 1384 CGAGAAAAACCTCAACCGGCTATGATTGCTCACCCACTTTTGAATGTTTTCAGATTAGAGCT 1443  
Qy 598 TrpHisLeuThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPhe 617  
Db 1444 TGGCATTTAACTGATGGATTCAATGAAAAATTTGAAAAATGCCGTAGACTATGACATGTTT 1503  
Qy 618 LeuLysLeuSerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgVal 637  
Db 1504 CTCAACTCAGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTCTATAACCGTGTA 1563  
Qy 638 LeuHisGlyAspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheVal 657  
Db 1564 TTACATCGTGATAACACATCAATTAAGAAAACTTGGCATTCAAAAGAAAAAACCAATTTTGT 1623  
Qy 658 ValValAsnGlnSerLeuAsnArgGlnGlyIleThrTyrThrAsnTyrAspGluPheAsp 677  
Db 1624 GTAGTCAATCAGTCATTAAATATAGCAAGGCAATTAATTTATTAATATGACGAATTTGAT 1683  
Qy 678 AspLeuAspGluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIle 697  
Db 1684 GATTAGATGAAGTAGAAGATATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATT 1743  
Qy 698 AspIleLeuLysAspIle 703  
Db 1744 GATATCTTAAAGATATT 1761

## RESULT 14

US-11-194-246-190/c

; Sequence 190, Application US/11194246

; Publication No. US20050272089A1

; GENERAL INFORMATION:

; APPLICANT: Mott, John

; APPLICANT: Trepod, Catherine

; APPLICANT: Arvidson, Staffan

; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET

; TITLE OF INVENTION: USE

; FILE REFERENCE: 00592.US1 (M&amp;R 268.05920101)

; CURRENT APPLICATION NUMBER: US/11/194,246

; CURRENT FILING DATE: 2005-08-01

; PRIOR APPLICATION NUMBER: US/10/274,586

; PRIOR FILING DATE: 2002-10-21

; PRIOR APPLICATION NUMBER: US 60/345,438

; PRIOR FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 621

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 190

; LENGTH: 2736

; TYPE: DNA

; ORGANISM: ARTIFICIAL

; FEATURE:

; OTHER INFORMATION: Sequence of the lpp coding sequence and flanking regions.  
US-11-194-246-190

Alignment Scores:





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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

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Title: US-10-642-248-2

Perfect score: 5108

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA\_Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5108	100.0	2920	5	US-10-217-613-2
2	5108	100.0	2920	7	US-10-642-248-1
3	5108	100.0	2937	5	US-10-011-768B-8
4	5108	100.0	2937	5	US-10-011-771B-8
5	5108	100.0	2937	10	US-11-109-855-8
6	5104	99.9	2916	6	US-10-326-185-94
7	5104	99.9	2916	10	US-11-096-190-8

Alignment Scores:  
Pred. No.: 0  
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Best Local Similarity: 100.00%  
Query Match: 100.00%  
Length: 2920  
Matches: 972  
Conservative: 0  
Indels: 0

ALIGNMENTS

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; Sequence 2, Application US/10217613  
; Publication No. US20030113845A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL  
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND U:  
; FILE REFERENCE: 35541.081  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 2920  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-10-217-613-2

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Sequence 44, Appli



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Db 2221 TTCGTTATGTTTACATGTTGATAAGAAATCATCTTACACCCAGATATCAAAAAAGAAATA 2280
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAnsnAspIleSerTyrTyr 780
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Qy 801 LeuAnsnLeuAnsnCysGluTyrIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2401 TTAATCTAAATTTGGAATACATCATCTTTTGTATATCATGACAGCTATTCGTTAAAAAT 2460
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2461 GACAGCTATGCTTATATGAAAAATATGATGTCGCGCATGAATTTCTCAGCATTAACACAT 2520
Qy 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLysLeuIleLysThrTyrPhe 860
Db 2521 GATTGGATCGAGAAATCAATCGCATCCACCATTTAAAAAGCTCATTTAAAACTTATTTT 2580
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyValAsrGlnGlyMetPheMetThr 880
Db 2581 AATGCAATGACTTAAAGATGATGAATGTGAAGGGGCATCAACAGGTATGTTATGAGC 2640
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTAATTAAGAAGTCATCACATCTTGCCAGTCA 2700
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleThrPheGlnPheAlaLeuLeuIle 920
Db 2701 ATTGATAGTGTCCAGATATATACACTGAGGATATTTGTTTCCAATTTGCACCTTTAATC 2760
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db 2761 TTAGAAAAAGAAACCGCGCATGTATTTAATAAACAATCGACCTGACCTATATGCTTGG 2820
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2821 GAACGAAATTAACATGGCAATGAACAAATTTGAAGTGCAGAAAAAGAGAGAGAAATATA 2880
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2881 CCTGTTAAACAGTTCATTATTATTAAGTATAACTCTA 2916
RESULT 2
US-10-642-248-1
; Sequence 1, Application US/10642248
; Publication No. US20040132143A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; APPLICANT: Jing, Wei
; TITLE OF INVENTION: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND METHO
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 3554.097
; CURRENT APPLICATION NUMBER: US/10/642,248
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
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; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/842,484
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/199,538
; PRIOR FILING DATE: 2000-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-10-642-248-1
Alignment Scores:
Pred. No.: 0 Length: 2920
Score: 5108.00 Matches: 972
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:
US-10-642-248-2 (1-972) x US-10-642-248-1 (1-2920)
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Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AAATTTATTTGAAAGTCGCGGAAATCTATGACGCGAAATTTGTTGAAATTTTCAAAATTA 120
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 121 AAATGCAAGAAAGAAATCTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTTCTGTAA 180
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 181 AAAGAAGAAAGAAAGTCAATGTTTGGATAGTCGTTAGATATTGCAACACACACTGTTACT 240
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db 241 TCCACGCTAAAAAATATTAGTACTTTCTGACTCGGAAAAAACACCGTTAAAAAATAAATGG 300
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 301 AAATTTGCTCACTCAGAGAAGAAATCTGANAATGCGGAGGTAAGAGCGGTCGCCCTTGTAC 360
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 361 AAAGATTTTCCCAAGATCTGGTTTTAGCGCCTTTACCTGATCATGTTAATGATTTTACA 420
Qy 141 TrpTyrLysLysArgLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 421 TGGTACAAAAAGCGAAGAAAGAAAGACTTGGCATAAAAACCTGAAACATCAACATCTTGT 480
Qy 161 SerIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
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Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAAACCAAAAAACACATTTACCCGTTTGAGGTTATCGTGACAGATGATGCTAGTAGGAA 600
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
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Db 601 GATCTATACCGATCATTCGCCATATAGAAATTAATTTGGATATTCGCTACGTCAGACAA 660  
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Db 661 AAAGATAACGGTTTCAAGCGCAGTCCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 720  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAenProLeuTyrValHisSerTyr 260  
Db 721 GACTTTATTTGGCTTACTCGCATGTGATATGGCGCAATCCATTTATGGGTTTCATCTTAT 780  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProAArgLysTyrIleAsp 280  
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Qy 281 ThrGlnHisIleAspProLysAspPheLeuAenAlaSerLeuLeuGluSerLeuPro 300  
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Qy 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
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Qy 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAspSerProPheArgPhe 340  
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Qy 341 PheAlaAlaGlyAenValAlaPheAlaLysLysTyrLeuAenLysSerGlyPheAsp 360  
Db 1021 TTTGCGCGGGTAATGTGCTTTCGCTTAAATAATGGCTTAAATAATCCGGTTTCTTTGAT 1080  
Qy 361 GluGluPheAenHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1081 GAGGAATTTAATCACTACGCGGGTGAAGAGATGTGAATTTGGATATTCGCTTATTCGCTTAC 1140  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1141 GGTAAGTTCTTTAAACTATTGATGGCATTATGGCTTACCATTCAAGGCCACAGGTANA 1200  
Qy 401 GluAenGluThrAspArgGluAlaGlyLysAenIleThrLeuAspIleMetArgGluLys 420  
Db 1201 GAAATGAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAAG 1260  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAenArgValPro 440  
Db 1261 GTCCCTTATATCTATAGAAAATTTTACCATAAGAGATTCGCATATCAATAGAGTACCT 1320  
Qy 441 LeuValSerIleTyrIleProAlaTyrAenCysAlaAenTyrIleGlnArgCysValAsp 460  
Db 1321 TTAGTTTCAATTTATATCCAGCTTATTAACCTGTGCNAATATATTCAACGTTGCGTAGAT 1380  
Qy 461 SerAlaLeuAenGlnThrValValAspLeuGluValCysIleCysAenAspGlySerThr 480  
Db 1381 AGTCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTAAACGATGTTCAACA 1440  
Qy 481 AspAenThrLeuGluValIleAenLysLeuTyrGlyAenAenProArgValArgIleMet 500  
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Qy 501 SerLysProAenGlyGlyIleAlaSerAlaSerAenAlaValSerPheAlaLysGly 520  
Db 1501 TCTAAACCAATGGCGAATAGCTTCAGATCAATATGACGCGGTTTTCTTTGCTTAAGGT 1560  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1561 TATTACATGGGCAGTTAGATTTCAGATGATTTCTTGAGCCTGATGCGAGTTGAACCTGTGT 1620  
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Qy 561 AenProAspGlySerLeuIleAlaAenGlyTyrAenTyrProGluPheSerArgGluLys 580

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Db 1741 CTCACAACCGCTATGATGCTCCACCTTTAGAAATGTTACGATTTAGAGCTTGGCATTTA 1800  
Qy 601 ThrAspGlyPheAenGluLysIleGluAenAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1801 ACTGATGGATTCAATGAAAAAATTGAAATCGCGTAGACTATGACATGTTCTCTCAACTC 1860  
Qy 621 SerGluValGlyLysPheLysHisLeuAenLysIleCysTyrAenArgValLeuHisGly 640  
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Qy 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysAenHisPheValValValAen 660  
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Qy 661 GlnSerLeuAenArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Db 1981 CAGTCAATTAATAGACAGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040  
Qy 681 GluSerArgLysTyrIlePheAenLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
Db 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGAGATTGATCTTA 2100  
Qy 701 LysAspIleLysIleIleGlnAenLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2101 AAAGATATTAAATTCATCCAGATAAAGATGCCAATAATCGCAGTCAGTATTTTTTATCCC 2160  
Qy 721 AsnThrLeuAenGlyLeuValLysLysLeuAenAsnIleIleGluTyrAenLysAenIle 740  
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Qy 741 PheValIleValLeuHisValAspLysAenHisLeuThrProAspIleLysLysGluIle 760  
Db 2221 TTCGTTATTGTTCTACATGTTGATAAGATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAenIleLeuAenAenAspIleSerTyrTyr 780  
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Qy 781 ThrSerAenArgLeuIleLysThrGluAlaHisLeuSerAenIleAenLysLeuSerGln 800  
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Qy 801 LeuAenLeuAenCysGluTyrIleIlePheAspAenHisAspSerLeuPheValLysAen 820  
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Qy 841 AspTyrIleGluLysIleAenAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
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Qy 941 GluArgLysLeuGlnTrrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
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Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Db 2881 CCTGTTAAAGTTCAATTTAATAGTATATACTCTA 2916

RESULT 3  
US-10-011-768B-8  
; Sequence 8, Application US/10011768B  
; Publication No. US20030073221A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Kumari, Khamana  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/10/011,768B  
; CURRENT FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: Pastuerella Multocida  
US-10-011-768B-8

Alignment Scores:  
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Score: 5108.00 Matches: 972  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-642-248-2 (1-972) x US-10-011-768B-8 (1-2937)

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Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
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Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 319 AAATTGCTCACTGAGAAGAAATCTGAAATGCGGAGTAAAGAGCGGTCCGCTTGTACCA 378  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
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Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
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Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
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Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
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Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
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Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
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Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1279 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1338  
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Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
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Qy 521 TyTyriIleGlyGlnLeuAenSerAspAspTyriLeuGluProAspAlaValGluLeuCys 540
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Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyriAsnTrpProGluPheSerArgGluLys 580
Db 1699 AATCCGGATGGTAGCTTAATCGCTAAATGGTTACAAATGGCCAGAAATTTTCACGAGAAAAA 1758
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
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Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyriAspMetPheLeuLysLeu 620
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Qy 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyriPhe 860
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Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2599 AATGACAATGCTTAAAAAAGTATGAATGTGAAGGGGGCATCACAAAGGTATGTTTATGACG 2658
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Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2659 TATGCGCTTAGCGATGAGCTTCTGACGATATTATTAAGAAGTCAATCACTCTTCCAGTCA 2718
Qy 901 IleAspSerValProGluTyriAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 2719 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACATTAATC 2778
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyriMetProTrp 940
Db 2779 TTAGAAAAAGAAAAACCGGCATGTGATTATAAAAAACATCGACCCCTGACTTATATGCCCTGG 2838
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2839 GAACGAAATTTACATGGAACAAATGAACAAATTTGAAGTGCAAAAAGAGAGAAATATA 2898
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Db 2899 CCTGTTAAACAAGTTCATTATTATATAGTATAACTCTA 2934
RESULT 4
US-10-011-771B-8
; Sequence 8, Application US/10011771B
; Publication No. US20030082780A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H.
; APPLICANT: DeAngelis, Paul
; APPLICANT: Kumari, Kshama
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof
; FILE REFERENCE: 3554.011
; CURRENT APPLICATION NUMBER: US/10/011,771B
; PRIORITY FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 09/178,851
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: US 60/064,435
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Pasteurella Multocida
US-10-011-771B-8
Alignment Scores:
Pred. No.: 0 Length: 2937
Score: 5108.00 Matches: 972
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-10-642-248-2 (1-972) x US-10-011-771B-8 (1-2937)
Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyriAsnSerAsnAspTyriGlnLeuAlaLeu 20
Db 19 ATGAATACATTATCACAAAGCAATAAAGCAATATAACGCAATGACTATCAATTAGCACTC 78
Qy 21 LysLeuPheGluLysSerAlaGluIleTyriGlyArgLysIleValGluPheGlnIleThr 40
Db 79 AAATTTTCAAAAGTCGGCGGAAATCTATGGACGGGAAATTTGTTGAATTTCAAAATTACC 138
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 139 AAATGCAAGAAAAAATCTCAGCACATCTCTCTGTTAAATTCAGCACATCTTCTTGTAAT 198
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 199 AAAGAAGAAAAAGTCAATGTTTGGATAGTTCGTTAGATATTGCAACACACTGTACTT 258
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db 259 TCCAACGTAAAAAAATTTAGTACTTTCTGACTCGGAAAAAACACGTTAAAAAATAAATGG 318
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101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValAlaArgAlaValAlaLeuValPro 120 QY  
139 AAATGTCTCACTGAGAGAAATCTGAAATCGGAGGTAGAGCGGTGTTACCA 378 Db  
121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140 QY  
379 AAAGATTTTCCAAAGATCTGGTTTACCGCTTTTACCTGATCATGTGTAATGATTTTACA 438 Db  
141 TrpTyrLysLysArgLysLysArgLysGluLysProGluHisGlnHisValAlaGlyLeu 160 QY  
439 TGGTACAAAAGCGAAGAAAGACTTGGCATAAAACCTGAACTCAACATGTTGGGCTT 498 Db  
161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180 QY  
499 TCTATATCGTTACACATTCATCGACCAACAAATTTATCGATTACATTAGCCGTGTTA 558 Db  
181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200 QY  
559 GTAAACCAAAAAACACATTTACCGGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618 Db  
201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220 QY  
619 GATCTATCACCGATCATTTCCGCAATATGAAATTAATTTGGATATTCGCTACGTCAGACAA 678 Db  
221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuAlaGluAlaLysTyr 240 QY  
679 AAAGATAACGGTTTTCAAGCCAGTCCGCTCGAATATGGGATATACGCTTAGCAAAATAT 738 Db  
241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260 QY  
739 GACITTAATGGCTTACTCGACTGTGATATGGCCCAATCCATTATGGGTTTCATTTCTAT 798 Db  
261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280 QY  
799 GTTCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCAAAGAAAATACATCGAT 858 Db  
281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300 QY  
859 ACACAACATATTAGCCCCAAAGACTTCTTAATAACGGGAGTTTCCTTGAATCATTACCA 918 Db  
301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320 QY  
919 GAAAGTGAACCAATAATAGTTGTTCCCGCAAAAGGGAGGAACAGTTTCTCTCGATTGG 978 Db  
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361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380 QY  
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381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400 QY  
1159 GGTAGTTTCTTTAAACATTTATGTCGATTATGGCTTATCGCTCAACAGAGCCACAGGTAAA 1218 Db  
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421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440 QY  
1279 GTCCCTTATCTATAGAAAACCTTTTACCAATGAGAAGATTCGCATATCAATAGATACCT 1338 Db  
441 LeuValSerIleTyrIleProLysThrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460 QY  
1339 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACGGTTGCGTAGAT 1398 Db

461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480 QY  
1399 AGTGCACCTGAATCAGACTGTTGTGATCTCAGGTTTGTATTGTTAAACGATGGTTCAACA 1458 Db  
481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500 QY  
1459 GATAATACCTTTAGAGTGATCAATAGCTTTATGGTTAATTAATCTCTAGGGTACGCATCATG 1518 Db  
501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520 QY  
1519 TCTAAACCAATGCGGAATAGCCTCAGCTCAATTCAGCCGTTCTTTTGTCTAAAGGT 1578 Db  
521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540 QY  
1579 TATTACATTGGCAGTTTAGATTTCAGATGATTTCTTCAGCCTGATGAGTTGAATCTGTGT 1638 Db  
541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560 QY  
1639 TTAAGAAGATTTTAAAGATTAACCGCTAGCTGTGTTTATACCACTATATAGAAACGTC 1698 Db  
561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580 QY  
1699 AATCCGATGGTAGCTTAATCGCTAATGGTTTACAATTTGGCCAGAAATTTTCACGAGAAAA 1758 Db  
581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600 QY  
1759 CTCAACCGGCTATGATTTGCTCACCACTTTAGAAATGTTTCAGATTAGAGCTTTGGCATTTA 1818 Db  
601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620 QY  
1819 ACTGATGGATTCAATGAAAAAATTTGAAAATCCCGTAGACTATGACATGTTCTCTCAACTC 1878 Db  
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661 GlnSerLeuAsnArgGlnGlyIleThrTyrThrAsnTyrAspGluPheAspAspLeuAsp 680 QY  
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681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700 QY  
2059 GAAAGTAGAAGATATTTTCAATAAACCCTGATATCAAGAAGACAGATGATATCTTA 2118 Db  
701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720 QY  
2119 AAAGATATTAATAATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2178 Db  
721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740 QY  
2179 AATACATTAAACCGCTTAGTGAAAAAACTAAACAATATTTTGAATATAATAAATAATA 2238 Db  
741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760 QY  
2239 TTCGTTATGTTTACATGTTGTAAGAATCATCTTACCCAGATATCAAAAAAGAAATA 2298 Db  
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2299 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTTAC 2358 Db  
781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800 QY  
2359 ACGAGTAATAGATTAATAAATACTGAGCGCATTTTAAGTAATTAATAAATAAATAAGTCAG 2418 Db  
801 LeuAsnLeuAsnCysGluTyrIlePheAspAsnHisAspSerLeuPheValLysAsn 820 QY  
2419 TTAATCTAAATTTGGAATACATCATTTTGTGTAATCATGACAGCCTATTCGTTAAAAAT 2478 Db  
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Db 2599 AATGACAATGACTTTAAAAAGTATGAATGTGAAGGGGCATCACAAAGGTATGTTATGACG 2658
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Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrYrMetProTrp 940
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Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
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Db 2899 CCTGTTAAACAAGTTTCATTATTAATAGTATAACTCTA 2934
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## RESULT 5

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US-11-109-855-8
; Sequence 8, Application US/11109855
; Publication No. US20050202540A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H.
; APPLICANT: Deangelis, Paul
; APPLICANT: Kumari, Kshama
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof
; FILE REFERENCE: 3554.011
; CURRENT APPLICATION NUMBER: US/11/109,855
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US 09/178,851
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: US 60/064,435
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Pastuerella Multocida
US-11-109-855-8
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Pred. No.: 0 Length: 2937
Score: 5108.00 Matches: 972
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
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US-10-642-248-2 (1-972) x US-11-109-855-8 (1-2937)

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Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
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Qy 321 ArgLeuGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
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Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
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Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
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 Db 1399 AGTCACCTGAATCAGACTGTTGTGATCTCGAGGTTTGTATTGTGTAAACGATGCTTCAACA 1458  
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 Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
 Db 2719 ATTGATAGTGGCAGAAATATAACACATGAGGATATTTGGTTCCAATTTGACACTTTTAATC 2778  
 Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940  
 Db 2779 TTAGAAAAAGAAAAACCGCCCATGTATTTAAATAAAACATCGACCCCTGACTTATATGCTTGG 2838  
 Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
 Db 2839 GAACGAAATTTACAAATGGAACAAATGAAACAAATTTGAAGTGCAGAAAGAGGAGAAATATA 2898  
 Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
 Db 2899 CCTGTTAAACAGTTTCATTTATTAATAGTATACTCTA 2934

RESULT 6

US-10-326-185-94  
 ; Sequence 94, Application US/10326185  
 ; Publication No. US20030175902A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sloma, Alan  
 ; APPLICANT: Behr, Regine  
 ; APPLICANT: Widner, William  
 ; APPLICANT: Tang, Maria  
 ; APPLICANT: Sternberg, David  
 ; APPLICANT: Brown, Stephen  
 ; TITLE OF INVENTION: Methods for Producing Hyaluronan In a Recombinant Host Cell  
 ; FILE REFERENCE: 10341.200-US  
 ; CURRENT APPLICATION NUMBER: US/10/326,185  
 ; CURRENT FILING DATE: 2002-12-20  
 ; PRIOR APPLICATION NUMBER: US 60/342,644  
 ; PRIOR FILING DATE: 2001-12-21  
 ; NUMBER OF SEQ ID NOS: 108  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 94  
 ; LENGTH: 2916  
 ; TYPE: DNA  
 ; ORGANISM: Pasteurella multocida  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(2916)  
 ; OTHER INFORMATION:  
 US-10-326-185-94

Alignment Scores: 0 Length: 2916  
 Pred. No.:

Score:	5104.00	Matches:	971
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.90%	Mismatches:	0
Query Match:	99.92%	Indels:	0
DB:	6	Gaps:	0
US-10-642-248-2 (1-972) x US-10-326-185-94 (1-2916)			
Qy	1	MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu	20
Db	1	ATGAATACATTTATCACAGCAATAAAGCAATATAACAGCAATGACTATCAATAGCACTC	60
Qy	21	LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr	40
Db	61	AAATTATTGAAAGTCCGGCGAAATCTATGGACGGAAATTTGTGAATTTCAAAATACC	120
Qy	41	LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn	60
Db	121	AAATGCCAGAAAACCTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTCTGTAAAT	180
Qy	61	LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeu	80
Db	181	AAAGAAGAAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACACAACTGTTACTT	240
Qy	81	SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr	100
Db	241	TCCAACGTAAAAAAATTTAGTACTTTCTGACTCGGAAAAAACACGTTAAAAAAATAAATGG	300
Qy	101	LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro	120
Db	301	AAATTGCTCACTGAGAAGAAATCTGAAATATGCGAGAGGTAGAGCGGTGCGCCCTGTACCA	360
Qy	121	LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr	140
Db	361	AAAGATTTTCCCAAGATCTGTTTTAGCGCCTTTACTCTGATCATCTGTTAATGATTTTACA	420
Qy	141	TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu	160
Db	421	TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAAACATCAACATGTTTGGTCTT	480
Qy	161	SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu	180
Db	481	TCATATTATCGTTACACACATTCATCGACCAGCAATTTTATCGATTACATTAGCCCTGTTTA	540
Qy	181	ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu	200
Db	541	GTAACCAAAAACACATTTACCCGTTTGAAGTTATCTGTCAGACAGATGATGGTAGTCAGGAA	600
Qy	201	AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln	220
Db	601	GATCTATCACCGATCATTCGCAATATGAAATAATTAATTTGGATATTCGCTACGTCAGACAA	660
Qy	221	LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr	240
Db	661	AAAGATAACGGTTTTCAAGCCAGTCCGCTCGAATATGGATTTACGCTTAGCAGCAAAATAT	720
Qy	241	AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr	260
Db	721	GACTTTATGGCTTACTCGACTGTGATATGCGCCAAATCCATTTATGGTTTCACTCTTAT	780
Qy	261	ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp	280
Db	781	GTTTCAGAGCTATTAGAAAGATGATTTTAAACAATTCATTTGTTCCAGAAAAATACATCGAT	840
Qy	281	ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro	300
Db	841	ACACACATATGTACCCAAAAGACTTCTTAATTAACCGGAGTTTCTGTTGAATCATTTACCA	900
Qy	301	GluValLysThrAsnAsnSerValAlaLysGlyGluGlyThrValSerLeuAspTyr	320
Db	901	GAAGTGAACCAATAATAGTGTTCGCCCAAAAGGGGAAGCAACAGTTTCTCTGGATTGG	960
Qy	321	ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe	340
Db	961	CGCTTAGAACATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCCTTTCCGTTTT	1020
Qy	341	PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrPheAsnLysSerGlyPhePheAsp	360
Db	1021	TTTTCGGCGGGTAATGTTGCTTTTAAATAATGCTAAATTAATTAATTAATTAATTAAT	1080
Qy	361	GluGluPheAsnHisTyrPheGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr	380
Db	1081	GAGGAATTTAATCACCTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGCTTAC	1140
Qy	381	GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys	400
Db	1141	GGTAGTTTTCTTTAAAACATATTGATGCAATATGCGCTACCATCAAGAGCCACCCAGGTAA	1200
Qy	401	GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys	420
Db	1201	GAAAAATGAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG	1260
Qy	421	ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro	440
Db	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT	1320
Qy	441	LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp	460
Db	1321	TTAGTTTTCAATTTATATCCAGCTTATTAAGTGTGCAAACTATATTCAACGTTGCGTAGAT	1380
Qy	461	SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr	480
Db	1381	AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAAACGATGGTTCAACA	1440
Qy	481	AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet	500
Db	1441	GATAATACCTTAGAAGTGATCAATAGCTTTATGGTAATAATCTTAGGGTACGCATCATG	1500
Qy	501	SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly	520
Db	1501	TCATAACCAAAATGGCGAATAGCTCAGCATCAAAATGCAGCCGTTCTTTTGTAAAGGT	1560
Qy	521	TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys	540
Db	1561	TATTACATGGGCAGTTAGATTAGATTGATTATCTTGAGCCTGATGCACTGGAACCTGT	1620
Qy	541	LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal	560
Db	1621	TTAAAAAGAAATTTTAAAGATAAAACGCTAGCTGTGTGTTTATACCACTAATAGAAACGTC	1680
Qy	561	AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys	580
Db	1681	AATCCCGATGGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTCCAGGAAAAA	1740
Qy	581	LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrPheLeu	600
Db	1741	CTCACACGCTATGATGTTGCTCACCACTTTAGAAATGTTACAGATTAGAGCTTGGCATTTA	1800
Qy	601	ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu	620
Db	1801	ACTGATGGATTCAATGAAAAAATTTGAAAAATTCGCGTAGACTATGACATGTTTCCCTCAAACTC	1860
Qy	621	SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly	640
Db	1861	AGTGAAGTTGGAANAATTTAAACATCTTAATAAATCTGCTATAACCGGTATTACATGGT	1920
Qy	641	AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn	660
Db	1921	GATAACACATCAATTAAGAAACTTGGCATTCAAAGAAAAAACCAATTTTGTGTAGTCAAT	1980
Qy	661	GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp	680
Db	1981	CAGTCATTAATAAGCAAGGCATAACTTATTATAATTTATGACCAATTTGATGATTTAGAT	2040
Qy	681	GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu	700

2041 GAAAGTGAAGATATATTTTCAATAAAACCGCTGAATATCAAGAGGATGTATCTTA 2100  
Db  
701 LysAspIleValIleGluAsnLysAspAlaValSerIlePheTyrPro 720  
Qy  
2101 AAAGATATTAATCATCCAGATTAAGATGCCAAATCGGAGTCAGTATTTTATCC 2160  
Db  
721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Qy  
2161 AATACATTAACGGCTTAGTGAAATACTAACAATATTAATGAATATAATAAATAATA 2220  
Db  
741 PheValIleValLeuHisValAspLysAsnHisIleThrProAspIleLysGluIle 760  
Qy  
2221 TTCGTTATTTGTTTACATGTTGATAAGAATCATCTTACACGAGATATCAAAAAAGAAATA 2280  
Db  
761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAspIleSerTyrTyr 780  
Qy  
2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
Db  
781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Qy  
2341 ACGAGTATAGTATTAATAAAACTGAGCGCATTTAAGTAAATTAATAAATAAAGTCAG 2400  
Db  
801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLysPheValLysAsn 820  
Qy  
2401 TTAAATCTAAATTTGTGAATACATCATCTTTTGATAATCATGACAGCCTATTCGTTAAAAAT 2460  
Db  
821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Qy  
2461 GACAGCTATGCTTATATGAAAAATATGATGTCGCGCATGAATTTCTCAGCATTAACAT 2520  
Db  
841 AspTyrIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
Qy  
2521 GATTGATCGAGAAATCAATCGGCATCCACATTTAAAGACTCATTAAGCTTATTTT 2580  
Db  
861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Qy  
2581 AATGACATGACTTAAAGATGATGAATGTGAAAGGGGCATCAAGAGTATGTTATGACG 2640  
Db  
881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Qy  
2641 TATGCGCTAGCGCATGAGCTTCTGAGATTTATTAAGAGTATCATCACATCTTGCCAGTCA 2700  
Db  
901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuLeuIle 920  
Qy  
2701 ATTGATAGTGTCCAGATATTAACACTGAGGATATTTGGTCCATTTGACATTTTATC 2760  
Db  
921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940  
Qy  
2761 TTAGAAAAAGAAACCGGCCATGTATTTAATAAAACATCGACCTGACTTATATGCTTGG 2820  
Db  
941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Qy  
2821 GAACGAAAAATTAACAATGGAACAATTAACAATTTGAAGTGAAGGAGGAGGAGGAAAAATA 2880  
Db  
961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Qy  
2881 CCTGTTAAACAAGTTTCAATTAATTAATGATTAATCTTA 2916  
Db

## RESULT 7

US-11-096-190-8  
; Sequence 8, Application US/11096190  
; Publication No. US20050221446A1  
; GENERAL INFORMATION:  
; APPLICANT: Widner, William  
; APPLICANT: Sloma, Alan  
; APPLICANT: Thomas, Michael D.  
; APPLICANT: Tang, Maria  
; TITLE OF INVENTION: Methods For Producing A Hyaluronic Acid In A Bacillus Cell  
; FILE REFERENCE: 10596.200-US  
; CURRENT APPLICATION NUMBER: US/11/096,190  
; CURRENT FILING DATE: 2005-03-31  
; PRIOR APPLICATION NUMBER: 60/558,507  
; PRIOR FILING DATE: 2004-03-31

; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 8  
; LENGTH: 2916  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-096-190-8

Alignment Scores:  
Pred. No.: 0 Length: 2916  
Score: 5104.00 Matches: 971  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 99.92% Indels: 0  
DB: 10 Gaps: 0

US-10-642-248-2 (1-972) x US-11-096-190-8 (1-2916)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 1 ATGAATACATTTATCACAGCAATATAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 61 AAATTTATTTGAAAGTCGCGGAAATCTATGACGCGAAATTTGTGAATTTCAATTTACC 120  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 121 AATGCCAAGAAAACTCTCAGCACATCTTCTGTTAATTCAGCACATCTTTCTGTAAT 180  
Qy 61 LysGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 181 AAAGAAGAAAAAGTCAATGTTTGGGATAGTCGTTAGATATTGCAACAACAATCTGTACT 240  
Qy 81 SerAsnValLysLysLeuValLysSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100  
Db 241 TCCACGCTAAAAAAATTAGTACTTCTTGACTCGGAAAAAACAACGTTAAAAAATAATGG 300  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 301 AATTTGCTCACTGAGAGAAATCTGAAATCGGAGGTAGAGCGGTGCGCCTGTGACCA 360  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 361 AAAGATTTCCCAAGATCTGGTTTATAGCGCTTTACCTGATCATGTTTAATGATTTTACA 420  
Qy 141 TrpTyrLysLysArgLysLysArgLysProGluHisGlnHisValGlyLeu 160  
Db 421 TGGTACAAAAAGCGGAAAGAACCTTGGCATAAACCTGAAACATCAACATGTTGGTCTT 480  
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 481 TCTATTATCGTTTACAACTCAATCGACCACTTTTATCGATTACATTAGCCTGTTTA 540  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 541 GTAAACCAAAAAACACATTTACCCGTTTCAAGTTATCGTGACAGATGATGGTAGTCAGAA 600  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 601 GATCTTATCACCAGATCATTTCCGCAATATAAATTTGGATATTTCCGCTACGCTACAGAA 660  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 661 AAAGATAACGGTTTCAAGCCGCTCCGCTCGGATATATGGGATTTAGCTTACCAAAATAT 720  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
Db 721 GACTTTATTTGGCTTACTCGACTGATGATGGCCAAATCCATTATGGTTCATCTTAT 780  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 781 GTTGACAGAGCTATTAGAAGATGATGATTTAAACAAATCATTTGGTCCCAAGAAAAATACATCGAT 840

QY 281 ThrGlnHisIleAspProLysAspPheLeuAenAenAlaSerLeuLeuGluSerLeuPro 300  
DB 841 ACACAAATATTGACCCAAAGACTCTCTTAATAACCGGAGTTTGCTTGAATCAATACCA 900  
QY 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
DB 901 GAACTGAAACCAATATAGTTGTCGCGCAAAAGGGGAGGACAGTTCTCTGGATTGG 960  
QY 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAspSerProPheArgPhe 340  
DB 961 CGCTTAGAACAAATTCGAAAAACACAGAAATCTCCGCTTATCCGATTCGCCCTTCCGTTTT 1020  
QY 341 PheAlaAlaGlyAenValAlaPheAlaLysIleThrLeuAenLysSerGlyPhePheAsp 360  
DB 1021 TTTGCGCGGGGTAATGTTGCTTTCGCTAAAAAAATGGCTAAATAATCCGGTTTCTTTGAT 1080  
QY 361 GluGluPheAenHisIleTyrGlyGlyValGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
DB 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 1140  
QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
DB 1141 GGTAGTTTCTTTAAACTATTTGATGGCATTTATGGCTTACCATCAAGAGCCACCAGGTAAA 1200  
QY 401 GluAenGluThrAspArgGluAlaGlyAenIleThrLeuAspIleMetArgGluLys 420  
DB 1201 GAAATGAAACCGCATCGTAAGCGGGAATAATATTACGCTCGATATATTATGAGAGAAAAG 1260  
QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAenArgValPro 440  
DB 1261 GTCCCTTATATATAGAAACTTTTACCATAAGAGATTCGCATATCAATAGATACCT 1320  
QY 441 LeuValSerIleTyrIleProAlaTyrAenCysAlaAenTyrIleGlnArgCysValAsp 460  
DB 1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTCGCTAGAT 1380  
QY 461 SerAlaLeuAenGlnThrValValAspLeuValCysIleCysAenAspGlySerThr 480  
DB 1381 AGTCACATGAATACAGACTGTTGTTGATCTCGAGTTTGTATTTGTAAACGATGGTTCAACA 1440  
QY 481 AspAenThrLeuGluValIleAenLysLeuTyrGlyAenAenProArgValArgIleMet 500  
DB 1441 GATTAATACCTTAGAAGTGATCAATAGCTTTATCGTAAATAATCTCCTAGGATACGATCATG 1500  
QY 501 SerLysProAenGlyIleAlaSerAenAlaAlaValSerPheAlaLysGly 520  
DB 1501 TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCAGCGCTTCTTTTGCTTAAAGGT 1560  
QY 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
DB 1561 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCGATTGAATCTGTGT 1620  
QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
DB 1621 TTAAGAAGATTTTAAAGATTAACCGCTAGCTTGTGTTTATACCATTAATAGAAAACGTC 1680  
QY 561 AsnProAspGlySerLeuIleAlaAenGlyTyrAenTrpProGluPheSerArgGluLys 580  
DB 1681 AATCCGGATGGTAGCTTAATCGCTAAATGGTTTACAATTTGGCCAGAAATTTTCCAGGAGAAAA 1740  
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
DB 1741 CTCACACGGCTATGATTGCTCACCACTTTTGAATGTTTCAGATTTAGAGCTTGGCATTTA 1800  
QY 601 ThrAspGlyPheAenGluLysIleGluAenAlaValAspTyrAspMetPheLeuLysLeu 620  
DB 1801 ACTGATGATTCAATGAAAAAATTTGAAAATGCGCTAGCATATGATGATGTTCTTCAAACTC 1860  
QY 621 SerGluValGlyLysPheLysHisLeuAenLysIleCysTyrAenArgValLeuHisGly 640  
DB 1861 AGTGAAGTTGGAAAAATTTAAACATCTTTAAATAATCTGCTATAACCGCTGTATTACATGGT 1920

QY 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValValAsn 660  
DB 1921 GATTAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 1980  
QY 661 GlnSerLeuAenArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680  
DB 1981 CAGTCATTAATAAGACAGGCATAACTTATTAATAATATGACGAAATTTGATGATTTAGAT 2040  
QY 681 GluSerArgLysIlePheAenLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
DB 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
QY 701 LysAspIleLysIleGlnAenLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
DB 2101 AAAGATATTAAATCATCCAGATAAAGATGCCAAATTCGCACTCAGTATTTTATATCCC 2160  
QY 721 AsnThrLeuAenGlyLeuValLysLysLeuAenAsnIleIleGluTyrAenLysAenIle 740  
DB 2161 ATACATTTAAACCGCTTAGTGAATAAACTAAACAATATTATTGAATATATAAAAAATATA 2220  
QY 741 PheValIleValLeuHisValAspLysAenHisLeuThrProAspIleLysLysGluIle 760  
DB 2221 TTCGTTATTGTTCTCATGTTGATTAAGAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
QY 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAenAenAspIleSerTyrTyr 780  
DB 2281 CTAGCCTTCTATCATTAACATCAAGTGAATATTTTACTAAATTAATGATATCTCATATTAC 2340  
QY 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAenIleAenLysLeuSerGln 800  
DB 2341 ACCAGTAATAGATTAATAAAAACTGAGGCGCATTTAAGTAATATTATAAATAAAGTCAG 2400  
QY 801 LeuAenLeuAenCysGluTyrIleIlePheAspAenHisAspSerLeuPheValLysAen 820  
DB 2401 TTAATCTAAATTTGTAATACATCATTTTGTAAATCATGACAGCCTATTTCGTTAAAAAT 2460  
QY 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAenPheSerAlaLeuThrHis 840  
DB 2461 GACAGCTATGCTTATATGAATAAATATGATGTCGGCATGNAATTTCTCAGCATTAACACAT 2520  
QY 841 AspTrpIleGluLysIleAenAlaHisProProPheLysLysLeuIleLysThrTyrPhe 860  
DB 2521 GATTGGATCGAGAAATCAATCGCATCCACCATTTTAAAAAGCTCATTTAAACCTTATTTT 2580  
QY 861 AsnAspAenAspLeuLysSerMetAenValLysGlyAlaSerGlnGlyMetPheMetThr 880  
DB 2581 AATGACAAATGACTTAAAGAGTATGAATGTGAAGGGGCATCAAGAGGTATGTTTATGACG 2640  
QY 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
DB 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGTCATCATCTTTCAGCTCA 2700  
QY 901 IleAspSerValProGluTyrAenThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
DB 2701 ATTGATAGTGTGCAGAAATATAACACTGAGGATATTGTTCCCAATTTGCACATTTAATC 2760  
QY 921 LeuGluLysLysThrGlyHisValPheAenLysThrSerThrLeuThrTyrMetProTyr 940  
DB 2761 TTAGAAAAAGAAAAACCGCCCATGTATTATTAATAAACATCGACCTGATCTTATATGCCCTGG 2820  
QY 941 GluArgLysLeuGlnTrpThrAenGluGlnIleGluSerAlaLysArgGlyGluAenIle 960  
DB 2821 GAACGAAATTAACATGGACAAATGAACAAATTTGAAGTGCNAAGAGAGGAGAAATATA 2880  
QY 961 ProValAenLysPheIleIleAenSerIleThrLeu 972  
DB 2881 CCTGTTAAACAAGTTTCATTATTATTAATAGTATAACTCTA 2916

## RESULT 8

US-09-879-959-9

; Sequence 9, Application US/09879959

; Patent NO. US20020160489A1

; GENERAL INFORMATION:

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; APPLICANT: Weigel, Paul H
; APPLICANT: Kumari, Khama
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION
; FILE REFERENCE: 3554.049
; CURRENT APPLICATION NUMBER: US/09/879,959
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/469,200
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: pasteurella multocida
US-09-879-959-9

Alignment Scores:
Pred. No.: 0 Length: 2937
Score: 5104.00 Matches: 971
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.92% Indels: 0
DB: 3 Gaps: 0

US-10-642-248-2 (1-972) x US-09-879-959-9 (1-2937)

QY 1 MetAenThrLeuSerGlnAlaIleLysAlaTyraenSerAsnAspTyxGlnLeuAlaLeu 20
Db 19 ATGAATACATATATCAAGCATATAAAGCATATAACAGCATATCAATATAGCACTC 78

QY 21 LysLeuPheGluLysSerAlaGluLeuTyrglyArgLysIleValGluPheGlnIleThr 40
Db 79 AAATTTATTTGAAAGTCGCGGAAATCTATGGACGGAATTTGTTGAAATTTCAAATACC 138

QY 41 LysCysLysGluLysLeuSerAlaHisProSerValaenSerAlaHisLeuSerValaen 60
Db 139 AAATGCCAAGAAATCTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTTCTGTAAT 198

QY 61 LysGluGluLysValaenValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 199 AAAGAAGAAATAGTCAATGTTTGGATAGTCGCTAGATATTTGCAACACACTGTTACTT 258

QY 81 SerAenValLysLysLeuValLeuSerAspSerGluLysAenThrLeuLysAenLysTrp 100
Db 259 TCCAAAGTAAATTAATAGTACTTTCTGACTCGGAAATACACGTTAAATTAATATGG 318

QY 101 LysLeuLeuThrGluLysLysSerGluAenAlaGluValArgAlaValAlaLeuValPro 120
Db 319 AAATTTGCTCACTCAGAGAATATCTGAAATGCGGAGGTAAAGCGCGTCCGCTTGTACCA 378

QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAenAspPheThr 140
Db 379 AAAGATTTTCCCAAGATCTGTTTGGATAGTCGCTTACCTGATCATGATTAATGATTTACA 438

QY 141 TrpTyrlLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 439 TGGTCAAAAGCGAAGAAAGAGACTTGGCATAAACCTGAACATCAACATGTTGGTCTT 498

QY 161 SerIleIleValThrThrPheAenArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 499 TCTATTATCGTTACAACTTCAATCGACGAGCAATTTTATCGATTACATTAGCCTGTTTA 558

QY 181 ValAenGlnLysThrHisTyrlProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 559 GTAAACCAAAACCAATACCTCCGTTTGAAGTTATCTGACAGATGATGAGTAGTCAGGAA 618

QY 201 AspLeuSerProIleLeuArgGlnTyrlGluAenLysLeuAspIleArgTyrlValArgGln 220
Db 619 GATCTATACCGATCATTCGCCAATATGAATTAATTTGGATATTCGCTACGTCAGACAA 678
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QY 221 LysAspAenGlyPheGlnAlaSerAlaAArgAenMetGlyLeuArgLeuAlaLysTyrl 240
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QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProbenProLeuTrpValHiserTyrl 260
Db 739 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAATCCATATATGGTTTCACTTAT 798

QY 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrlIleAsp 280
Db 799 GTTCAGAGCTATTAGAGATGATGATTAAACATCATTTGTCCTCAAGAAATATACATCAT 858

QY 281 ThrGlnHisIleAspProLysAspPheLeuAenAenAlaSerLeuLeuGluSerLeuPro 300
Db 859 ACACAACATATTGACCCCAAGACTTCTTAATAACCGAGTTTGTCTGAATCATTTACCA 918

QY 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320
Db 919 GAAGTGAACCAATATAGTTGTCGCCCAAGGGAAGAACAGTTTCTCTGGATTGG 978

QY 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAspSerProPheArgPhe 340
Db 979 CGCTTAGAACATTTGCAAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTTCGTTT 1038

QY 341 PheAlaAlaGlyAenValAlaPheAlaLysLysTrpLeuAenLysSerGlyPheAsp 360
Db 1039 TTTGCGCGGGTAATGTTGCTTAAATAATGCTTAAATAATGCTTAAATAATGCTTAAATA 1098

QY 361 GluGluPheAenHisTrpGlyGlyGluAspValGluPheGlyTyrlArgLeuPheArgTyrl 380
Db 1099 GAGGAATTTAATCACTGGGGTGGAGAAATGTTGGAATTTGGATATTCGCTTATTCGCTTAC 1158

QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrlHisGlnGluProGlyLys 400
Db 1159 GGTAGTTTCTTTAAACTATTGATGGCATATTGGCTTACCATCAAGAGCCACAGGTAA 1218

QY 401 GluAenGluThrAspArgGluAlaGlyLysAenIleThrLeuAspIleMetArgGluLys 420
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QY 421 ValProTyrlIleTyrlArgLysLeuLeuProIleGluAspSerHisIleAenArgValPro 440
Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT 1338

QY 441 LeuValSerIleTyrlIleProAlaTyrlAenCysAlaAenTyrlIleGlnArgCysValAsp 460
Db 1339 TTAGTTTCAATTTATATCCAGCTTATACTGTGCNAACATATATTCNAGCTTTCGCTAGAT 1398

QY 461 SerAlaLeuAenGlnThrValValAspLeuGluValCysIleCysAenAspGlySerThr 480
Db 1399 AGTGCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAACCATGTTCAACA 1458

QY 481 AspAenThrLeuGluValIleAenLysLeuTyrlGlyAenAspProArgValArgIleMet 500
Db 1459 GATAATACCTTAGAAGTGCATCAATTAAGCTTTATGTTAATAATCCCTAGGGTAGCATCATG 1518

QY 501 SerLysProAenGlyGlyIleAlaSerAlaSerAenAlaAlaValAenSerPheAlaLysGly 520
Db 1519 TCTAAACCAATATGGCGGAATAGCTTCAGCATCAATATGACGCGTTCCTTTGCTAAAGGT 1578

QY 521 TyrlTyrlIleGlyGlnLeuAspSerAspTyrlLeuGluProAspAlaValGluLeuCys 540
Db 1579 TATTACATTTGGCAGTTAGATTACATGATTTATCTTGGAGCTGATGATGAGTGAATCTGT 1638

QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrlThrAenArgAenVal 560
Db 1639 TTTAAAGAAATTTTAAAGATATAAGCTAGCTGTTGTTTATACCACTAATATAAGAACGTC 1698

QY 561 AenProAspGlySerLeuIleAlaAenGlyTyrlAenTrpProGluPheSerArgGluLys 580
Db 1699 AATCGGATGGTAGCTTAATCGCTAATGTTTACATTTGCCAGAAATTTTTCACGAGAAAAA 1758
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Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
Db 2719 ATTGATAGTGGCCAGAAATATACACTGAGGATATTGGTCCAAATTTGCACITTTTAATC 2778  
Qy 921 LeuGluIysIysThrGlyHisValPheAsnIysThrSerThrLeuThrTyrMetProTrp 940  
Db 2779 TTAGAAAAGAAACCGCCATGTATTTAAATAAAACATCGACCTGACTTATATGCTTTGG 2838  
Qy 941 GluArgIysLeuGlnTrpThrAsnGluGlnIleGluSerAlaIysArgGlyGluAsnIle 960  
Db 2839 GAACGAAAATTTACAATGGACAAATGAACAAATTGAAAAGTGCAAAAGAGGAGGAAAAATATA 2898  
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Db 2899 CCTGTTAAACAAGTTCATTTATTAATAGTATACTCTA 2934  
RESULT 10  
US-10-309-560-7  
; Sequence 7, Application US/10309560  
; Publication No. US20030235893A1  
; GENERAL INFORMATION: PAUL H  
; APPLICANT: WEIGEL, PAUL H  
; APPLICANT: KUMARI, KSHANA  
; TITLE OF INVENTION: HYALURONAN SYNTHASES AND METHODS OF MAKING AND USING SAME  
; FILE REFERENCE: 35541.082  
; CURRENT APPLICATION NUMBER: US/10/309,560  
; CURRENT FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: 60/336,105  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-10-309-560-7  
Alignment Scores:  
Pred. No.: 0 Length: 2937  
Score: 5104.00 Matches: 971  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 99.92% Indels: 0  
DB: 6 Gaps: 0  
US-10-642-248-2 (1-972) x US-10-309-560-7 (1-2937)  
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Db 79 AAATTAATTGAAAAGTCGGCGGAAATCTATGAGCGGAAAATTGTTGAATTTCAAAATTACC 138  
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Qy 121 LysAspPheProIysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
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Qy 141 TrpTyrIysIysArgIysIysArgLeuGlyIleIysProGluHisGlnHisValGlyLeu 160  
Db 439 TGGTACAAAAGCGAAGAAAGACATTGGCATAAAACCTGAAACATCAACATGTGTGGTCTT 498  
Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 499 TCTATTATCGTTACAACATTCATTCGACCGCAATTTTATCGATTACATTTAGGCTGTITA 558  
Qy 181 ValAsnGlnIysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 559 GTAAACCAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnIysLeuAspIleArgTyrValArgGln 220  
Db 619 GATCTATCACCGATCATTCGCCAATATGAAAATAAATTTGGATATTCGCTACGTCAGACAA 678  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
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Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
Db 739 GACTTTTATGGCTTACTCGAGTGTATATGGCGCCAAATCCATATATGGGTTCATCTTAT 798  
Qy 261 ValAlaLeuLeuLeuGluAspAspLeuThrIleIleGlyProArgIysTyrIleAsp 280  
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Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
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Qy 381 GlySerPhePheIysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyIys 400  
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Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
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Qy 421 ValProTyrIleTyrArgIysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1279 GTCCCTTATATCTATAGAAAACCTTTTACCATAATAGAGATTCGCATATCAATAGAGTACCT 1338  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1339 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACCTGCGTAGAT 1398  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480

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Db 1399 AGTGCATGATCAGACTGTTGATCTCGAGGTTGTTATTTGTAACGATGGTTCAACA 1458
Qy 481 AspAenThrLeuGluValIleAenLysLeuTyrglyAenAenProArgValArgIleMet 500
Db 1459 GATAATACCTTAGAAGTGATCAATTAAGCTTTATGGTAAATATCTCAGGTCAGCATG 1518
Qy 501 SerLysProAenGlyGlyIleAseAseAseAenAlaValSerPheAlaLysGly 520
Db 1519 TCTAAACCAATGGCGAATAGCTCAGCATCAATGACGCGTTTCTTTGCTAAAGGT 1578
Qy 521 TyrTrileGlyGlnLeuAseAseAsePyrLeuGluProAseAlaValGluLeuCys 540
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Qy 541 LeuLysGluPheLeuLysAseLysThrLeuAlaCysValTyrThrThrAenArgAenVal 560
Db 1639 TTAAGAAGAAATTTTAAAGATATAAAGCTAGCTTGTGTTTATACCATTAATAGAAACGTC 1698
Qy 561 AenProAseGlySerLeuIleAlaAenGlyTyrAenTrpProGluPheSerArgGluLys 580
Db 1699 AATCCGATGGTAGCTTAATCGCTAATGTTTACAAATGGCCAGAAATTTTCACGAGAAAAA 1758
Qy 581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1759 CTCACACGGCTATGATTGCTCACCATTTTGAATGTTTACGATTAGAGCTTGGCATTTA 1818
Qy 601 ThrAseGlyPheAenGluLysIleGluAenAlaValAsePyrAseMetPheLeuLysLeu 620
Db 1819 ACTGATGATTCAATGAAAGAAATTTGAAATGCCGTAGACTATGACATGTTCTCTCAAACTC 1878
Qy 621 SerGluValGlyLysPheLysHisLeuAenLysIleCysTyrAenArgValLeuHisGly 640
Db 1879 AGTGAAGTTGGAAAAATTTTAAACATCTTAATAAATCTCTAATAACCGTGATTACATGGT 1938
Qy 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValAse 660
Db 1939 GATAACACATCAATTAAGAACTTGGCATTCAAAGAAACCAATTTTGTGTAGTCAAT 1998
Qy 661 GlnSerLeuAenArgGlnGlyIleThrTyrTyrAenTyrAseGluPheAseAseLeuAse 680
Db 1999 CAGTCATTAATAGACAGGCATACTTATTATATATATGACGAATTTTGATGATTAGAT 2058
Qy 681 GluSerArgLysTyrIlePheAenLysThrAlaGluTyrGlnGluLysIleAsePheLeu 700
Db 2059 GAAAGTAGAAAGTATATTTTCAATAAACCCTGAAATATCAAGAAAGATTGATATCTTA 2118
Qy 701 LysAsePheIleIleGlnAenLysAseAlaLysIleAlaValSerIlePheTyrPro 720
Db 2119 AAAGATATTAATAATCATCAGATTAAGATGCCAAATCGCAGTCAGTATTTTATATCCC 2178
Qy 721 AenThrLeuAenGlyLeuValLysLysLysAenAenIleIleGluTyrAenLysAse 740
Db 2179 AATACATTTAAACGGCTTAGTGAATAAACTTAACAAATATTATTGAAATATAAATAATA 2238
Qy 741 PheValIleValLeuHisValAseLysAenHisLeuThrProAsePheLysLysGluLe 760
Db 2239 TTCGTTATTGTTCTACATGTTGATGAAGATCATCTTTACACCAATATCAAAAAAGAAATA 2298
Qy 761 LeuAlaPheTyrHisLysHisGlnValAenIleLeuAenAseAsePheSerTyrTyr 780
Db 2299 CTAGCCTTCTATCATTAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2358
Qy 781 ThrSerAenArgLeuIleLysThrGluAlaHisLeuSerAseAseAseLysLeuSerGln 800
Db 2359 ACGAGTATATAGATTATAAAAACTCAGCGCATTTTAAGTAAATATTAAATAAATAAGTCAG 2418
Qy 801 LeuAenLeuAseCysGluTyrIlePheAseAenHisAseSerLeuPheValLysAse 820
Db 2419 TTAATACTAAATGTGAATACATCAATTTTGTGAATATCATGACAGCCTATTCGTTAAAAAT 2478
Qy 821 AseSerTyrAlaTyrMetLysLysTyrAseValGlyMetAsePheSerAlaLeuThrHis 840
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Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538
Qy 841 AspTrileGluLysIleAenAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2539 GATTGATCGAAGAAATCAATGCGCATCCACCACTTTAAAGAGCTCATTTAAACCTTATTTT 2598
Qy 861 AseAseAenAsePheLysSerMetAenValLysGlyAlaSerGlnGlnGlyMetPheMetThr 880
Db 2599 AATGACAACTGACTTAAAGATATGAATGTGAAAGGGGCATCACAAAGGTATGTTTATGACG 2658
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
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Db 2719 ATTGATAGTGGCAGAAATATACACTGAGGATATTTGGTTTCCAATTTGCACATTTAATC 2778
Qy 921 LeuGluLysLysThrGlyHisValPheAenLysThrSerThrLeuThrTyrMetProTrp 940
Db 2779 TTAGAAAAAGAAACCGGCCATGTATTTAATAAACAATCGACCTGACTTATATGCTTGG 2838
Qy 941 GluArgLysLeuGlnTyrThrAenGluGlnIleGluSerAlaLysArgGlyGluAseIle 960
Db 2839 GAACGAAATTTACAAATGCAAAATGAACAAATGAAAGTGCAAAAGAGGAGAAATATA 2898
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## RESULT 11

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US-09-842-484A-3
; Sequence 3, Application US/09842484A
; Publication No. US20030104601A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL L.
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 4605.003
; CURRENT APPLICATION NUMBER: US/09/842,484A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/199,538
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-09-842-484A-3
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Alignment Scores:
Pred. No.: 0 Length: 2979
Score: 4502.50 Matches: 845
Percent Similarity: 93.21% Conservative: 61
Best Local Similarity: 86.93% Mismatches: 59
Query Match: 88.15% Indels: 7
DB: 3 Gaps: 2
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US-10-642-248-2 (1-972) x US-09-842-484A-3 (1-2979)

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Db 121 AAATATTATTGAGAAGTCTGCTGAAACCTTACGGCGGAAAAAATCGTTGAATTCCAAATTATC 180
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAse 60
Db 181 AAATGTAAGAAAGAAACTC-----TCGACCAATTTCT-----TATGTAACT 219
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QY 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
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QY 181 ValAsnGlnLysThrHisTrpProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 580 GTCAATCAGAAAAACAACCTACCCTTTGAAGTCTGTTGCAGATGATGGTAGTAGGAA 639  
QY 201 AspLeuSerProIleIleArgGlnTrpGluAsnLysLeuAspIleArgTrpValArgGln 220  
Db 640 AACTTACTTACCATTGTGCAAAAATACGAAACAAAACCTTGACATAAAGTATGTAAGCAA 699  
QY 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTrp 240  
Db 700 AAAGATTATGGATATCAATTTGTGTCAGTTCAGAACTTAGGTTTACGTACAGCAAAAGTAT 759  
QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTrp 260  
Db 760 GATTTTGTCTCGATTCTAGACTGCGATATGCGACCAACAATATATGGGTTTCATCTTAT 819  
QY 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTrpIleAsp 280  
Db 820 CTTACAGAACTATTAGAAGACAATGATATTGTTTAAATGGACCTAGAAAAATATGTGGAT 879  
QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 880 ACTCATAATATTACCGCAGAACCAATCTCTTAACGATCCATATTTAATAGAATCACTACCT 939  
QY 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 940 GAAACCCCTACAAATAACAATCCTTCGATTACATCAAAAGAAATATATCGTTGGATTGG 999  
QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 1000 AGATTAGAACATTTCAAAAAAACCCGATAATCTAGCTCTATGTGATTCCTCGTTTCGTTAT 1059  
QY 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
Db 1060 TTTAGTTGCGGTATGTTGCAATTTCTAAAGAATGGCTAAATAAAGTAGGTGGTTCGAT 1119  
QY 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTrpArgLeuPheArgTrp 380  
Db 1120 GAAGAAATTTAATCATTTGGGGGGCGAAGATGTAGAAATTTGGTTACAGATTTATGGCCAAA 1179  
QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTrpHisGlnGluProProGlyLys 400  
Db 1180 GGCTGTTTTTCAGAGTAATTGACGGCGGAATGGCATAACCATCAAGAACCCCTCGGTAAA 1239  
QY 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGlyLys 420  
Db 1240 GAAAAATGAAACAGACCCGGAAGCTGGTAAAAAGTATTACGCTTAAAAATTTGTGAAAGAAAAG 1299  
QY 421 ValProTrpIleTrpArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440

Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCATAAGAGATTTCACATATTTCATAGATACCT 1359  
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Db 1360 TTAGTTTCTATTATATCCCGCTTATAACTGTGCAAAATATATATTCAAAAGATGTGTAGAT 1419  
QY 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1420 AGTGCTCTCTTAATCAAACTGTGTGCAITCTCGAGGTTTGTTATTGTAAACGATGGTTCAACA 1479  
QY 481 AspAsnThrLeuGluValIleAsnLysLeuTrpGlyAsnAsnProArgValArgIleMet 500  
Db 1480 GATAATACCTTAGAAGTGATCAATAAGCTTTATGTTAAATCTCTAGGTCAGCATCATG 1539  
QY 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
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QY 521 TrpTrpIleGlyGlnLeuAspSerAspAspTrpLeuGluProAspAlaValGluLeuCys 540  
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QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTrpThrThrAsnArgAsnVal 560  
Db 1660 TTAAGAAGATTTTAAACAGATAAAGCTTAGCTTGTTGTATATACCCTAATAGAAACGTC 1719  
QY 561 AsnProAspGlySerLeuIleAlaAsnGlyTrpAsnTrpProGluPheSerArgGluLys 580  
Db 1720 AATCCGGATGTAGCTTAATCGCTAATGTGTACAATTTGGCCAGAAATTTTCACGAGAAAA 1779  
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1780 CTCACAACCGCTATGATGCTCACCATTAGAAATTTAGAAATTTTACGATTAGAGCTTGGCATTTA 1839  
QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTrpAspMetPheLeuLysLeu 620  
Db 1840 ACGGATGGATTTAACGGAATATTGAAAACGCGCTGATGATGACATGTTCTTTAAACTC 1899  
QY 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTrpAsnArgValLeuHisGly 640  
Db 1900 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCCGCTATTACATGGT 1959  
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1960 GATAACACATCCATTAAAGAACTCGGCATTCAAAAGAAAACCATTTTGTGTAGTCAAT 2019  
QY 661 GlnSerLeuAsnArgGlnGlyIleThrTrpTrpAsnTrpAspGluPheAspLeuAsp 680  
Db 2020 CAGTCATTAAATAGACAAGGCATCAATTATTATAATTATGACAAATTTGATGATTTAGAT 2079  
QY 681 GluSerArgLysTrpIlePheAsnLysThrAlaGluTrpGlnGluGluIleAspIleLeu 700  
Db 2080 GAAAGTAGAAAGTATATCTTCAATAAAACCGCTGAATATCAAGAGAAAATGGATATTTTA 2139  
QY 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTrpPro 720  
Db 2140 AAAGATCTTAAATCATTCAAAATAAAGATGCCAAATCGCAGTCAGTATTTTCTATCCC 2199  
QY 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTrpAsnLysAsnIle 740  
Db 2200 NATACATTAAACCGCTTAGTGAATAAACTTAACAATATTATTGAATATAATAAATAATA 2259  
QY 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Db 2260 TTCGTTATTATTCTACATGTGTGATAAGATCATCTTACACCAGACATCAAAAAGAAATA 2319  
QY 761 LeuAlaPheTrpHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTrpTrp 780  
Db 2320 TTGGCTTTCTATCATGAAGCACCAGGGAATATTTTACTAAATATGACATCTCATATTAC 2379  
QY 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2380 ACGAGTAATAGACTAATAAAACTGAGGCACATTTAAGTAATATTATAAATTTAAGTCAG 2439





; CURRENT APPLICATION NUMBER: US/10/197,153

; CURRENT FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: 09/437,277

; PRIOR FILING DATE: 1999-11-10

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 4

; LENGTH: 2979

; TYPE: DNA

; ORGANISM: Pasteurella multocida

US-10-197-153-4

Alignment Scores:

Pred. No.: 0 Length: 2979

Score: 4502.50 Matches: 845

Percent Similarity: 93.21% Conservative: 61

Best Local Similarity: 86.93% Mismatches: 59

Query Match: 88.15% Indels: 7

DB: 9 Gaps: 2

US-10-642-248-2 (1-972) x US-10-197-153-4 (1-2979)

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Db 61 ATGAATACATTTATCACAAGCAATAAAGCATATACAGCAATGACTATGAATTAGCACTC 120
Qy 21 LysLeuPheGluLysSerAlaGluLeuTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 121 AAATATTATTGAGAAGCTGCTGAAACCTACGGCGGCAAAATCGTTGAATTCAAATTTATC 180
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAen 60
Db 181 AAATGTAAGAAACATC-----TCGACCAATTCI-----TATGTAAGT 219
Qy 61 LysGluGluLysValAenValCysAspSerProLeuAenAspIleAlaThrGlnLeuLeuLeu 80
Db 220 GAAAGATAAAAAACAGTGTTCGATAGCTCATTAGATATATGCAACACAGCTCTTACTT 279
Qy 81 SerAenValLysLeuValLeuSerAspSerGluLysAenThrLeuLysAenLysTrp 100
Db 280 TCCACAGTAAATAAATACTCTATCCGAATCAGAAAAACAGTTTAAAAATAAATGG 339
Qy 101 LysLeuLeuThrGluLysLysSerGluAenAlaGluValArgAlaValAlaLeuValPro 120
Db 340 AAATCTATCACTGGGAAAAAATCGAGAACCGAGAAATCAGAAAGTGGAACTAGTACCC 399
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAenAspPheThr 140
Db 400 AAAGATTTTCTTAAAGATCTTGTCTTCTCCATTCGACAGATCATGTTAATGATTTTACA 459
Qy 141 TrpTyrLysLysArgLysArgLeuGlyIleLysProGluHisGlnHisValGluLysLeu 160
Db 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATATAAGCCCTGTAATAAGAAATATCGGCTT 519
Qy 161 SerIleIleValThrThrPheAenArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 520 TCTATTATTCTTACATTTAATCGTACCGGTATTTAGATATATACCGTTAGCCCTGTTG 579
Qy 181 ValAenGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 580 GTCAATCAGAAAAACAACTACCCATTTGAAGTCGTTGTTGTCAGATGATGTTAGTAAAGAA 639
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAenLysLeuAspIleArgTyrValArgGln 220
Db 640 AACTTACTTACCATTTGTGCAAAAAATACGAAACAAACCTTGACATAAAGTATGTAGACAA 699
Qy 221 LysAspAenGlyPheGlnAlaSerAlaAlaArgAenMetGlyLeuArgLeuAlaLysTyr 240
Db 700 AAAGATTATGGATATCAATTTGTGCGAGTCAGAAACTTAGTTAGTTTACGTACACAAAGTAT 759
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAenProLeuTrpValHisSerTyr 260
Db 760 GATTTTGTCTCGATCTAGACTGCGATATGGCACCACAAACATTTATGGGTTCTATCTTAT 819
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Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db 820 CTTACAGAACTATTAGAAGACAATGATGATTTGTTTAAATGGACCTAGAAAAATATGTGGAT 879
Qy 281 ThrClnHisIleAspProLysAspPheLeuAenAenAlaSerLeuLeuGluSerLeuPro 300
Db 880 ACTCATATATTATCCGAGAACAAATCTCTTAACCATCCATATTTATAGATCACTACCT 939
Qy 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320
Db 940 GAAACCCGCTACAATAACAATCTCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 999
Qy 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAspSerProPheArgPhe 340
Db 1000 AGATTAGAACATTTCAAAAAAACCGATAATCTACGTCTATGTGATTTCTCCGTTTCGTAT 1059
Qy 341 PheAlaAlaGlyAenValAlaPheAlaLysLysTrpLeuAenLysSerGlyPhePheAsp 360
Db 1060 TTTAGTTGCGGTAAATGTTGCATTTTCTAAAGATGGCTAAATAAAGTAGGTGGTTGCT 1119
Qy 361 GluGluPheAenHisTrpGlyGlyValGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1120 GAAGAAATTAATCATTTGGGGGGCGAAGATGCTAGAAATTTGTTACAGATTTATTTGCCAAA 1179
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1180 GGCTGTTTTTTCAGAGTAATTCACGGCGGAATGCGATACCATCAAGAACCCACCTGGTAAA 1239
Qy 401 GluAenGluThrAspArgGluAlaGlyAenIleThrLeuAenIleMetArgGluLys 420
Db 1240 GAAATGAACACAGACCCGGAAGCTGGTAAAGATTTACGCTTTAAATTTGTGAGAAAGAA 1299
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAenArgValPro 440
Db 1300 GTACTTACATCTATAGAAAGCTTTTACCATAAGAGATTCACATATTTACATAGATACCT 1359
Qy 441 LeuValSerIleTyrIleProAlaTyrAenCysAlaAenTyrIleGlnArgCysValAsp 460
Db 1360 TTAGTTTCTATTATATCCCGCTTATAAATGTCGAAATATATTTCAAGATGTTGTAGAT 1419
Qy 461 SerAlaLeuAenGlnThrValValAspLeuValCysIleCysAenAspGlySerThr 480
Db 1420 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTGTATTGTTGACGATGTTTCAACA 1479
Qy 481 AspAenThrLeuGluValIleAenLysLeuTyrGlyAenAenProArgValArgIleMet 500
Db 1480 GATTAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATATCTTAGGGTACGATCATG 1539
Qy 501 SerLysProAenGlyGlyIleAlaSerAlaSerAenAlaAlaValSerPheAlaLysGly 520
Db 1540 TCTAAACCAATGCGGAATAGCCTCAGCATCAAAATGCGCGCTTCTTTTGTCTAAAGGT 1599
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540
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Qy 561 AenProAspGlySerLeuIleAlaAenGlyTyrAenTrpProGluPheSerArgGluLys 580
Db 1720 AATCGGATGTTAGCTTAATCGTAAATGTTTACAAATGCGCCAGAAATTTTACGAGAAAAA 1779
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1780 CTCACACGGCTATGATGCTCACCATTTTAGAAATGTTTACGATTTAGAGCTTTGGCATTTA 1839
Qy 601 ThrAspGlyPheAenGluLysIleGluAenAlaValAspTyrAspMetPheLeuLysLeu 620
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Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
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Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660
Db |||||
Qy 1960 GATAACACATCCATTAAAGAACTCGGCATTCAAAAGAAACCACTTTTGGTTAGTCAAT 2019
Db |||||
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db |||||
Qy 2020 CAGTCATTAAATGACAAGGCATCAATATTATTAATTTATGACAAATTTGATGATTTAGAT 2079
Db |||||
Qy 681 GluSerArgLysThrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db |||||
Qy 2080 GAAGTAGAAGTATATCTTCAATAAAACCGCTGATATCAAGAAGAAATGGATATTITA 2139
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Qy 701 LysAspIleLysIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
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Qy 2140 AAAGATCTTAAACTCAATCAAAATAAAGATGCCAAATCGCAGTCAGTATTTCATATCCC 2199
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Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnIleIleGluTyrAsnLysAsnIle 740
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Qy 2200 AATACATTAACCGCTTAGTGAATAAACTAAACAATATTATTGAATATAATAAAATATA 2259
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Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
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Qy 2260 TTGGTTAATTATCTACATGTTGTAAGAATCATCTTACACGACATCAAAAAGAAATA 2319
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Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAspIleSerTyrTyr 780
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Qy 2320 TTGGCTTCTATCATAGCACCAGTCAATATTTTACTAATAATGACATCTCATATTAC 2379
Db |||||
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db |||||
Qy 2380 ACCAGTAATAGACTAATAAACTGAGCGCACTTTAAGTAATATTAAATAAATTAAGTCAG 2439
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Db |||||
Qy 2440 TTTAAATCTTAAATGTAATGATCATATTTTGGATTAATCATGACAGCCATTTCGTTTAAANAT 2499
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Db |||||
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RESULT 14

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US-11-042-530-3
; Sequence 3, Application US/11042530
; Publication No. US20050164984A1
; GENERAL INFORMATION:
; APPLICANT: DEANGLIS, PAUL L.
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 4605,007
; CURRENT APPLICATION NUMBER: US/11/042,530
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: 60/199,538
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/842,484
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-042-530-3
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Alignment Scores:
Pred. No.: 0 Length: 2979
Score: 4502.50 Matches: 845
Percent Similarity: 93.21% Conservative: 61
Best Local Similarity: 86.93% Mismatches: 59
Query Match: 88.15% Indels: 7
DB: 10 Gaps: 2
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US-10-642-248-2 (1-972) x US-11-042-530-3 (1-2979)

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Db 121 AAATTATTGAGAGTCTGCTGNAACCTACGGCGGAGAAAATCGTTGNAATTCGAATATTC 180
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Db 181 AAATGTAAAGAAAACTC-----TCGACCAATTC-----TATGTAAGT 219
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 220 GAAGATAAAAAAACAAGTGTTCGATAGTCTCAATTAGATATCCGACACAGCTCTTACTT 279
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Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 340 AAATCTATCACTCGGAAAAAATCGAGAACCGCAGAAATCAGAAAGGTGGAACTAGTACCC 399
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Db 460 TGTACAAAATCGAAAAAAGCTTAGGTATATAAGCCTGTAATAAAGCAATATCGGTCTT 519
Qy 161 SerIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 520 TCTATTATTATTCCTACATTTAATCGTAGCCGTATTTTAGATATAACGTTAGCGCTGTTG 579
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspPheGlySerGlnGlu 200
Db 580 GTCAATCAGAAAAACAACTACCATTTGAAGTCGTTGTTGTCAGATGATGTAGTAGAGAA 639
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db |||||
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221 LysAspAsnGlyPheGlnAlaSerAlaalaArgAsnMetGlyLeuArgLeuAlaLysTyr 240 Qy  
700 AAGATTATGATATCAATTTGTGTCAGTCAAGAACCTTAGGTTCACGTACAGCAAAAGTAT 759 Db  
241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260 Qy  
760 GATTTCCTCGATTCAGATCGCATATGGCACCACCAACAATATATGGTTCATTCAT 819 Db  
261 ValAlaGluLeuLeuGluAspAspLeuThrIleGlyProArgLysTyrIleAsp 280 Qy  
820 CTTACAGAACTATTAGAACACATGATATTTGTTAAATTTGGACCTAGAAAAATATGTGGAT 879 Db  
281 ThrGlnHisIleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro 300 Qy  
880 ACTCATATATATACCGCAGAACATTCCTTACGATCCATATTTAATAGATCACTACT 939 Db  
301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320 Qy  
940 GAAACCGCTACAAATACATCTTCGATTACATCAAAAGGAATATATCGTTGGATTGG 999 Db  
321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340 Qy  
1000 AGATTAGAACATTTCAAAAAAACCGATAATCTACGCTCTATGTGATTCCTCCGTTTCGTTAT 1059 Db  
341 PheAlaAlaGlyAsnValAlaPheAlaLysTyrLeuAsnLysSerGlyPhePheAsp 360 Qy  
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361 GluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380 Qy  
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381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400 Qy  
1180 GCCTGTTTTTTCAGAGTAATTCACGGCGAATGGCATACCATCAAGAACCACTCGTAAA 1239 Db  
401 GluAsnGluThrAspArgGluAlaGlyAsnIleThrLeuAspIleMetArgGluLys 420 Qy  
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421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440 Qy  
1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGATACCT 1359 Db  
441 LeuValSerIleTyrProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460 Qy  
1360 TTAGTTTCTATTATATCCCGCTTATTAATCTGTGCAATTTATTTCAAGATGTGTAGAT 1419 Db  
461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480 Qy  
1420 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1479 Db  
481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500 Qy  
1480 GATAATACCTTGAAGTATCAATAGCTTTATGTTAATATCCCTAGGGTAGCATCATG 1539 Db  
501 SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520 Qy  
1540 TCTAAACCAATGGCGAATAGCTCAGCATCAATGTCAGCGCTTCTTTTGTCTAAAGGT 1599 Db  
521 TyrTyrIleGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540 Qy  
1600 TATTACATTTGGGCGATTAGATTAGATGATATCTTTGAGCCTGATGTCAGTTGAACCTGTGT 1659 Db  
541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560 Qy  
1660 TTAAGAAATTTTAAAGATATAAACCTGAGCTTGTGTTTATACCACTAATAGAACGTC 1719 Db  
561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580 Qy  
1720 AATCCGGATGGTAGCTTAATCGCTAATGTTACAAATGGCCAGAAATTTTTCACGAGAAAA 1779 Db

581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTyrPheIleu 600 Qy  
1780 CTCACAAACGGCTATGATTGCTCACCATTTTAGAATGTTTACGATTAGAGCTTGGCATTTA 1839 Db  
601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620 Qy  
1840 ACGGATGGATTTAACGAAAAATTTGAAACGCCGTGGATATATGACATGTTCTTTAAACTC 1899 Db  
621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640 Qy  
1900 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAATCTGCTATTAACCGGTATTACATGGT 1959 Db  
641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660 Qy  
1960 GATAACACATCCATTAAGAACTCGCATTCGCAATTCATAATATATGACAAATTTGTGTAGTCAAT 2019 Db  
661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680 Qy  
2020 CAGTCATTAATAGACAGGCATCAATTTATTAATATATGACAAATTTGTATGATTTAGAT 2079 Db  
681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700 Qy  
2080 GAAAGTAGAAAGTATATCTTCATATAAACCCCTGATATCAAGAAGAAATGGATATTTTA 2139 Db  
701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720 Qy  
2140 AAAGATCTTAACATTCATTCAAAAATAAGATGCCAAAAATCGCAGTCAGTATTTCTATGCC 2199 Db  
721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740 Qy  
2200 AATACATTTAAACGGCTTAGTGAATAAACTAAACCAATATTTATGTAATATAATAAAATA 2259 Db  
741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760 Qy  
2260 TTCGTTATTTATCTACATGTTGTAAGAAATCATCTTACCCAGACATCAAAAAAGAAATA 2319 Db  
761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780 Qy  
2320 TTGGCTTTCTATCATACCAACCAAGTGAATATTTTACTAAATATATGACATCTCATATTAC 2379 Db  
781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800 Qy  
2380 ACGAGTAATAGACATAATAAAACTGAGGCACATTTTAAGTAAATATTAATAAATAAGTAC 2439 Db  
801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820 Qy  
2440 TTAATCTTAAATTTGTAATATCATCATTTTGAATATCATGACAGCTATTCGTTAAATAT 2499 Db  
821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840 Qy  
2500 GACAGCTATGCTTATATGAAAAATATCATGTGCGCATGAAATTTCTCAGCATTAACACAT 2559 Db  
841 AspTyrIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860 Qy  
2560 GATTGGATCGAGAAAAATCAATCGCATCCACCATTTAAAAAGCTGATTTAAACCTATTTT 2619 Db  
861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880 Qy  
2620 AATGCAATGCTTAAGAGATGTAATGTGAAGGGGATCAAGAGTATGTTTATGAAG 2679 Db  
881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900 Qy  
2680 TATGGCTTACCGCATGAGCTTCGAGGATTTAAAGAAGTCATCACATCCCTGCCAATCA 2739 Db  
901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGluPheAlaLeuLeuIle 920 Qy  
2740 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTCCAAATTTGCACTTTTAAATC 2799 Db  
921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940 Qy  
2800 TTGAAGAAAGAAACCCGCCATGATTTTATAAATAATCGACCTGACTTATATGCTTGG 2859 Db

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QY 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2860 GAACGAAATTTACAAATGGACAAATGAAACAATTCAAAGTGCAGAAAGGCGAAATATC 2919

QY 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2920 CCGTTAAACAGTTCAATTAATAGTATTAACGCTA 2955

RESULT 15
US-09-842-484A-1
; Sequence 1, Application US/09842484A
; Publication No. US20030104601A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL L.
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 4605.003
; CURRENT APPLICATION NUMBER: US/09/842.484A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/199,538
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-09-842-484A-1

Alignment Scores:
Pred. No.: 0 Length: 2979
Score: 4490.50 Matches: 843
Percent Similarity: 93.11% Conservative: 62
Best Local Similarity: 86.73% Mismatches: 60
Query Match: 87.91% Indels: 7
DB: 3 Gaps: 2

US-10-642-248-2 (1-972) x US-09-842-484A-1 (1-2979)

QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 61 ATGAATACATTTATCACAAGCAATTAAGACATATTAACGCAATGACTATGAATTAGCACTC 120

QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 121 AAATATTGAGAAAGTCTGTGGAACCTACGGGCGAATAATCGTTGAATTCCAAATATC 180

QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 181 AAATGTAAAGAAANAATC-----TCGACCAATTC-----TATGTAAGT 219

QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 220 GAAGATAAAAAACACAGTGTGTGCGATAGCTCATTAGATATCGCAACACAGCTCTACTT 279

QY 81 SerAsnValLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
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QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 340 AAATCTATCACTGGGAAAAAATCGGAGAACCGAGAAATCAGAAAGGTGGAACCTAGTACCC 399

QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
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QY 141 TrpTyrLysLysArgLysLeuGluGlyIleLysProGluHisGlnHisValGlyLeu 160
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QY 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 520 TCTATTATTCTCACAATTAATCGTAGCCGTATTTAGATATATAACGTTAGCCTGTTG 579
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QY 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 580 GTCAATCAGAAACAACATACCATTGGAAGTCGTTGTTGCAGATGATGTTAGTAGTAAGAA 639

QY 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 640 AACTTACTTACCATTGTCGCAAAAATACGAAACAAAACCTTGACATAAAGTATGTAGACAA 699

QY 221 LysAspAsnGlyPheGlnAlaSerAlaIleArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 700 AAAGATTATGGATATCAATTTGTGTGCGAGTCAGAAACTTAGGTTTACGTCACAGCAAGTAT 759

QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260
Db 760 GATTTTGTCTCGAATCTAGACTCGGATATGGCACCACAATATTAATGCGGTTCATCTTAT 819

QY 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db 820 CTTACAGAACTATTAGACACAATGATATTGTTTAAATTGGACCTAGAAAAATATGTGGAT 879

QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 880 ACTCATAATATTACCGCAGAACAAATTCCTTAACGATCCATATTTAATAGAAATCACTACCT 939

QY 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320
Db 940 GAAACCGCTACAAATAACAAATCTTCGATTACATCAAAAGGAATAATATCTGTTGGATTGG 999

QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 1000 AGATTAGAACATTTCAAAAAAACCGGATAATCTACGTCATGTGATTCTCGCTTTCGTTAT 1059

QY 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360
Db 1060 TTTGTTGCGGGTAATGTTCATTTCTAAAGAAATGGCTAAATAAAGTAGGTTCGTTCCGAT 1119

QY 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1120 GAAGAATTTAATCATTTGGGGGGCGGAAGATGTAGAAATTTGGTTACAGATTTATTTGCCAAA 1179

QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1180 GGCTGTTTTTTCAGAGTAATTGACGGCGGAATGCCCATCCATCAAGAACCCACCTGGTAAA 1239

QY 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db 1240 GAAAAATGAACAGAACCGGAAGCTGGTAAAAAGTATTACGCTTAAAAATTTGTAAGAAAG 1299

QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCANTAGAGATTACATATTTCATAGAAATACCT 1359

QY 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
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QY 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1420 AGTGCTCTTAATAACAACTGTTGTCGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA 1479

QY 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
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QY 501 SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
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QY 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1600 TATTACATTCGGCAGTTAGATTTCAGATGATTATCTTGAGCCTGTATGCAGTTGAACCTGTGT 1659
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Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1660 TTAAGAAGATTTTAAAGATATAAACCCTAGCTTGTGTATATACCACTAATAGAAACGTC 1719
Qy 561 AsnProaspGlySerLeuLeuAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580
Db 1720 AATCCGATGGTAGCTTAATCGCTAATGGTGTACAAATGGCCAGAAATTTTCACGAGAAAAA 1779
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1780 CTCACACGGCTATGATTGCTCACCAATTTTGAAGATGTTTACGATTAGAGCTTGGCATTTA 1839
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1840 ACGATGGATTACGAAAAATATTGAAAAACCGCGTGGATTATGACATGTTCTTTAAACTC 1899
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1900 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAAACCGCGTATTACATGGT 1959
Qy 641 AspAsnThrSerIleLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660
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Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680
Db 2020 CAGTCATTAAATAGACAGGCATCAATTTATTAATTAATGACAAATTTTGATGATTAGAT 2079
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluLysIleAspIleLeu 700
Db 2080 GAAAGTAGAAGTATATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTA 2139
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2140 AAAGATCTTAAACTCATTTCAAAATAAAGATGCCAAAATCGCAGTCAGTATTTCTATCCC 2199
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740
Db 2200 AATACATTAACCGCTTAGTGAAANAACTAAACATATTTATGATATTAATAAATAATA 2259
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2260 TTCGTTATTATCTACATGTTGATAAGAATCATCTTACACCAGACATCAAAAAAGAAATA 2319
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuAsnAsnAspIleSerTyrTyr 780
Db 2320 TTGGCTTTCTATCATAGCACCAGTGAATATTTTACTAAAAATATGACATCTCATATTAC 2379
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
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Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
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Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
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Qy 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
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Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
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Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSer 900
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Db 2920 CCCGTTAAACAAGTTTCATTATTAATAGTATAACGCTA 2955
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Search completed: January 9, 2006, 02:27:35  
Job time : 1698 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 8, 2006, 16:53:15 ; Search time 7680 Seconds

(without alignments)  
5921.490 Million cell updates/sec

Title: US-10-642-248-2

Perfect score: 5108

Sequence: 1 MNTLSQAKAYNSNDYQAL.....SAKGENIPVKNKFIINSITL 972

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool\_p/US10642248/runat\_06012006\_125010\_26878/app\_query.fasta\_1.1159  
-DB=EST -OPWT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptio -NORM=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10642248 @CGN 1 1 8010 @runat\_06012006\_125010\_26878 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hc1:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gsa1:\*  
10: gb\_gsa2:\*  
11: gb\_gsa3:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	225	4.4	1223	9	CC799180
C 2	220	4.3	878	10	C2545903
C 3	220	4.3	2110	9	BH770860
C 4	214.5	4.2	807	10	CL696206
5	210.5	4.1	832	10	C2541282
6	207	4.1	773	10	CL673825
C 7	201	3.9	720	10	CL677451

C	9	201	3.9	742	10	CL652986
C	10	197.5	3.9	829	10	CL683612
C	11	195	3.8	475	1	CZ541577
C	12	189.5	3.7	753	9	AI724383
C	13	188	3.7	655	9	BH387189
C	14	183.5	3.6	724	7	BH861035
C	15	173	3.4	468	10	BH861035
C	16	173	3.4	662	10	BH861035
C	17	171	3.3	1500	11	CJ414912
C	18	170	3.3	647	7	CL680585
C	19	169.5	3.3	3796	4	PRIO129d
C	20	168.5	3.3	3683	4	AG948871
C	21	162.5	3.2	1497	9	DQ049456
C	22	161	3.2	630	3	Homo sapi
C	23	161	3.2	846	10	CJ390966
C	24	160.5	3.1	595	3	Mus muscu
C	25	160	3.1	541	3	AK028506
C	26	160	3.1	563	3	AK019995
C	27	159.5	3.1	846	8	BH770718
C	28	159.5	3.1	2748	4	BH770718
C	29	158	3.1	297	10	BH770718
C	30	154.5	3.0	6021	4	AG936607
C	31	152.5	3.0	777	9	CR857560
C	32	152	3.0	1330	9	BH382993
C	33	151	3.0	507	8	BZ576465
C	34	151	3.0	897	8	CR230043
C	35	150.5	2.9	783	5	DR846253
C	36	150.5	2.9	849	7	BU365467
C	37	150.5	2.9	929	7	CK187525
C	38	150	2.9	853	9	CK187848
C	39	150	2.9	9664	9	BZ573948
C	40	149.5	2.9	1863	4	BH771023
C	41	148.5	2.9	603	3	CNS0A8M6
C	42	148.5	2.9	662	9	BH368787
C	43	147.5	2.9	812	7	BH395862
C	44	147.5	2.9	1737	10	AG935970
C	45	147.5	2.9	2607	4	AY403817

ALIGNMENTS

RESULT 1  
CC799180/c  
LOCUS CC799180 1223 bp DNA linear GSS 03-SEP-2004  
DEFINITION CC799180 Rumen metagenome subtractive hybridization library  
uncloned organism genomic clone HHX01C01, genomic survey  
sequence.

ACCESSION CC799180.1 GI:40539296

VERSION CC799180

KEYWORDS GSS

SOURCE uncloned organism

ORGANISM uncloned organism

REFERENCE 1 (bases 1 to 1223)

AUTHORS Galbraith, E.A., Antonopoulos, D.A. and White, B.A.

TITLE Suppressive subtractive hybridization as a tool for identifying

genetic diversity in an environmental metagenome: the rumen as a

model

JOURNAL Environ. Microbiol. 6 (9), 928-937 (2004)

PUBMED 15305918

COMMENT Contact: Galbraith EA

Department of Animal Sciences

University of Illinois

1207 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 217 244 4305

Fax: 217 333 8804

Email: galbraith@uiuc.edu

Insert Length: 1223 Std Error: 0.00

Class: PCR-based subtractive hybridization.

Location/Qualifiers

1..1223

/organism="uncultured organism"

FEATURES  
source



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Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 286 CGAACAACAAACGGCGGTTTCATCCGCGTATGAAGTATTAAGCGGCTCCGGA 227
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAlaValGluLeuCys 540
Db 226 TGCTATATCTGCTTCTTGGACAGCGATGACACTTATGAACCGGACTTTATCCGACACTG 167
Qy 541 LeuLysGluPheLeuLysAsp 547
Db 166 GTGAGTAAAGTCACACAGGAT 146

RESULT 3
BH770860/c 2110 bp DNA linear GSS 01-MAY-2002
LOCUS BH770860
DEFINITION LLMGtag598 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.
ACCESSION BH770860
VERSION BH770860.1 GI:20373817
KEYWORDS Lactococcus lactis subsp. cremoris
SOURCE Lactococcus lactis subsp. cremoris
ORGANISM Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
REFERENCE 1 (bases 1 to 2110)
AUTHORS Bolotin,A., Ehrlich,S.D. and Sorokin,A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbiologie
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is rgeP (56%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 2082.
Location/Qualifiers
1..2110
/organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
/sub_species="Cremoris"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/notes="Vector: pSGMU2; Site 1: SmaI; Library of
chromosomal fragments of L.lactis strain MG1363 was
prepared by partial AluI digestion or by sonication."

ORIGIN
Alignment Scores:
Pred. No.: 2,53e-13 Length: 2110
Score: 220.00 Matches: 136
Percent Similarity: 39.81% Conservative: 112
Best Local Similarity: 21.28% Mismatches: 206
Query Match: 4.31% Indels: 186
DB: 9 Gaps: 30

US-10-642-248-2 (1-972) x BH770860 (1-2110)
Qy 411 AsnIleThrLeuAspIleMetArgGluLysValProTyrIleTyrArgLysLeuLeuPro 430
Db 1793 AATTGTGAGTGTACAAATGCTCAGATCT-----TACCATTACAACTTCGG 1749
Qy 431 IleGluAsp-----SerHisIle-AsnArgValProLeu----- 441
Db 1748 ATGGATGAATATCGTTTCAGGAATAGAACATATTATCTTTTAAGTAGTGAATATGACAA 1689
Qy 442 ----ValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAs 460
Db 1688 AAAAGTATCAGTCGTAGTGACATGCTACAAATCAGGAAAATTTATGAAGATGCTTAGC 1629

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Qy 460 pSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerTh 480
Db 1628 TAGCAITTTTTCGCAAACTCATCAGAAACATTGAACCTTCTAGTTTAAATGATGGTCGAC 1569
Qy 480 rAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnPro-----ArgValAr 498
Db 1568 AGATGATCTTGGTCGAGTAAATTTCAAAAGTGTGAAGAATCACCATTCTGCTGAAACTCA 1509
Qy 498 gIleMetSerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAl 518
Db 1508 TTATTTTTCAGGAGAAATAGAGGTCTAGCTTTTGTACGAATATGATGCTTTAACTAAGAG 1449
Qy 518 aLysGlyTyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAlaValG 538
Db 1448 CACAGGCGATTTTACTTTTGTGTAGTAGTAAATTTCTTAATGCTGACCATATTGA 1389
Qy 538 uLeuCysLeuLysGluPheLeu---LysAspLysThrLeuAlaCysValTyrThrAs 557
Db 1388 AAAGTTACTGACAGAGCTGTTAGCAACAGATTTCAGATATTGCGCTATTGTCAGCTATGGGA 1329
Qy 557 nArgAsn-----ValAsnProAspGlySerLeuIleAlaAsnGlyTyrAs 572
Db 1328 TTTTAATGCTCAAAAAGACCTTCTTCGCCAGAT----- 1295
Qy 572 nTrpProGluPheSerArgGluLysLeuThrThrAlaMetIleAlaHisPheArgMe 592
Db 1294 ----TTAGAATATAGCTTTTAAAAAACAACTAGAGGGAATCTGTATTGATCTTCTGCTCAT 1239
Qy 592 tPheThrIleArgAlaTrpHisLeuThrAsp---GlyPheAsnGluLysIleGluAsnAl 611
Db 1238 G-----GTTAGGACCTCAAAAATTTGCTGACATAAAATTTGATGAATCTTTAAATAATAA 1185
Qy 611 aVal-----AspTyrAspMetPheLeuLysLeuSerGluValGlyLysPheLysHisLe 629
Db 1184 AACACTTGAGATATTATGATTTTGTGTTAGGATTAATC----- 1148
Qy 629 uAsnLysIleCysTyrAsnArgValLeuHisGlyAspAsnThrSerIleLysLysLeuGl 649
Db 1147 -----ATTAATAATGAGCAAAACCTATTATT 1122
Qy 649 yIleGlnLys---LysAsnHisPheValValValAsnGlnSerLeuAsnArgGlnGly 668
Db 1121 TGTTTCAAAATACAAAATTGAATTATTCGAGTTTTAGAACAACTCTTGAGTCAAGAGGA-- 1064
Qy 668 eThrTyrTyrAsnTyr----- 673
Db 1063 -AATTGGGAAAACCTATTATCAATCGTATTTTATATACCAATAGTACAGTAAAAAAT 1005
Qy 674 -----AspGluPheAs 677
Db 1004 TCCGTGCACTGATAGAGCGCTCCAAAACAACTTACTACTTTGGGTAGATAAATATCA 945
Qy 677 pAspLeuAspGluSerArg---LysTyrIlePheAsnLysThrAlaGluTyrGlnGluGl 696
Db 944 AAACCTTACAAAATGATGACAGACAGACACTTGTGATAAAGCTCAAGAGTATCTTGAACA 885
Qy 696 uIleAspIleLeuLysAspIleLysIleGlnAsnLysAspAlaLysIleAlaValSe 716
Db 884 AGAAGAGCGATGAAA-----AAAACAAATAGCTGACAAAGATATCCCATATTGCT----- 836
Qy 716 rIlePheTyrProAsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleGluTyr 736
Db 835 -----ANTCAAGAAAGTATGATTTCTGAAATTAATACTAATTTCTTTTGCATA 792
Qy 736 r-----AsnLysAsnIlePheVa 742
Db 791 TCGGCTAATAATAAGTGATACATCCCTTAGGAAAGAGGATGAACAATAAATTTATCTCT 732
Qy 742 lIleValLeuHisValAspLysAsnHisLeuThrPro----- 754
Db 731 ATACGTA-----CATTTAACCGAAAATACCGAGTTTGAGTCCCACTTT 590

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Qy 755 -----AspileLysLysGluLeuAlaPheThyHisLysHisGlnValAs 770
Db 689 ATTACCAATTGAACCAATACCGCAAAATTTGATGNAAGTTTCTTCATTTCAAATAGT 630
Qy 770 nileLeuLeuAsnAspIleSerTyTyTySerAsnArgLeuIleLysThrGluAl 790
Db 629 -TTAATGGATGAAATGCCITAGCTACACTGACAGCGCAAAATCTCATT-----GACGG 577
Qy 790 aHisLeuSerAsnIleLeuLys-----LeuSerGlnLeuAsnLeuAs 804
Db 576 TTTTATCAACAGTGAATAAATAGGGCTATGACTTTTGTGCTGACAGCGATGAACA 517
Qy 804 nCysGluTyrllePheAspAsnHisAspSerLeuPheValLysAsnAspSer----- 822
Db 516 TTATGGATTGMAAAACTTCATCTATGATTCGGTACCAATATATGATGATCTGTTT 457
Qy 823 -----TyAlaTyMetLysLysTyTyAspValGlyMe 833
Db 456 TGGACCAAGTTTACGATTTTGAAGGAATTTTCTAAGCTTTAATAA---GATTCAAATGT 400
Qy 833 tAsnPheSerAlaLeuThrHisAspTrpIleGluLysIleAsnAlaHisProPheLys 853
Db 399 TGATTTCTGGGAATTACTAATAACCGAAGTCATATAAGTAAACCATGCGGAGCCCGTGA 340
Qy 853 sLysLeu-----IleLysThrTyPheAsnAspAsnAspLeuLysSerMe 868
Db 339 AGCAATTTGTTTACCAGATCATATTCAAGTTATTTTGTAAATTACAAACAAAATAATGT 280
Qy 868 tAsnValLysGlyAlaSerGlnGlyMetPheMetThrTyAlaLeuAlaHisGluLeuLe 888
Db 279 AAAAAGTAAGCT-----TTTGAAGATTTTGGCAAAATATTGAAGTTT 235
Qy 888 uThrIleLysGluValIleThrSerCysGlnSerIleAspSerValProGluTyAs 908
Db 234 AGATGATGTGTGAAGTCATTTGAAAATATGAACA-----GCAATGACGAAATAT-- 183
Qy 908 nThrGluAspIleTrpPheGlnPheAlaLeuLeuLysLysThrGlyHisVa 928
Db 182 -TTTGAAGATGCTGGCTTT-----AAATCAGAGATTAAT 151
Qy 928 lPheAsnLysThrSerThrLeuThrTyMetProTrpGluArgLysLeuGlnTrp 946
Db 150 TTTTGAC-----ACAGTAAAGAGAGTGG 126

RESULT 4
CL696206
LOCUS
DEFINITION
CL696206 807 bp DNA linear GSS 10-JUL-2004
PRI018b_G12.2 - PRI018b.BR (807) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION
VERSION CL696206.1 GI:50218114
KEYWORDS GSS.
SOURCE
ORGANISM Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Nemodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 807)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7

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FEATURES
source
Class: fosmid ends
Location/Qualifiers
1..807
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores: 2,25e-13 Length: 807
Pred. No.: 214,50 Matches: 63
Score: 41.54% Conservative: 50
Percent Similarity: 23.16% Mismatches: 118
Best Local Similarity: 4.20% Indels: 41
Query Match: 7
Gaps: 7
DB: 7

US-10-642-248-2 (1-972) x CL696206 (1-807)
Qy 436 IleAsnArgValProLeuValSerIleTyrlleProAlaTyAsnCysAlaAsnTyrlle 455
Db 19 ATGAACAGCACCAATAAACTTAGCCTTTTATTCCTTATATAATCGGGCGATGATTC 78
Qy 456 GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys 475
Db 79 CGCACTTGATGAAATCTTAATACGCAAACTCGACTGCTCGGAAATCATTAATTATT 138
Qy 476 AsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrlleGlyAsnAsnPro 495
Db 139 AAGATGGTTTCAACGGATATTTCTGTGAAATGACAAAGATTATTCACGAGAAATATCCG 198
Qy 496 ArgValArgIleMetSerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaVal 515
Db 199 CAGCTTCGTTGTTGTCATCAGCGAATCTGGCGCATCGTGGCGGTAATCGTGGGATT 259
Qy 516 SerPheAlaLysGlyTyrlleGlyGlnLeuAspSerAspTyrlleGluProAsp 535
Db 259 GAAGTGGCAACGGCAATATGTCGCTTTTGTGATGCTGACGATGAAGTCTATCCACC 318
Qy 536 AlaValGluLeuCysLeuLysGluPheLeuLysAsp-----LysThrLeuAlaCysVal 553
Db 319 ATGTACGAACGCTGATGTTTTTGGCGTTAGAGGACGACCTCGACGTGGCGAGTGC--- 375
Qy 554 TyThrThrAsnArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyrlleAsnTrp 573
Db 376 -----AACGCTGACTGCTGTTTTCGTGAAACGGAGAAACCTGG 414
Qy 574 ProGluPheSerArgGluLysLeuThrAla----- 584
Db 415 CAATCCATCCCAACCGATCGCTTCTCAACCGGCGCTTAAACGGCCCGGACTGGCTG 474
Qy 585 MetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPhe 604
Db 475 CGGATGGGGCTTCTTCGCGCGCTGGACTCAGCTTGTCTGGATGGGGGTTTATCCCGT 534
Qy 605 AsnGluLysIleGluAsnAlaValAspTyrlleAspMetPheLeuLysLeuSerGluValGly 624
Db 535 GATGTTATTGTTAAAAATAACATTAATTTATTCGCGGATTACATCATCAGGATATTGTC 594
Qy 625 -----LysPheLysHisLeuAsnLysIleCysTyrlle 634
Db 595 TGGACAACAGAATTTCATGTTTAAACGGCTGCGTGGCGGATATACCGAGCAATCATATAT 654
Qy 635 AsnArgValLeuHisGlyAspAsnThrSerIleLysLysLeu----- 648
Db 655 AATATATTCTGCAT-----AATAGTCAGTGCAGTGGTTCATAGACACAGGAATAAA 708
Qy 649 GlyIleGlnLysLysAsnHisPheValValAsnGlnSerLeuAsnArgGlnGlyIle 668
Db 709 AACCTTAATTATCAACGTCACATATATTAAGATTACCCTGCTGCTGGAGAAATTAATCGA 768

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QY 669 ThrTyrTyrAsn-----TyrAspGluPhe 676
Db 769 AATTATCGCGACAAAATATGATTATCCGGAATTT 804

RESULT 5
CZ541282 832 bp DNA linear GSS 13-MAY-2005
LOCUS SRRA-aad37b05.g1 Strongyloides ratti whole genome shotgun library
DEFINITION (SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Strongyloides ratti
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoides; Strongyloidea; Strongyloides.
1 (bases 1 to 832)
Mitreva, M., McCarter, J.P., Thompson, F., Viney, M., Pape, D.,
Ritter, E., Martin, J., Wylie, T., Dante, M., Waterston, R.H.,
Clifton, S.W. and Wilson, R.
Strongyloides ratti the rat parasitic nematode
Genome Survey sequences from the rat parasitic nematode
Strongyloides ratti
Unpublished (2005)
Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@wustl.edu
Genomic DNA was provided by Fiona Thompson
(F.Thompson@bristol.ac.uk) and Mark Viney
(Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol,
UK.
Class: shotgun.
FEATURES
source
location/Qualifiers
1..832
/mol_type="genomic DNA"
/strain="Isotemale line ED321 heterogonic"
/db_xref="taxon:34506"
/dev_stage="infective larval stage (iL3)"
/lab_host="GS10"
/clone_lib="Strongyloides ratti whole genome shotgun
library (SRAAGSS 004)"
/note="Vector: pOTW13; Site 1: BstX1; Site 2: BstX1;
Strongyloides ratti genomic DNA was randomly sheared,
end-repaired and size fractionated to enrich for 2-4 kb
fragments. Genomic DNA was provided by Fiona Thompson
(F.Thompson@bristol.ac.uk) and Mark Viney
(Mark.Viney@bristol.ac.uk) at the University of Bristol,
Bristol, UK. Sequencing by Washington University Genome
Sequencing Center, St. Louis, MO."
ORIGIN
Alignment Scores:
Pred. No.: 6,89e-13 Length: 832
Score: 210.50 Matches: 67
Percent Similarity: 49.34% Conservative: 45
Best Local Similarity: 29.52% Mismatches: 60
Query Match: 4.12% Indels: 56
DB: 10 Gaps: 10
US-10-642-248-2 (1-972) x CZ541282 (1-832)

QY 423 TyrIleTyrArgLysLeuLeuProGluAspSerHisIleAsnArgValProLeuVal 442
Db 179 TATATTGTGAAAAATAC-----CAATGCTGAAGTT 211

QY 443 SerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAspSerAla 462
Db 212 TCCATCATACACCTCGTACAAATCTTCAAAATTTCTGGAGAACAAATACGCTCTGTA 271

QY 463 LeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThrAspAsn 482
Db 272 CAAAACCAGACTTTTACAGATTGGGAATGGCTGATTACAGATGACAGATCTACAGACAAT 331

QY 483 ThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIle--MetSer 501
Db 332 TCTGTAGAAATGATTGAGAAAATA-----AACGATCCGAGAAATAAAACTTTACTGTTGCA 385

QY 502 LysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGlyTyr 521
Db 386 GAAAAAACGAGGAGGAGCAGCATGCAAGAAATATTTTCAATAAAATGCTACAGGAAGA 445

QY 522 TyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCysLeu 541
Db 446 TTTATCACCTTTCTGGATGCAGATGATTTTGGGAACCAAGAAATTTCTTCAGGAA---ATG 502

QY 542 LysGluPheLeuLysAspLysThrLeuAlaCysValTyrThr-----Asn 557
Db 503 ACTGCTTTTATGAAAAATNAACACGCAGAAATTCCTACTTACTTATGCAAGATGTGAT 562

QY 558 ArgAsnValAsnPro-----AspGly 564
Db 563 GAAATTTAAAGCTTAAATTTGAAGACTTCAAGCAGATTAAGAGTACTTTTCGATAAT 622

QY 565 -----SerLeuIleAlaAsnGlyTyrAsn----- 572
Db 623 TTATTAAAAACCTGCCGCTCTCTTTTATTATCTTCTATGATGATTTTAAAGAGTGGGT 682

QY 573 -----TrpProGluPheSerArgGlu-LysLeu----- 581
Db 683 ATAGATATATTTCCCGGAAGGAAGTAAACGTAAGATCATGTAATGTGGCTCAATTTGGTC 742

QY 582 -ThrThrAlaMetIleAlaHisPheArgMetPheThr---IleArgAlaTrpHisLe 600
Db 743 AAAAAATTTCCCGGTGGGAACCACTTCCGAAACATGACAAATAATACAGGA-ATGCACGC 801

QY 600 uThrAspGlyPheAsnGlu 606
Db 802 AACAAAGTGGTTTCCAGAA 820

RESULT 6
LOCUS CL673825 773 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0110c C05.2 - PRI0110c.BR (773) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL673825
VERSION CL673825.1 GI:50176112
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS 1 (bases 1 to 773)
TITLE Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
1468147
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: 17
Class: fosmid ends.
Location/Qualifiers
1..773
FEATURES
source

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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 1.55e-12 Length: 773
Score: 207.00 Matches: 65
Percent Similarity: 39.34% Conservative: 42
Best Local Similarity: 23.90% Mismatches: 111
Query Match: 4.05% Indels: 54
DB: 10 Gaps: 7

US-10-642-248-2 (1-972) x CL673825 (1-773)
QY 436 IleAsnArgValProLeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIle 455
Db 18 ATGAACAGCAGCAATAAATAGTGTATTATTCGGTTATATATCGCGCGATGATTC 77
QY 456 GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys 475
Db 78 CGCACTTGATGGAATCTTAAATACGCAACCTGGACTGCTCTGGGAATCATATTATT 137
QY 476 AsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnPro 495
Db 138 AACGATGGTTCAACGGGATAATCTGTTGAATAGCAAAATATTACGCAGAAACTATCCG 197
QY 496 ArgValArgIleMetSerLysProAsnGlyIleAlaSerAlaSerAlaAlaVal 515
Db 198 CACGTTGTTTGTGCATCAGGCGAATGCTGGCGCATCGGTGGCGGTAAATCGTGGGATT 257
QY 516 SerPheAlaLysGlyTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAsp 535
Db 258 GAAGTGGCAACGGCAATATGCTTTGTCGATGCTGACCATGAGTCTATCCACC 317
QY 536 AlaValGluLeuCysLeuLysGluPheLeuLysAsp-----LysThrLeuAlaCysVal 553
Db 318 ATGTACGAAACGCTGATGACCATGGCGTTAGAGACGACCTCGACGTGGCGCAGTGC--- 374
QY 554 TyrThrThrAsnArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyr 573
Db 375 -----AACGTCGACTGTTGTTTCGTGAAACGGGAGAAACCTGG 413
QY 574 ProGluPheSerArgGluLysLeuThrAla-----LysPheLysHisLeuAsnLysIleCysTyr 584
Db 414 CAATCCATCCCAACCGATCGCTTCGCTCAACGGCGTCTTAACCGCGCGGACTGGCTG 473
QY 585 MetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPhe 604
Db 474 CGGATGGGGCTTCTTCGCGCGGTGGACTCAGCTTCTCGATGGGGGTTTATCGCGGT 533
QY 605 AsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeuSerGluValGly 624
Db 534 GATGTTATTCTTAAAAATAACATTAAATTTATTTCGCGGATTATCATCATCAGGATATTGTC 593
QY 625 -----LysPheLysHisLeuAsnLysIleCysTyr 634
Db 594 TGGACAACAGAAATTCATGTTTAACGGCTCGTGGCGGATATACCGGCAATCATATTAT 653
QY 635 AsnArgValLeuHisGlyAspAsnThrSerIleLysLysLeuGlyIleGlnLysAsn 654
Db 654 AAATATTATTCGCAAT-----AATACGTCACTGAGTCG----- 686
QY 655 HisPheValValAsnGlnSerLeuAsnArgGlnIleThrTyrTyrAsnTyrAsp 674
Db 687 -----TTGCATAGACAAAGGGAATAAAAAACCTTAATTAT--- 719
QY 675 GluPheAspAspLeuAspGluSerArgLysTyrIle 686
Db 675 -----
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Db 720 -----CAACGTCACATATT 734

RESULT 7
CL677451/c
LOCUS
DEFINITION
CL677451 720 bp DNA linear GSS 09-JUL-2004
PRI0120b.D10.2 - PRI0120b.BR (720) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.

ACCESSION
VERSION CL677451.1 GI:50183459
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 720)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
JOURNAL
PUBMED
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..720
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

FEATURES
source
1..720
ORIGIN
Alignment Scores:
Pred. No.: 6.87e-12 Length: 720
Score: 201.00 Matches: 45
Percent Similarity: 47.30% Conservative: 25
Best Local Similarity: 30.41% Mismatches: 68
Query Match: 3.94% Indels: 10
DB: 10 Gaps: 2

US-10-642-248-2 (1-972) x CL677451 (1-720)
QY 436 IleAsnArgValProLeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIle 455
Db 509 ATGAACAGCAGCAATAAATAGTGTATTATTCGGTTATATATCGCGCGATGATTC 450
QY 456 GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys 475
Db 449 CGCACTTGATGGAATCTTAAATACGCAACCTGGACTGCTCGGAAATCATATTATT 390
QY 476 AsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnPro 495
Db 389 AACGATGGTTCAACGGGATAATCTGTTGAATAGCAAAAGTATTATTCACGAGAAACTATCCG 330
QY 496 ArgValArgIleMetSerLysProAsnGlyIleAlaSerAlaSerAlaAlaVal 515
Db 329 CACGTTCTGTTTGTGATCAGCGCATCGTGGCGCATCGTGGCGGTAAATCGTGGGATT 270
QY 516 SerPheAlaLysGlyTyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAsp 535
Db 269 GAAGTGGCAACGGGCAATATGTCGCTTTTGTGATGCTGACGATGAAGTCTATCCACC 210
```

```

QY 536 AlavalGluLeuCysLeuLysGluPheLeuLysAasp-----LysThrLeuAlaCysVal 553
Db 209 ATGTACGAACGCTGATGACCATGCGCTTATAGAGCAGACCTCGCGGCGCAGTGC--- 153
QY 554 TyrThrThrAsnArgAsnValAsnProAspGlySerLeuLeuAlaAsnGlyTyrAsnTrp 573
Db 152 -----AACGCTGACTGCTGTTTTCGTGAAACGGGAGAAACCTGG 114
QY 574 ProGluPheSerArgGluLysLeu 581
Db 113 CAATCCATCCCCACCGATCGCCTT 90

RESULT 8
CL652986 742 bp DNA linear GSS 09-JUL-2004
LOCUS PRI0116b.D06 - PRI0116b.B21 (742) Mixed stage fosmid library of P.
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL652986 GI:50131764
VERSION CL652986
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 742)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppAD8: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raif.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..742
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

FEATURES
source
Location/Qualifiers
1..829
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 7,228-12 Length: 742
Score: 201.00 Matches: 45
Percent Similarity: 47.30% Conservative: 25
Best Local Similarity: 30.41% Mismatches: 68
Query Match: 3.94% Indels: 10
DB: 10 Gaps: 2

US-10-642-248-2 (1-972) x CL652986 (1-742)

QY 436 IleAsnArgValProLeuValSerIleTyrProAlaTyrAsnCysAlaAsnTyrIle 455
Db 145 ATGAACAGCAGCAACAACTAGTGTATTATTCGTTATATGCGGCGCATGATTC 204
QY 456 GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys 475
Db 205 CGCACTTGATGAACTCTTAAATACGCAACCTGGACTGCTCTGGAATCATATTATT 264
QY 476 AsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnPro 495

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```

Db 265 AACGATGGTTCAACGGATAATTCTGTGAAATAGCAAAAGTATTACGAGAAAACACTATCCG 324
QY 496 ArgValArgIleMetSerLysProAsnGlyGlyIleAlaSerAlaSerAlaValAlaVal 515
Db 325 CAGTTTCGTTTGTTCATCAGCGAATGCTGGCGCATCGTGCGGTAAATCGTGGGATT 384
QY 516 SerPheAlaLysGlyTyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAsp 535
Db 385 GAAGTGGCAACGGCAAAATATGTCGCTTTTGTGATGCTGACGATGAAGTCTATCCACC 444
QY 536 AlavalGluLeuCysLeuLysGluPheLeuLysAasp-----LysThrLeuAlaCysVal 553
Db 445 ATGTACGAACGCTGATGACCATGCGCTTATAGAGCAGACCTCGCGGCGCAGTGC--- 501
QY 554 TyrThrThrAsnArgAsnValAsnProAspGlySerLeuLeuAlaAsnGlyTyrAsnTrp 573
Db 502 -----AACGCTGACTGCTGTTTTCGTGAAACGGGAGAAACCTGG 540
QY 574 ProGluPheSerArgGluLysLeu 581
Db 541 CAATCCATCCCCACCGATCGCCTT 564

RESULT 9
CL683612 829 bp DNA linear GSS 09-JUL-2004
LOCUS PRI0137b.E11.2 - PRI0137b.BR (829) Mixed stage fosmid library of P.
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL683612 GI:50191365
VERSION CL683612
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 829)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppAD8: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raif.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..829
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

FEATURES
source
Location/Qualifiers
1..829
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 8,678-12 Length: 829
Score: 201.00 Matches: 45
Percent Similarity: 47.30% Conservative: 25
Best Local Similarity: 30.41% Mismatches: 68
Query Match: 3.94% Indels: 10
DB: 10 Gaps: 2

US-10-642-248-2 (1-972) x CL683612 (1-829)

```

Qy 436 IleAsnArgValProLeuValSerIleTyrIleProAlaTyrAenCysAlaAenTyrIle 455  
 Db 564 ATGACAGCACCATAAATAGTGTATTATTCGTTATATATATGCGGCGATGATTC 505  
 Qy 456 GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys 475  
 Db 504 CGCAGTGTATGGAATCTTTAATTACGCAACCTGGAGCTGCTCTGGAATCATTTATT 445  
 Qy 476 AsnAspGlySerThrAspAenThrLeuGluValIleAenLysLeuTyrGlyAsnAspPro 495  
 Db 444 AACGATGTTCAACGGATAATCTTGTGTAATAGCAAAATGATTACGCGAGAAATATCCG 385  
 Qy 496 ArgValArgIleMetSerLysProAsnGlyIleAlaSerAlaSerAenAlaVal 515  
 Db 384 CAGCTTGTTGTGATCAGCGAATGCTGCGCCATCGGTGGCGCTAATCGTGGGATT 325  
 Qy 516 SerPheAlaLysGlyTyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAsp 535  
 Db 324 GAAGTGGCAACGGGCAATATGTCCTTTGTCGATGCTGACGATGAAGTCTATCCACC 265  
 Qy 536 AlaValGluLeuCysLeuLysGluPheLeuLysAsp-----LysThrLeuAlaCysVal 553  
 Db 264 ATGTACGAAACGCTGATGACCATGCGCTTAGAGACGACCTCGACGTGGCGCAGTGC--- 208  
 Qy 554 TyrThrThrAenArgAenValAenProAspGlySerLeuIleAlaAenGlyTyrAenTyr 573  
 Db 207 -----AACGCTGATGCTGTTTTCGTGAAACGGGAGAAACCTGG 169  
 Qy 574 ProGluPheSerArgGluLysLeu 581  
 Db 168 CAATCCATCCCCCGATCGCCTT 145

RESULT 10  
 CZ541577 841 bp DNA linear GSS 13-MAY-2005  
 LOCUS SRAA-aad39b05.g1 Strongyloides ratti whole genome shotgun library  
 DEFINITION (SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.

ACCESSION CZ541577  
 VERSION CZ541577.1 GI:64667882  
 KEYWORDS GSS.

SOURCE Strongyloides ratti  
 ORGANISM Strongyloides ratti  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 Panagrolaimoidea; Strongyloidea; Strongyloides.

REFERENCE 1. (bases 1 to 841)  
 Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D.,  
 Ritter,E., Martin,J., Wylie,T., Dante,M., Waterston,R.H.,  
 Clifton,S.W. and Wilson,R.

TITLE Genome Survey sequences from the rat parasitic nematode  
 Strongyloides ratti

JOURNAL Unpublished (2005)  
 COMMENT Contact: Mitreva M  
 Washington University in St. Louis  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: nematode@watson.wustl.edu  
 Genomic DNA was provided by Fiona Thompson  
 (F.Thompson@bristol.ac.uk) and Mark Viney  
 (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol,  
 UK.

Class: shotgun.  
 Location/Qualifiers  
 1. .841  
 /organism="Strongyloides ratti"  
 /mol\_type="genomic DNA"  
 /strain="isofemale line ED321 heterogonic"  
 /db\_xref="taxon:34506"  
 /dev\_stage="infective larval stage (iL3)"  
 /lab\_host="GS10"  
 /clone\_lib="Strongyloides ratti whole genome shotgun  
 library (SRAAGSS 004)"

FEATURES  
 source

/note="Vector: pOTW13; Site 1: BatX1; Site 2: BatX1;  
 Strongyloides ratti genomic DNA was randomly sheared,  
 end-repaired and size fractionated to enrich for 2-4 kb  
 fragments. Genomic DNA was provided by Fiona Thompson  
 (F.Thompson@bristol.ac.uk) and Mark Viney  
 (Mark.Viney@bristol.ac.uk) at the University of Bristol,  
 Bristol, UK. Sequencing by Washington University Genome  
 Sequencing Center, St. Louis, MO."

## ORIGIN

Alignment Scores: 2,26e-11 Length: 841  
 Pred. No.: 197,50 Matches: 48  
 Score: 56,55% Conservative: 34  
 Percent Similarity: 56,55% Mismatches: 46  
 Best Local Similarity: 33,10% Indels: 17  
 Query Match: 3,87% Gaps: 5  
 DB: 10

US-10-642-248-2 (1-972) x CZ541577 (1-841)

Qy 423 TyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAenArgValProLeuVal 442  
 Db 179 TATATTTGTAATAAATAC-----CAAAATGCGCTGAAGTT 211  
 Qy 443 SerIleTyrIleProAlaTyrAenCysAlaAenTyrIleGlnArgCysValAspSerAla 462  
 Db 212 TCCATCATTTACCCCTGCTACAATTTCTCACAATTTCTGGAATAACAATAAGCTGTGA 271  
 Qy 463 LeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThrAspAen 482  
 Db 272 CTAAACCAACTTTTACAGATTTGGGAATGCGTGTATACAGATCAGATCTACAGACAAT 331  
 Qy 483 ThrLeuGluValIleAenLysLeuTyrGlyAsnAsnProArgValArgIle---MetSer 501  
 Db 332 TCTGTGTAATGATGTAATAATA-----AACGATCCGAGATAAACTTACTGTTGCA 385  
 Qy 502 LysProAsnGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGlyTyr 521  
 Db 386 GAAAAAACGGAGGACGACATGCAAGAAATATTTTCATTAATAAATGCTACAGGAAGA 445  
 Qy 522 TyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCysLeu 541  
 Db 446 TTTATCACCTTTCTGCGATGCGATGATTTTGGGAACCAAGAAATTTCTTCAAGAA---ATG 502  
 Qy 542 LysGluPheLeuLysAspLysThrLeuAlaCysValTyrThr-----Asn 557  
 Db 503 ACTGCTTTTATGAAAAATCAAAACGCGAGAAATTCCTACTCTTACTTATGCAAGATGTGAT 562  
 Qy 558 ArgAsnValAenPro 562  
 Db 563 GAAAAATTTCAAGCCT 577

## RESULT 11

AI724383 475 bp mRNA linear EST 19-JUL-2000  
 LOCUS RHIZ1\_34\_H11.Y2\_A001 Rhizome1 (RHIZ1) Sorghum halepense cDNA, mRNA  
 DEFINITION sequence.

AI724383

AI724383.1 GI:5043235

VERSION

KEYWORDS

SOURCE

ORGANISM

Sorghum halepense

Sorghum halepense

1 (bases 1 to 475)

An EST database from Sorghum: Sorghum halepense rhizomes

Unpublished (2000)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.

Cordonnier-Pratt,M.-M., Gingle,A., Pratt,L.H. and Paterson,A.  
 An EST database from Sorghum: Sorghum halepense rhizomes

[illegible]

```

Db      191  -----:::|||||-----TCCTGGTTAGCCCTATCTACTGGCCAGAGAAAT 159
Qy      560  ValAsnProAspGlySerLeuIleAlaAsn-----GlyTyrAsnTTP 573
Db      158  ATT-----ATTATAGGAAGACCGCTAATTACTCATGG 126

RESULT 13
BH861035/c
LOCUS      655 bp      DNA      linear      GSS 12-FEB-2003
DEFINITION
312 Listeria monocytogenes pUC18 library Listeria monocytogenes
genomic clone 10-63 similar to CDP-glycerol (gct)-Listeria
monocytogenes, genomic survey sequence.
ACCESSION
BH861035
VERSION    BH861035.1 GI:28317965
KEYWORDS   GSS.
SOURCE     Listeria monocytogenes
ORGANISM   Listeria monocytogenes
REFERENCE  1 (bases 1 to 655)
AUTHORS    Call,D.R., Borucki,M.K. and Besseer,T.E.
TITLE      Mixed-genome microarrays reveal multiple serotype and
lineage-specific differences among strains of Listeria
monocytogenes
JOURNAL    J. Clin. Microbiol. 41 (2), 632-639 (2003)
PUBMED     12574259
COMMENT    Contact: Monica Borucki
Animal Disease Research Unit
USDA-ARS
3003 ADBF, WSU, Pullman, WA 99164, USA
Tel: 509 335 7407
Fax: 509 335 8328
Email: mborucki@vetmed.wsu.edu
PCR Primers
FORWARD: M13F
BACKWARD: M13R
Insert Length: 655 Std Error: 0.00
Seq primer: M13F, M13R
Class: plasmid ends.
FEATURES   Location/Qualifiers
source     1..655
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            /mol_type="genomic DNA"
            /strain="multiple"
            /db_xref="taxon:1639"
            /clone="10-63"
            /notes="Vector: pUC18; Shotgun library prepared by Amplicon
Express (Pullman, WA)"
ORIGIN
Alignment Scores:
Pred. No.: 1.9e-10 Length: 655
Score: 188.00 Matches: 37
Percent Similarity: 67.12% Conservative: 12
Best Local Similarity: 50.68% Mismatches: 22
Query Match: 3.68% Indels: 2
DB: 9 Gaps: 1

US-10-642-248-2 (1-972) x BH861035 (1-655)
Qy      440  ProLeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysVal 459
Db      236  CCTTTAGTAGTGAATTATTCAGTTTATAATAGTAGAAGATGTCACAAACGCTGTTG 177
Qy      460  AspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySer 479
Db      176  GATTTCAGTTCTTGAGCAACATATCATCAACCTCGAAGTTATCGTAGTATATGATGGAGCG 117
Qy      480  ThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIle 499
Db      116  ACTGATAATTTCAGTAAAGTCATAAAAGTATCTCAGATAAT-----CGAATTCGTTAT 63

US-10-642-248-2 (1-972) x CJ414912 (1-724)
Qy      500  MetSerLysProAsnGlyGlyIleAlaSerAlaSerAsn 512
Db      62  TTTRAAAGAAATGCGGACAGCTACTGCCCCGAAT 24

RESULT 14
CJ414912
LOCUS      724 bp      mRNA      linear      EST 21-JUN-2005
DEFINITION
Molgula tectiformis cDNA clone mclv020a11 5', mRNA sequence.
ACCESSION
CJ414912
VERSION    CJ414912.1 GI:68107179
KEYWORDS   EST.
SOURCE     Molgula tectiformis
ORGANISM   Molgula tectiformis
REFERENCE  1 (bases 1 to 724)
AUTHORS    Gyoja,F., Satou,Y. and Satoh,N.
TITLE      Expressed genes in Molgula tectiformis
JOURNAL    Unpublished (2005)
COMMENT    Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
When you want to obtain this EST clone, please send an e-mail to
Nori Satoh (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka
Satou (yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES   Location/Qualifiers
source     1..724
            /organism="Molgula tectiformis"
            /mol_type="mRNA"
            /db_xref="taxon:30286"
            /clone="mclv020a11"
            /tissue_type="whole animal"
            /dev_stage="larva"
            /clone_lib="Molgula tectiformis unpublished cDNA library,
larva"
ORIGIN
Alignment Scores:
Pred. No.: 7.45e-10 Length: 724
Score: 185.50 Matches: 63
Percent Similarity: 40.32% Conservative: 37
Best Local Similarity: 25.40% Mismatches: 77
Query Match: 3.59% Indels: 71
DB: 7 Gaps: 9

US-10-642-248-2 (1-972) x CJ414912 (1-724)
Qy      442  ValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAspSer 461
Db      38  GTATCTATTATATTACTCTCTACAAATGCGAAAGATGGCTAGAGAGTCTTTGGCTTCA 97
Qy      462  AlaLeuAsnGlnThrValVal---AspLeuGluValCysIleCysAsnAspGlySerThr 480
Db      98  ATATATTCTCAAAACCTACCAAGGATCCATGGAACTATGTATCTACACGATTGTAGTACT 157
Qy      481  AspAsnThrLeuGluValIleAsn-----LysLeuTyrGlyAsnAsnProArg 496
Db      158  GATAATTCCTTACAAATTTTGGAAAGCTGGACAAATTAAGTTAGAGGATAAAACATTAAA 217
Qy      497  ValArgIleMetSerLysProAsn-----GlyGlyIleAlaSerAlaSerAsn 512
Db      218  GTTGTGTGCTGACTCATATATATATTATGATGGACCATTAGTGTGTTGTTATGCGAAGAT 277
Qy      513  AlaAlaValSerPheAlaLysGlyTyrTyrIleGlyGlnLeuAspSerAspAspTyrLeu 532
Db      278  AGAGCAGTCCGAATCAAGCAGTGGTGAATATTATTTATGTTTGTGGACAGTGTATGATCTT 337
Qy      533  GluProAspAlaValGluLeuCysLeuLysGluPheLeuLysAspLysThrLeuAlaCys 552

```

Db	338	ATGCCCAATCGCATAGAACTGCAAAATGGAAGCTGCTTTGGCATGCCGTAGCAATACTATT	397
Qy	553	ValTyrThrThrAsnArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyrAsn	572
Db	398	ATTGGGCACA	418
Qy	573	TTPProGluPheSerArgGluLysLeuThr	588
Db	419	GAACCCGCCCAACTCAACACAGATACACAAAATGGATCAACACACTAACACCTGCACAA	478
Qy	583	-----ThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTTPHisLeu	600
Db	479	CTATACACACAAATGTACACTTCACATGGAGCCCACTGTAGTCATGCCCAACTTGGTTTATG	538
Qy	601	ThrAspGlyPheAsnGluLysIleGluAsnAlaVal	612
Db	539	-----CATAAAAATGTTACATAAGTGTGTGCATTTCTGAAGCTGGAAAG	586
Qy	613	-----AspTyrAspMetPheLeuLysLeuSerGluValGly	624
Db	587	GGAACACGGGAAGACTATCTCTTTTAAATCATTTAAACCTGGTGGAAACCTACAT	646
Qy	625	-----LysPheLysHisLeuAsnLysIleCysTyrAsnArgVal	637
Db	647	AGAGTANACCATGTTTACTAAAGTATCGACAT	679
Qy	638	LeuHisGlyAspAsnThrSerIle	645
Db	680	---CATGCAACGGCTACTAGTCTA	700

RESULT 15  
CL680585/c  
LOCUS  
DEFINITION  
CL680585 468 bp DNA linear GSS 09-JUL-2004  
PRI0129D\_BR (468) Mixed stage fosmid library of *P.  
pacificus* var. *California* *Pristionchus pacificus* genomic, genomic  
survey sequence.

**FEATURES**  
**SOURCE**

## ORIGIN

**Alignment Scores:**

Pred. No.:	5,99e-09	Length:	468
Score:	173.00	Matches:	40
Percent Similarity:	46.27%	Conservative:	22
Best Local Similarity:	29.85%	Mismatches:	62
Query Match:	3.39%	Indels:	10
DB:	10	Gaps:	2

US-10-642-248-2 (1-972) x CL680585 (1-468)

	Qy	450	AsnCysAlaAsnTyrlleGlnAArgCysValAspSerAlaLeuAenGlnThrValValAasp	466
	Dd	467	AATCGGGAGATGATTTCGCACACTTGATGAATCTTTAAATACCAACCCTGGACTGCT	408
	Qy	470	LeuGluValCysIleCysAsnAspGlySerThrAspaEnthrLeuGluValileAsnLys	489
	Dd	407	CTGGAATCATTAATAAACGATGGTTCACGGTAATCTGTGTGAATAGCAAAGTAA	348
	Qy	490	LeuTyGlyAsnAsnPraArgValArgIleMetSerLysProAsnNGlyGlyIlealaSer	509
	Dd	347	TACGCAGAAAACATAATCCGCGTTTCGTTGTGTCATCAGCGGAATCTCGGCCATCGGTG	288
	Qy	510	AlaSerAsnAlaLaValSerPheAlaLysGlyTyTyrlleGlyGlnLeuAspSerAap	529
	Dd	287	GCGCGTAATCGTGGGATTGAAGTGGCACGGGCAAAATATGCTGCTTTTGTGATGCTGAC	228
	Qy	530	AspTyrlleuGluPurAspAlaValGlulLeuCysLeuLysGluPheLeuLysAap-----	547
	Dd	227	GATCAAGTCTATATCCCAACATGTACGAACCGCTGATGACCATGCGGCTTAGAGACGACNCTA	168
	Qy	548	LysThrLeuAlaCysValTyThrThraAsnArgAsnValAsnProAspGlySerLeulle	567
	Dd	167	GACGTGGCGCAGTGC-----AACCGTGCAGTGGTGTTCGT	132
	Qy	568	AlaAsnGlyTyTrAsnTrpProGluPheSerArgGluLysLeu	581
	Dd	131	GAACCGGAGAAACCTGGCAATCATATCCCAACCGATCGCCTT	90

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Job time : 7697 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 8, 2006, 13:05:42 ; Search time 1191 Seconds  
(without alignments)  
5439.195 Million cell updates/sec

Title: US-10-642-248-2  
Perfect score: 5108  
Sequence: 1 MNTLSQAIKAYNSNDYQLAL.....SAKRGENIPVKNFIINSITL 972

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -ENDS=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10642248 @CGN 1.1.1096 @runat\_06012006\_125009\_26862 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 21.\*

- 1: geneseqn1980s.\*
- 2: geneseqn1990s.\*
- 3: geneseqn2000s.\*
- 4: geneseqn2001as.\*
- 5: geneseqn2001bs.\*
- 6: geneseqn2002as.\*
- 7: geneseqn2002bs.\*
- 8: geneseqn2003as.\*
- 9: geneseqn2003bs.\*
- 10: geneseqn2003cs.\*
- 11: geneseqn2003ds.\*
- 12: geneseqn2004as.\*
- 13: geneseqn2004bs.\*
- 14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5104	99.9	2916	9 ABT44090	Abt44090 Pasteurel
2	5104	99.9	2937	2 AAX58857	Aax58857 Pasteurel
3	5104	99.9	2917	3 AAZ35589	Aaz35589 P. multoc
4	5104	99.9	2937	10 ADC77478	Adc77478 Pasteurel

5	5104	99.9	2937	10	ADD93325	Add93925 Pasteurel
6	4502.5	88.1	2979	6	ABA05098	Aba05098 Pasteurel
7	4502.5	88.1	2979	11	ADP75650	Adp75650 Pasteurel
8	4502.5	88.1	2979	14	AEA04966	Aea04966 Chondroit
9	4490.5	87.9	2979	3	AAA27449	Aaa27449 P. multoc
10	4490.5	87.9	2979	6	ABA05097	Aba05097 Pasteurel
11	4490.5	87.9	2979	11	ADP75667	Adp75667 Pasteurel
12	3964	77.6	2271	11	ADP75668	Adp75668 Pasteurel
13	3705	72.5	2136	11	ADP75698	Adp75698 Pasteurel
14	3697	72.4	2112	14	AEA04964	Aea04964 Hyaluron
15	3693	72.3	2112	3	AAA27448	Aaa27448 P. multoc
16	3693	72.3	2112	11	ADP75718	Adp75718 Pasteurel
17	3690	72.2	2112	11	ADP75692	Adp75692 Pasteurel
18	3690	72.2	2112	11	ADP75693	Adp75693 Pasteurel
19	3689	72.2	2112	11	ADP75665	Adp75665 Pasteurel
20	3689	72.2	2112	11	ADP75695	Adp75695 Pasteurel
21	3689	72.2	2112	11	ADP75680	Adp75680 Pasteurel
22	3689	72.2	2112	11	ADP75689	Adp75689 Pasteurel
23	3689	72.2	2112	11	ADP75663	Adp75663 Pasteurel
24	3689	72.2	2112	11	ADP75687	Adp75687 Pasteurel
25	3689	72.2	2112	11	ADP75683	Adp75683 Pasteurel
26	3688	72.2	2112	11	ADP75658	Adp75658 Pasteurel
27	3688	72.2	2112	11	ADP75681	Adp75681 Pasteurel
28	3688	72.2	2112	11	ADP75684	Adp75684 Pasteurel
29	3688	72.2	2112	11	ADP75686	Adp75686 Pasteurel
30	3688	72.2	2112	11	ADP75694	Adp75694 Pasteurel
31	3688	72.2	2112	11	ADP75696	Adp75696 Pasteurel
32	3688	72.2	2112	11	ADP75690	Adp75690 Pasteurel
33	3688	72.2	2112	11	ADP75659	Adp75659 Pasteurel
34	3686	72.2	2112	11	ADP75664	Adp75664 Pasteurel
35	3686	72.2	2112	11	ADP75682	Adp75682 Pasteurel
36	3686	72.2	2112	11	ADP75688	Adp75688 Pasteurel
37	3686	72.2	2112	11	ADP75666	Adp75666 Pasteurel
38	3686	72.2	2112	11	ADP75691	Adp75691 Pasteurel
39	3686	72.2	2112	11	ADP75697	Adp75697 Pasteurel
40	3684	72.1	2112	11	ADP75685	Adp75685 Pasteurel
41	3607	70.6	2061	11	ADP75679	Adp75679 Pasteurel
42	3506	68.6	2007	11	ADP75678	Adp75678 Pasteurel
43	3471	68.0	1980	11	ADP75674	Adp75674 Pasteurel
44	3414	66.8	1953	11	ADP75657	Adp75657 Pasteurel
45	3336	65.3	1902	11	ADP75675	Adp75675 Pasteurel

ALIGNMENTS

RESULT 1  
ABT44090  
ID ABT44090 standard; DNA; 2916 BP.

XX

AC ABT44090;

XX

DT 17-OCT-2003 (first entry)

XX

DE Pasteurella multocida hyaluronan synthase DNA.

XX

KW Hyaluronic acid; glycosaminoglycan; hyaluronan synthase; antirheumatic;

KW UDP-glucose 6-dehydrogenase; UDP-glucose pyrophosphorylase; orthopaedic;

KW UDP-N-acetylglucosamine; ophthalmological; dermatological; joint surgery;

KW eye; rheumatology; dermatology; adhesion; development; cell motility;

KW cancer; angiogenesis; wound healing; ds; gene.

XX

OS Pasteurella multocida.

XX

PN WO2003054163-A2.

XX

PD 03-JUL-2003.

XX

PF 20-DEC-2002; 2002WO-US041067.

XX

PR 21-DEC-2001; 2001US-0342644P.

XX

PA (NOVO ) NOVOZYMES BIOTECH INC.

XX

PI Sloma A, Behr R, Widner W, Tang M, Sternberg D, Brown S;  
 XX WPI; 2003-559139/52.  
 DR P-PSDB; ABJ72189.  
 XX  
 PT Producing a hyaluronic acid (e.g. for use in eye and joint surgery,  
 PT orthopedics, rheumatology or dermatology) comprises cultivating a  
 PT Bacillus host cell and recovering the hyaluronic acid from the  
 PT cultivation medium.  
 XX  
 XX Claim 132; Page 186-190; 218pp; English.  
 XX  
 CC The invention relates to a novel method which comprises producing a  
 CC hyaluronic acid via cultivating a Bacillus host cell under conditions  
 CC suitable for production of the hyaluronic acid and subsequently  
 CC recovering the hyaluronic acid from the cultivation medium. The most  
 CC abundant heteropolysaccharides of the body are the glycosaminoglycans, of  
 CC which hyaluronic acid is an example. A number of enzymes are involved in  
 CC the biosynthesis of hyaluronic acid including hyaluronan synthase, UDP-  
 CC glucose 6-dehydrogenase, UDP-glucose pyrophosphorylase and UDP-N-  
 CC acetylglucosamine. The molecules of the invention demonstrate  
 CC ophthalmological, antirheumatic and dermatological activities, whilst the  
 CC method itself may be useful for producing a hyaluronan in a recombinant  
 CC host cell. The hyaluronan generated may be used in eye and joint surgery,  
 CC orthopaedics, rheumatology or dermatology and may exhibit further uses  
 CC within the fields of adhesion, development, cell motility, cancer,  
 CC angiogenesis and wound healing. The current sequence is that of the DNA  
 CC of the invention which encodes a protein that plays a role in the  
 CC synthesis of hyaluronic acid  
 XX  
 SQ Sequence 2916 BP; 1067 A; 481 C; 506 G; 862 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 2916  
 Score: 5104.00 Matches: 971  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.90% Mismatches: 0  
 Query Match: 99.92% Indels: 0  
 DB: 9 Gaps: 0

US-10-642-248-2 (1-972) x ABT44090 (1-2916)

Qy 1 MetAsnThrLeuSerGlnAlaIleuSerAsnSerAsnAspTyrGlnLeuAlaLeu 20  
 Db 1 ATGAATATCATTTATCACAAGCAATTAAGACATATTAACAGCAATGATCAATTAAGCACT 60  
 Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
 Db 61 AAATATTTGNAAGTTCGGCGGAATCTATGGACGGAAATTTGTTGAATTTCAATTTACC 120  
 Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
 Db 121 AAATGCCAAGAAAGAACTCTCAGCACATCTTCTGTTAATTCAGCACATCTTCTGTAAAT 180  
 Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
 Db 181 AAAGAAGAAAAGTCAATGTTTGGCGATGTCGTTAGATATTGCAACACCACTGTTACTT 240  
 Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100  
 Db 241 TCCACGTTAAATAATTTAGTACTTTCTGACTCGGAAGAAAACACGTTTAAATAATTAATGG 300  
 Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
 Db 301 AAATGTCTACTGAGAGAAATCTGAAATTCGCGAGGTAGAGCGTTCGCTTGTACCA 360  
 Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
 Db 361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
 Qy 141 TrpTyrLysLysArgLysValArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160  
 Db 421 TGGTACAAAAGCGAAAGAAAGACTTTGGCAATAAAACCTGAAACATCAACATGTTGGTCTT 480

Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleuSerIleThrIleuAlaCysLeu 180  
 Db 481 TCTATTATCGTTTACAACATTTCAATCACCAGCAATTTTATCGATTACATTAGCTGTGTTA 540  
 Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
 Db 541 GTAAACAAAACAAACACATTTACCGTTTGAAGTTATCGTGCAGATGATGTTAGTACAGAA 600  
 Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
 Db 601 GATCTATCACCAGATCATTCGCCAATATGAAATAAATTCGATATTCGCTACGTCAGACAA 660  
 Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetClyLeuArgLeuAlaLysTyr 240  
 Db 661 AAAGATAACCGTTTTCACGCCAGTCGCTCGGAATATGCGATTAGCGTTAGCAAAATAT 720  
 Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
 Db 721 GACTTTATGGCTTACTCGACTGTGATATGGCCCAATCCATATGGGTTCATTCTTAT 780  
 Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
 Db 781 GTTGCAGAGCTATTAGAACGATGATGATTAACAATCATTTGGTCCAAGAAAATACATCGAT 840  
 Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
 Db 841 ACACAACATATTGACCCAAAGACTTCTTAAATTAACGCGAGTTTGTCTGTAATCATTAACA 900  
 Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
 Db 901 GAAGTGAACCAATTAATAGTGTTCGCCAAAGGGGAGGAACAGTTTCTCTGGATTGG 960  
 Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
 Db 961 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCCTTCCGTTTT 1020  
 Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrTrpLeuAsnLysSerGlyPhePheAsp 360  
 Db 1021 TTTGCGCGGGTAAATGTTGCTTTTCGTTAAAAAATGGCTAAATAATCCCGGTTCTTTTGAT 1080  
 Qy 361 GluGluPheAsnHisTyrGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
 Db 1081 GAGAAATTTAATCCTCGGGTGGAGAGATGCGAATTTGGATATCGCTTATTTCCGTTAC 1140  
 Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
 Db 1141 GGTAGTTTCTTTAAACTATTGATGCAATTTATGGCTTACCATCAAGAGCCACCAGGTAAA 1200  
 Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
 Db 1201 GAAAAATGAACCGATCGTGAAGCGGAAAAAATATTACGCTGATATTATGAGAGAAAAG 1260  
 Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
 Db 1261 GTCCCTTATATCTATGAGAAACITTTTACCANTAGAGATTCGCATATCAATAGATACCT 1320  
 Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
 Db 1321 TTAGTTTCAATTTATATCCAGCTTATTAACGTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
 Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
 Db 1381 AGTGCATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA 1440  
 Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
 Db 1441 GATAATACCTTAGAAGTATCAATAGCTTTTATGGTAATAATCTTAGGGTAGCATCATG 1500  
 Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
 Db 1501 TCTAAACCAATGCGGAATAGCTTCAGCATCAATGACCGCTTCTTTTGTCTTAAAGGT 1560

Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1561 TATTACATTGGCGCAGTTAGATTTCAGATGATTATCTTTGAGCCTGATGCAAGTTGAACCTGTGT 1620  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
Db 1621 TTTAAAGAAATTTTAAAGAGATAAAACGCTAGCTGTGTGTTTATACCACTAAATAGAAAACGTC 1680  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580  
Db 1681 AATCCGATGAGTGTAAATCGCTAATGTTTACAAATGGCCAGAAATTTTCACGAGAAAA 1740  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaThrPheLeu 600  
Db 1741 CTCACACGGCTATGATTGCTCACCACTTTAGAAATGTTTACAGATTAGAGCTTGGCATTTA 1800  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1801 ACTGATGATTCAAATGAAAAAATTTGAAAAATGCGTAGACTATGACATGTTCTCTCAAACTC 1860  
Qy 621 SerGluValGlyPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGGTATTACATGCT 1920  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660  
Db 1921 GATAACACATCAATTAAGAACTTGGCATTCAAAAGAAAACCAATTTTGTGTAGTCAAT 1980  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680  
Db 1981 CAGTCATTAATAGACAAGGCATACTTATTATATAATTATGACGAATTTGATGATTTAGAT 2040  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluLysIleAspIleLeu 700  
Db 2041 GAAAGTAGAAGATATATTTTCAATAAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2100  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2101 AAAGATATTAATAATCATCCAGAAATAAGATGCAAAATCGCAGTCAGTATTTTATATCC 2160  
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Db 2161 AATACATTAAACGGCTTAGTGAATAAACTAAACAATATTTTGAATATAATAAAAAATATA 2220  
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Db 2221 TTCGTTATTGTTCTACATGTTGATGAATATCATCTTTACACCAAGATATCAAAAAAGAAATA 2280  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
Db 2281 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAATAATAGATATCTCATATTAC 2340  
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2341 ACGAGTATAGATTAATAAAAACTGAGCGGCATTTAAGTAATATTAATAAATAAAGTCAG 2400  
Qy 801 LeuAsnLeuAsnCysGluTyrIleLysPheAspAsnHisAspSerLeuPheValLysAsn 820  
Db 2401 TTTAAATCTAAATTTGTGAATACATCATCTTTTGTAAATCATGACAGCCTATTCGTTAAAAAT 2460  
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Db 2461 GACAGCTATGCTTATATGAATAAATAATGATGCGCATGAAATTTCTCAGCATTAAACAT 2520  
Qy 841 AspTyrIleGluLysIleAsnAlaHisProPheLysLeuLeuLysThrTyrPhe 860  
Db 2521 GATTGATCGAGAAATCAATGGCATCCACCATTTAAAAAGCTCATTAATAAACTTATTTT 2580  
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2581 AATGACAAATGACTTAAAAAGTATGAATGTCAAGGGGCATCAAGGTATGTTTATGAGC 2640  
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900

Db 2641 TATCGCGTAGCGCATGAGCTTCTGACCATTTATTAAGAAGTCATCACATCTTGCAGTCA 2700  
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuLeuIle 920  
Db 2701 ATTGATAGTGTGCCAGAAATATACACTGAGGATATTTGGTTCCAATTTGCACATTTAATC 2760  
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940  
Db 2761 TTAGAAAAAGAAAACCGCCCATGTATTTAATAAAAAACATCGACCTGACTTATATGCTTTGG 2820  
Qy 941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Db 2821 GAACGNAAAATTTACAAATGGACAAATGAACAAATTTGAAAGTGCNAAGAGGAGAAATATA 2880  
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Db 2881 CCTGTTAAAGTTTCATTTATTAATAGTATAACTCTA 2916  
RESULT 2  
AAx58857  
ID AAx58857 standard; DNA; 2937 BP.  
XX AAx58857;  
AC AAx58857;  
XX  
XX 16-AUG-1999 (first entry)  
XX  
XX Pasteurella multocida hyaluronate synthase pmHAS DNA.  
XX  
XX Hyaluronate synthase; pmHAS; hyaluronic acid; hyaluronan; ss.  
XX  
XX Pasteurella multocida.  
XX  
XX Key Location/Qualifiers  
FH 19..2937  
FT CDS /\*tag= a  
XX  
XX WO9923227-A2.  
XX  
XX 14-MAY-1999.  
XX  
XX 30-OCT-1998; 98WO-US023153.  
XX  
XX 31-OCT-1997; 97US-0064435P.  
XX  
XX 26-OCT-1998; 98US-00178851.  
XX  
XX (OKLA ) UNIV OKLAHOMA STATE.  
XX  
XX Weigel PH, Kumari K, Deangelis P;  
XX  
XX WPI: 1999-337486/28.  
XX  
XX P-PSDB; AAY06212.  
XX  
XX Nucleic acid encoding hyaluronate synthase for production of hyaluronic acid with controlled molecular weight and targeting specificity.  
XX  
XX Disclosure; Page 123-125; 125pp; English.  
XX  
XX This DNA sequence codes for the hyaluronate synthase (pmHAS, see AAY06212) of Pasteurella multocida Carter type A. The pmHAS enzyme has different kinetic optima with respect to pH and metal ion dependence, and different Km values compared with the HAS enzymes of Streptococcus equisimilis (see AAY06206) and Streptococcus pyogenes. Km values are about 2- to 3-fold higher. The invention provides recombinant vectors containing hyaluronate synthase DNA, especially S. equisimilis hyaluronate synthase DNA (see AAX58841), and prokaryotic or eukaryotic host cells which produce the enzyme and its hyaluronic acid product, particularly a product with modified structure or molecular size. The hyaluronic acid produced this way is purer than that produced by conventional methods  
XX  
XX Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

## Alignment Scores:

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Pred. No.: 0 Length: 2937
Score: 5104.00 Matches: 971
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.92% Indels: 0
DB: 2 Gaps: 0

US-10-642-248-2 (1-972) x AAX58857 (1-2937)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 19 ATGAATACATTTATCACAGCAATAAAGCAATATAACAGCAATGACTATCAATTAGCACTC 78
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 79 AAATTATTGAAAGTCGGCGAAATCTATGGACGGAAATTTGTTGAATTTCAAAATPACC 138
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 139 AAATGCCAGGAAATCTCTAGCAATCCCTCTCTGTTAAATTCAGCAATCTTTCTGTAAT 198
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeu 80
Db 199 AAAGAAGAAAGTCAATGTTTGGATAGTCGTTAGATATTGCAACACAACTGTTACTT 258
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100
Db 259 TCCAAACGTAAATAAATTAGTACTTTCTGACTCGGAGGAAACACGTTTAAAAAATAAATGG 318
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 319 AAATGTCTCACTGAGAGAAATCTGAAATTCGGAGGTAAGAGCGGTTCGCTTGTACCA 378
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 379 AAAGATTTCCCAAGATCTGTTTACGGCTTTACCTGATCATGTTAATGATTTTACA 438
Qy 141 TrpTyrLysLysArgLysLysArgGluGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 439 TGGTACAAAAGCGAAAGAAAGACTTGGCATATAAAACCTGAACATCAACATGTTGGTCTT 498
Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 499 TCTATTATCGTTACACATTCATCGACCAATTTATTCGATTACATGACCTGTTTA 558
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 559 GTAAACCAAAAACACATTTACCGCTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 619 GATCTATCACCGATCATTCGCAATATGAAATAAATTTGGATATTTCGCTACGTACAGCAA 678
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 679 AAAGATACCGGTTTTCAGCCAGTCCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 738
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrPvalHisSerTyr 260
Db 739 GACTTTATGGCTTACTCGACTGTGATATGCGCCAAATCCATTTATGGTTTCATCTTAT 798
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db 799 GTTCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGTTCCAGAAATAATACATCAT 858
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro 300
Db 859 ACAACAACATATGACCCAAAAGACTCTTTAAATACCGAGTTTGTCTGGAATCAATACCA 918
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320
Db 919 GAAGTGAAACCAATAATAGTGTTCGCGCAAAAGGGGAAGGAACAGTTTCTCTCGATTGG 978
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Qy 321 AtqLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 979 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCCTTTCCGTTT 1038
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPhePheAsp 360
Db 1039 TTTGCGCGGGTAATGTTGCTTTGCTAAAAAATGCTAAATATAATCCGCTTTCTTTGAT 1098
Qy 361 GluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1099 GAGGAATTTAAATCACTCGGGTGGAGAAGATGTGAAATTTGGATATCGCTTATTTCCGTTAC 1158
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1159 GGTAGTTCCTTTTAAACTATTGATGGCATTTAGCCCTACCATCAGAGCCACCGGTAAA 1218
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db 1219 GAAATGAAACCGATCGTGAAGCGGAAAAATATATTACGCTCGATATTATGAGAGAAAG 1278
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTTCGATATCAATAGAGTACCT 1338
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1339 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTTCAACGTTCCGTAGAT 1398
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1399 AGTGCATCGATCAGACTGTTGTTGATCTCGAGTTTGTATTGTTAACGATGTTCAACA 1458
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1459 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAACTCTAGGGTACGCATCATG 1518
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 1519 TCTAAACCAAAATGGCGAATAGCTCAGCATCAATTCGACCCGCTTCTTTTGTCTAAAGGT 1578
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1579 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCTCGATGTCAGTTGAACGTGT 1638
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560
Db 1639 TTAAGAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1698
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580
Db 1699 AATCCGATGGTAGCTTAATCGCTAATGGTTACATTTGGCCAGAAATTTCCAGAGAAAAA 1758
Qy 581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTyrHisLeu 600
Db 1759 CTCACAAACGCTATGATGCTCACCCTTTAGAAATGTTACAGATTAGAGCTTGGCATTTA 1818
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1819 ACTGATGATTTCAATGAAAAATTTGAAATGCGGTAGCTATGACATGTTTCTCTCAAACTC 1878
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1879 AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT 1938
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660
Db 1939 GATACACATCAATTAAGAACTTGGCAATTCAAAGAAAAACCAATTTTGTGTAGTCAAT 1998
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
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Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2119 AAAGATATTAAATCATCCAGATAAAGATGCCAAATCGCAGTCAGTATTTTATATCCC 2178
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnLeuIleGluTyrAsnLysAsnIle 740
Db 2179 AATACATTAAACGGCTTAGTGAAAAAATAAACAATATTTTGAATATAATAAAATATA 2238
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2239 TTCGTTATGTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2298
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnLeuLeuLeuLeuAsnAspIleSerTyrTyr 780
Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2358
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2359 ACGAGTAATAGATTAAATAAAACCTAGCGGCATTTAAGTAATATTAATAAATTAAGTCAG 2418
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2419 TTAATCTTAATTTGTAATACATCATTTTGTATATCATGACAGCTATTCGTTAAATAAT 2478
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2479 GACAGCTATGCTTATATGAAAAATATGATGTGCGCATGAATTTCTCAGCATTTAACACAT 2538
Qy 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2539 GATTGGATCGAGAAAAATCAATCGCATCCACCATTTAAAGAGCTCATTAAGAACTTATTTT 2598
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2599 AATGACATGACTTAAAGATGATGATGTGAAGGGGCATCACAGGTATGTTTATGAGC 2658
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSer 900
Db 2659 TATGCGTAGCGCATGAGCTTCTGACGATTATTAAGAAGTCATCACATCTTGGCCAGTCA 2718
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 2719 ATTGATAGTGTGCCAGATATATACACTGAGGATATTTGGTCCAAATTTGCACCTTTTAATC 2778
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db 2779 TTAGAAAAAGAAACCGCCCATGTATTTAATAAACAATCATGCCCTGACTTATATGCTTGG 2838
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2839 GAACGAAATTAACATGGCAAAATGAACAAATTTGAAGGTGCAAAAGAGAGAGAAATATA 2898
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## RESULT 3

AAZ35589

ID AAZ35589 standard; DNA; 2937 BP.

XX

AC AAZ35589;

XX

DT 06-AUG-2003 (revised)

DT 01-FEB-2000 (first entry)

XX

XX P. multocida hyaluronate synthase (PmHAS) nucleotide sequence.

XX Hyaluronate synthase; PmHAS; hyaluronan; hyaluronic acid; HA; cosmetic;

KW drug delivery; angiogenesis; wound healing; capsule synthesis;

KW

fowl cholera; shipping fever; ss.  
Pasteurella multocida.

Key Location/Qualifiers  
CDS 19..2937  
/\*tag= a  
/product= "PmHAS"  
/note= "Hyaluronate synthase"

KW WO9951265-A1.

XX

XX 14-OCT-1999.

XX

XX 01-APR-1999; 99WO-US007289.

XX

XX 02-APR-1998; 98US-0080414P.

XX

XX 26-OCT-1998; 98US-00178851.

XX (OKLA ) UNIV OKLAHOMA.

XX

XX Deangelis P;

XX

XX WPI; 2000-013032/01.

XX

XX P-PSDB; AAY43099.

XX

New isolated hyaluronate synthase nucleic acids, used for the production of hyaluronic acid, for developing antibiotics and vaccines and for diagnostic applications.

XX Claim 3; Page 113-114; 121pp; English.

XX

This is the Pasteurella multocida hyaluronate synthase (PmHAS) nucleic acid sequence. Hyaluronate acid (HA) or hyaluronan, is a polysaccharide that serves both structural and recognition roles in higher animals. Bacteria produce extracellular capsules of HA which mimic their host HA and aid escape from a host immune response. The invention includes a vector containing the PmHAS nucleotide sequence which can be used to express PmHAS in a foreign host. The HS nucleic acids can be used for production of HA. Also, specific changes to the HS coding sequence can result in the production of HA having a modified size distribution or structural configuration and functional properties. The HA products can be used in e.g. drug delivery, angiogenesis and wound healing. The HS nucleic acids can also be used to develop agents to block capsule synthesis by pathogens and act as antibiotics. The avirulent P. multocida strains can be used as vaccines for fowl cholera or shipping fever. (Updated on 06-AUG-2003 to correct OS field.)

XX Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 0 Length: 2937  
Score: 5104.00 Matches: 971  
Percent Similarity: 100.00% Conservativeness: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 99.92% Indels: 0  
DB: 3 Gaps: 0

US-10-642-248-2 (1-972) x AAZ35589 (1-2937)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20

Db 19 ATGATATACATTATCACAGCAATAAAAGCATATAACAGCAATGACTATCATATTAGCACTC 78

Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40

Db 79 AAAATTATTTGAAAAAGTCGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAATACC 138

Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60

Db 139 AAATGCCAAGAAAAAACTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTTCTGTAAT 198

Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 199 AAGAAGAAAAGTCAATGTTTGGATAGTCGCTAGATATTGCAACACAACTGTTACTT 258  
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
Db 259 TCCAACGTAAAAAATTTAGTACTTTCTGACTCGCGAAAAAACACGTTAAAAAATAAATGG 318  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValAlaValAlaLeuValPro 120  
Db 319 AAATTGCTCATCTGAGAGAGAAATCTGAAAATCGCGAGGTAAAGCGCTCGCCCTTGTACCA 378  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 379 AAAGATTTTCCCAAGATCTGGTTTTAGCGCTTTTACCCTGATCAATGTTAATGATTTTACA 438  
Qy 141 TrpTrpLysLysArgLysLysArgLeuGluGluLysProGluHisGlnHisValGluLys 160  
Db 439 TGGTACAAAAAGCGAAGAAAAGACTTGGCATAAAACCTGAACATCAACATGTTGGTCTT 498  
Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 499 TCTATTATCGTTACAACATTCATCGACCAACAAATTTTATCGATTTACATTAGCGCTGTTA 558  
Qy 181 ValAsnGlnLysThrHisTrpProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 559 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTACAGATGATGGTAGTCAGGAA 618  
Qy 201 AspLeuSerProIleIleArgGlnTrpGluAsnLysLeuAspIleArgTrpValArgGln 220  
Db 619 GATCTATCACCGATCATTCGCCATATGAAAATAAATTTGGATTTCCGTACGTCAGACAA 678  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTrp 240  
Db 679 AAAGATAACGGTTTTCAAGCCAGTCGCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 738  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTrp 260  
Db 739 GACTTTTATGGCTTACTCGACTGTGATGTCGCGCAAAATCCATTTATGGGTTTCATCTTAT 798  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTrpIleAsp 280  
Db 799 GTTGCAGAGCTATTAGAAGATGATGATTAACATCATTTGCTCCAGAGAAATACATCGAT 858  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 859 ACACAACATATTGACCCAAAAGACTTCTTAAATAACGCGAGTTTGTGTTGAATCATTACCA 918  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 919 GAAGTGAACCAATAATAGTTGTGCGCGAAGAGGGGAAGAACAGTTTCTCTGGATTGG 978  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 979 CGCTTAGACAAATTCGAAAAACAGAAAATCTCGCTTATCCGATTCGCTTCCGTTTT 1038  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPheAsp 360  
Db 1039 TTTGCGCGGGTAATGTTGCTTTCGCTAAAAAATGGCTAAATAATCCGGTTTTCTTTGAT 1098  
Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTrpArgLeuPheArgTrp 380  
Db 1099 GAGGAATTTAATCACTGGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGCTTAC 1158  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTrpHisGlnGluProProGlyLys 400  
Db 1159 GGTAGTTTCTTTAAAACTATTGATGGCATTTATGCTTACCATTCAAGGCCACCAAGTAAA 1218  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1219 GAAAATGAAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG 1278  
Qy 421 ValProTrpIleTrpArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440

Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCDAATAGAAGATTCGCATATCAATAGATACCT 1338  
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Db 1339 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGCTCGTAGAT 1398  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1399 AGTGCACCTGAATCAGACTGTTGTGATCTCGAGGTTTGTATTGTACGATGGTTCAACA 1458  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTrpGlyAsnAsnProArgValArgIleMet 500  
Db 1459 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCTTAGGGTAGCATCATG 1518  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1519 TCTAAACCAAAATGGCGAATAGCTCAGCATCAAAATGCGAGCCGTTCTTTTGTCTAAAGGT 1578  
Qy 521 TrpTrpIleGlyGlnLeuAspSerAspAspTrpLeuGluProAspAlaValGluLeuCys 540  
Db 1579 TATTACATTTGGGCGAGTTAGATTCCAGATGATTTATCTTGAGCCTGATGCGATTGAACCTGT 1638  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTrpThrThrAsnArgAsnVal 560  
Db 1639 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAAGTC 1698  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTrpAsnTrpProGluPheSerArgGluLys 580  
Db 1699 AATCCGGATGGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTCCAGAGAAAA 1758  
Qy 581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1759 CTCACAACGCGCTATGATGCTCACCACTTTAGAAATGTTACAGATTAGAGCTTGGCATTTA 1818  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTrpAspMetPheLeuLysLeu 620  
Db 1819 ACTGATGGATTCAATGAAAATAATGAAAATCGCGTAGACTATGACATGTTCTCTCAAACTC 1878  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTrpAsnArgValLeuHisGly 640  
Db 1879 AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTATAACCGCTGTATTACATGGT 1938  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1939 GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAT 1998  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTrpTrpAsnTrpAspGluPheAspAspLeuAsp 680  
Db 1999 CAGTCATTAAATAGACAGCGCATAACTTATTATAATATGACCAATTTTGATGATTTAGAT 2058  
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Db 2119 AAAGATATTAAAAATCATCCAGAAATAAGATGCCAAAATCGCAATTCAGTCAGTATTTTATATCCC 2178  
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Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Db 2239 TTCGTTATTGTTCTACATGTTGATAAGAAATCATCTTACACACAGATATCAAAAAAGAAATA 2298  
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Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800

Db 2359 ACGAGTAATAGATTAAATAAAACCTGAGCGCATTTTAAGTAATATTAATAAAATTAAGTCAG 2418

Qy 801 LeuAenLeuAenCysGluTyrIleIlePheAenHisAaspSerLeuPheValIysAen 820

Db 2419 TTAATCTAAATTTGTAATACATCATTTTGTATATCATGACAGCCTATTCTGTAAATAAT 2478

Qy 821 AapSerTyrAlaTyrMetIysLysTyrAapValGlyMetAenPheSerAlaLeuThrHis 840

Db 2479 GACAGCTATGCTTATATGAAATAATATGATGTCGCGCATGAAATTTCTCAGCATTAACACAT 2538

Qy 841 AapTrpIleGluLysIleAenAlaHisProPheLysLysLysLeuIleLysThrTyrPhe 860

Db 2539 GATTGCATCGAGAAAATCAATGCGCATCCACCATTAAAAAGCTCATTTAAATTTATTTT 2598

Qy 861 AenAapAenAapLeuLysSerMetAenValIysGlyAlaSerGlnGlyMetPheMetThr 880

Db 2599 AATGCAATGACTTAAAGATATGAATGTGAAGGGGCATCAAGGATGTTTATGACG 2658

Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900

Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTTAAGAAGTCATCACATCTTGCCAGTCA 2718

Qy 901 IleAapSerValProGluTyrAenThrGluAapIleTyrPheGlnPheAlaLeuLeuLe 920

Db 2719 ATTGATAGTGTCCAGAAATATAACACTGAGGATATTGTGTTCCAAATTTGCACTTTTAATC 2778

Qy 921 LeuGluLysLysThrGlyHisValPheAenLysThrSerThrLeuThrTyrMetProTrp 940

Db 2779 TTAGAAAAGAAAACCGGCATCTATTATTAATAAACATCGACCTGACTTATATGCTTGG 2838

Qy 941 GluArgLysLeuGlnTrpThrAenGluGlnIleGluSerAlaLysArgGlyGluAenIle 960

Db 2839 GAACGAAATTAACATGGAATATGAACAAATTAAGTGCATAAAGAGGAGAAATATA 2898

Qy 961 ProValAenLysPheIleIleAenSerIleThrLeu 972

Db 2899 CCGTTTAAACAAGTTTCAATTATTAATAGTATAACTCTA 2934

RESULT 4

ID ADC77478 standard; DNA; 2937 BP.

AC ADC77478;

XX 01-JAN-2004 (first entry)

XX Pasteurella multocida hyaluronate synthase (HAS) gene sequence.

DE hyaluronate synthase; HAS; streptococcal infection;

KW streptococcal bacteria; phagocytic cell; foreign microorganism;

KW polysaccharide capsule; hyaluronic acid capsule; HA capsule;

KW antibacterial compound; bacterial infection; gene; ds.

XX Pasteurella multocida.

XX Key Location/Qualifiers

FT CDS 19..2937

FT /\*tag= a

FT /product= "Pasteurella multocida hyaluronate synthase"

XX US2003092118-A1.

XX 15-MAY-2003.

XX 13-JUN-2002; 2002US-00172527.

XX 31-OCT-1997; 97US-0064435P.

PR 26-OCT-1998; 98US-00178851.

PR 21-DEC-1999; 99US-00469200.

PR 13-JUN-2001; 2001US-0297744P.

PR 13-JUN-2001; 2001US-0297788P.

XX (DEAN/) DEANGELIS P L.

PA (WEIG/) WEIGEL P H.

PA (KUMARI/) KUMARI K.

XX Deangelis PL, Weigel PH, Kumari K;

XX WPI; 2003-755179/71.

DR P-PSDB; ADC77479.

XX Recombinant host cell is a Bacillus cell comprising a recombinant vector

PT having purified nucleic acid segment with a coding region encoding

PT enzymatically active hyaluronan synthase.

XX Claim 106; SEQ ID NO 9; 79pp; English.

XX This invention relates to a recombinant Bacillus host cell containing a

CC recombinant vector including a nucleic acid segment with a coding region

CC encoding enzymatically active hyaluronate synthase (HAS), where the

CC coding region is under control of a promoter. The incidence of

CC streptococcal infections is a major health and economic problem

CC worldwide. Streptococcal bacteria can grow undetected by the body's

CC phagocytic cells which are responsible for recognising and engulfing

CC foreign microorganisms. One way the bacteria evades these cells is by

CC coating themselves with polysaccharide capsules, such as a hyaluronic

CC acid (HA) capsule. As HA is non-immunogenic, the encapsulated bacteria do

CC not illicit an immune response. The present invention provides a means of

CC preparing HA which may prove useful for the identification of novel

CC antibacterial compounds for the treatment of bacterial infection. The

CC present sequence is the DNA sequence which encodes the hyaluronate

CC synthase (HAS) of Pasteurella multocida, used in the method of the

CC invention.

XX SQ Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 2937

Score: 5104.00 Matches: 971

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.90% Mismatches: 0

Query Match: 99.92% Indels: 0

DB: 10 Gaps: 0

US-10-642-248-2 (1-972) x ADC77478 (1-2937)

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Db 19 ATGATACATTATCACAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACATC 78

Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40

Db 79 AAATTTATTTGAAAAGTCGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAAATACC 138

Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAen 60

Db 139 AAATGCCAAGAAAAAACTCTCAGCATCTCTCTGTTAATTCAGCACATCTTTCTGTAAT 198

Qy 61 LysGluGluLysValAenValCysAapSerProLeuAapIleAlaThrGlnLeuLeuLeu 80

Db 199 AAAGAAAGAAAAAGTCAATGTTTGGCATAGTCGCTTAGATATTGCAACACAACTGTACTIT 258

Qy 81 SerAenValLysLysLeuValLeuSerAapSerGluLysAenThrLeuLysAenLysTrp 100

Db 259 TCCAAACGTAATAAAAAATTAGTACTTCTTGACTCGGAAAAAAACACGTTAAAAATAAATGG 318

Qy 101 LysLeuLeuThrGluLysLysSerGluAenAlaGluValArgAlaValAlaLeuValPro 120

Db 319 AAATTTGCTCACAGAGAAATCTGAAAAATGCGAGGTGAAGACGGTCCGCCCTTTGATCCA 378

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Db 499 TCTATTATCGTTACAACATCAATCGACCGCAATTTTATCGATTACATTAGCCTGTTTA 558  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 559 GTAAACCAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 619 GATCTATCACCGATCAATCGCCATATGAAATTAATTTGGATATTCGCTACGTCAGACAA 678  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 679 AAAGATAACGGTTTCAAGCCAGTGCCTCGGAATATGGGATTACGCTTAGCAAAATAT 738  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
Db 739 GACTTTATGGCTTACTCGACTGTGATATGGCGCAATCCATTTATGGTTTCATCTTAT 798  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 799 GTTCACAGCTATTAGAAGATGATGATTTAAACATCATTTGGTCCAGAAAAATACATCGAT 858  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 859 ACACAACATATTGACCCAAAGACTTCTTAAATAACCGAGTTTGGCTTGAATCATTTACCA 918  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
Db 919 GAAGTGAACCAATAATAGTGTTCGCCCAAAAGGGGAAGAACAGTTTCTCGATTGG 978  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 979 CGCTTAGAACCAATTCGAAAAACAGAAAACTCTCGCTTATCCGATTCGCCTTTCGGTTT 1038  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPheAsp 360  
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Qy 361 GluGluPheAsnHisTrpGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1099 GAGGAATTTAATCACTCGGGTGGAGAGATGTGGAATTTGGATATCGCTTATCCGTTAC 1158  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
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Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
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Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
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Db 1699 AATCCGAGTGGTAGCTTAATCGCTAATGTTTACAATTTGGCCAGAAATTTTCACGAGAAAA 1758  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
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Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
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Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1879 AGTGAAGTTGAAAAATTTAAACATCTTAATAAAAAATCTGCTATAACCGTGTATTACATGGT 1938  
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Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluLysIleAspIleLeu 700  
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Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
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Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
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Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
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Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
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Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2359 ACAGTAAATAGATTAAATAAACTGAGCGCATTTAAGTAATATTATAATTAATTAAGTCAG 2418  
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
Db 2419 TTAATCTAAATTTGTGAATACATCATTTTTTGATAAATCATGCAGCCTTATTCGTTAAAAAT 2478  
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Db 2479 GACAGCTATCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538  
Qy 841 AspTrpIleGluLysIleAsnAlaHisProProPheLysLysLeuIleLysThrTyrPhe 860  
Db 2539 GATTGGATCGAGAAATCAATGCGCATCCACCTTTAAAAAGCTCATTTAAACTTATTTT 2598  
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2599 AATGACAAATGACTTAAAGATGAAATGTGAAAGGGGCATCACAAAGGTATGTTTATGACG 2658



QY 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
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QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
DB 979 CGCTTAGAACAAATTCGAAACACAGAAAATCTCCGCTTATCCGATTCGCTTCCTCCGTTTT 1038  
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QY 361 GluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
DB 1099 GAGGAATTTAATCACTCGGGTGGAGAAGATGTGAATTTGGATATCGCTTATTCCTGTTAC 1158  
QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
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DB 1219 GAAAAATCAAAACCGATCGTAAGCGGGAATAATATTACGCTCGATATTATGACAGAGAAAAG 1278  
QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
DB 1279 GTCCCTTATATCTATAGAAACCTTTTACCATAAGAAATTCGCATATCAATAGAGTACCT 1338  
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QY 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
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QY 501 SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
DB 1519 TCTAAACCAAAATGCGGAATAGCTCAGCATCAATGCACGCTTCTTTTGTCTAAAGGT 1578  
QY 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540  
DB 1579 TATTACATTTGGCAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCAGTTGAACCTGTG 1638  
QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
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QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrPheIleLeu 600  
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QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
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DB 2059 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2118  
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DB 2119 AAAGATATTAAATATCATCCAGATAAAGATGCCAAATCGCAGTCAGTATTTTTTATCTCC 2178  
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DB 2179 AATACATTAACCGCTTAGTGAATAAACTAAACAATATTATTCAATATAATAAATAATA 2238  
QY 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
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QY 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
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QY 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
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QY 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
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QY 841 AspTyrIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
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DB 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTAATAAAGAGTCATCACTTTCCAGTCA 2718  
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DB 2719 ATTGATAGTGTCCAGAAATATAACATGAGGATATTTGGTTCCAAATTTGCACITTTAATC 2778  
QY 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940  
DB 2779 TTAGAAAAAGAAAAACCGCCATGTATTATAATAAACATCGACCCCTGACTTATATGCTTGG 2838  
QY 941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
DB 2839 GAACGAAAAATTACAATGGACAAATGAACAAATTTGAAAGTGCAAAAAGAGGAGAAATAATA 2898  
QY 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
DB 2899 CCTGTTAACAAAGTTCAATTAATAGTATAACTCTA 2934  
RESULT 6  
ABA05098  
ID ABA05098 standard; DNA; 2979 BP.  
XX  
AC ABA05098;  
XX 22-FEB-2002 (first entry)  
XX  
DE Pasteurella multocida chondroitin synthase gene #2.  
XX

KW Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer;  
 KW eye application; joint application; moisturiser; drug delivery;  
 KW wound dressing; biocompatible film; ds.

XX Pasteurella multocida.

XX Key Location/Qualifiers  
 XX 61..2958  
 FT CDS /tag= a  
 FT /product= "chondroitin synthase"

XX WO200180810-A2.

XX 01-NOV-2001.

XX 25-APR-2001; 2001WO-US013395.

XX 25-APR-2000; 2000US-0199538P.

XX (DANG/) DE ANGELIS P L.

XX De Angelis PL;

XX WPI; 2002-049237/06.

DR P-PSDB; AAM47336.

XX New chondroitin synthase gene obtained from Pasteurella multocida, useful  
 PT as hyaluronan polysaccharide substitute in medical or cosmetic  
 PT applications, e.g. for eye or joint applications, for moisturizer or  
 PT wound dressings.

XX Claim 4; Page 120-121; 125pp; English.

XX The present invention relates to the coding sequence of the Pasteurella  
 CC multocida chondroitin synthase. A chondroitin polysaccharide may be used  
 CC as a hyaluronan polysaccharide substitute in medical or cosmetic  
 CC applications, for example in eye or joint applications, for moisturiser  
 CC or wound dressings. The enzyme may be used in covalently coupling  
 CC specific drugs, proteins or toxins to the structurally modified  
 CC chondroitin for general or targeted drug delivery or radiological  
 CC procedures, covalently cross linking the hyaluronic acid itself or to  
 CC other supports to achieve a gel or other three dimensional biomaterial  
 CC with stronger physical properties, and covalently linking hyaluronic acid  
 CC to a surface to create a biocompatible film or monolayer. The present  
 CC sequence is one version of the coding sequence of the invention

XX Sequence 2979 BP; 1130 A; 466 C; 495 G; 888 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 0 Length: 2979  
 Score: 4502.50 Matches: 845  
 Percent Similarity: 93.21% Conservative: 61  
 Best Local Similarity: 86.93% Mismatches: 59  
 Query Match: 88.15% Indels: 7  
 DB: 6 Gaps: 2

US-10-642-248-2 (1-972) x ABA05098 (1-2979)

QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
 DB 61 ATGAATACATTATACAGCAATAAAGCATATATAACAGCAATGACTATGAATTAGCACTC 120  
 QY 21 LysLeuPheGluLysSerAlaGluLeuTyrGlyArgLysIleValGluPheGlnIleThr 40  
 DB 121 AAATATTATTGAGAAGTCTCTGAAACCTACCGCGCGAAAAAATCGTTGAATTCCAAATTATC 180  
 QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
 DB 181 AAATGTAAAGAAAAAATCTC-----TCACCAATCT-----TATGTAGT 219  
 QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
 DB 220 GAAGATAAAAAAACAGTGTTCGGATAGCTCATTAGATATCGCAACACAGCTCTTACTT 279

QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
 DB 280 TCCAAACGTAAAAAATACTCTATCGAATCAGAAAAAACACAGTTTAAAAAATAAATGG 339  
 QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValAlaLeuAlaLeuValPro 120  
 DB 340 AAATCTATCTACTCGGAAAAAATCGGAGAACGAGAACTCAGAAAGGTGGAACTAGTACCC 399  
 QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
 DB 400 AAAGATTTTCTTAAAGATCTTGTCTTCCATTCAGATCATGTATGATGATTTTACA 459  
 QY 141 TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160  
 DB 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATTAAGCCTGTAATAAAGAAATATCGGTCTT 519  
 QY 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
 DB 520 TCTATTATTATTCCTACATTTAATCGTAGCCGTATTTTAGATATAAGCTTAGCTGTTG 579  
 QY 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
 DB 580 GTCATTCAGAAAAACAACTACCCATTTGAAGTCGTGTTGCAGATGATGTTAGTAAAGAA 639  
 QY 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
 DB 640 AACTTACTTACCAATGTGCAAAAAATACGAAACAACTTCACATAAAAGTAGTTAAGACA 699  
 QY 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
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 QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
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 QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
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 QY 361 GluGluPheAsnHisTrpGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
 DB 1120 GAAGAAATTTAATCATTTGGGGGGCGAAGATGTAGATTTGGTTACAGATTTATTTGCCAAA 1179  
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 DB 1180 GGCTGTTTTTTCAGAGTAATTCAGCGCGAATGGCATACCATCAAGAACCACTCGGTAAA 1239  
 QY 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
 DB 1240 GAAATGAAACAGACCGCGAAGCTGTGTAAGATTTTACGCTTAAATTTGTGAAAGAAAAG 1299  
 QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
 DB 1300 GTACCTTATCTATAGAAAGCTTTTACCAATAGAAGATTTCATATTTCATAGAATACCT 1359

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Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1420 AGTGTCTTAAATCAAACTGTTGCGATCTCGAGGTTGTATTGTTAAGTGGTTCAACA 1479
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1480 GATAAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCTTAGGGTACGCATCATG 1539
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGly 520
Db 1540 TCTAAACCAATGGCGAATAGCCTCAGCATCAAAATGACCGCTTCTTTTGTCTAAAGGT 1599
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1600 TATTACATTGGCGAGTTAGATTACAGATGATTATCTTGAGCTGATGCAAGTTGAAGTGT 1659
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Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
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Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
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Db 1960 GATPAACACATCCATTAGAATCTGGCATTCAAAGAAACCAATTTTGTGTAGTCAAT 2019
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
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Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2080 GAAAGTAGAAGTAGTATATCTTCAATAAAACCCGCTGAATATCAAGAAAGAAATGGATATTTA 2139
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2140 AAAGATCTTAAACTCATTCATAATTAAGATGCCAAATCCGACGTCAGTATTTTCTATCCC 2199
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740
Db 2200 AATACATTAACCGCTAGTGAATAAACTAAACCAATATATTGAAATATAATAAAAAATATA 2259
Qy 741 PheValIleValLeuHisValAspLysAsnHisIleLeuThrProAspIleLysGluIle 760
Db 2260 TTCGTATTATTCATACATGTTGTAAGAATCATCTTACACGAGCATCAAAAAAGAAATA 2319
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780
Db 2320 TTGGCTTTCATCATATAGCACCAAGTGAATATTTTACTAAATATATGACATCTCATATTAC 2379
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2380 ACGAGTAATAGACTAATAAAAACTGAGGCACATTTAAGTAATATTAATAAATTAAGTCAG 2439
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
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Db 2440 TTTAAATCTAAATTTGTGAATACATCATTTTGTATAATCATGACAGCCTATTTCGTTAAAAAT 2499
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2500 GACAGCTATGCTTATATGAAAAAATATGATGTCGCGATGAATTTCTCAGCATTAACACAT 2559
Qy 841 AspTrpIleGluLysIleAsnAlaHisProProPheIysLysLeuIleLysThrTyrPhe 860
Db 2560 GATTGGATCGAGAAAAATCAATGCGCATCCACCATTAAAAAGCTGATTTAAACCTATTATT 2619
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyValAsrGlnGlyMetPheMetThr 880
Db 2620 AATGACATGACTTAGAAGTATGATGCAAGGGGCATCACAAAGGTATGTTTATGAAG 2679
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2680 TATGCGCTACCGCATGAGCTTCTGCGATTTATTAAGAGTATCATCATCTGCAATCA 2739
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 2740 ATTGATAGTGTGCCGAATATATACTGAGGATATTGTTTCCAAATTTGCACATTTTAATC 2799
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940
Db 2800 TTAGAAAAGAAAACCGCCCATGTTATTTAATAAACAATCGACCTGACTTATATGCCTTG 2859
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2860 GAACGAAAAATTACAAATGGACAAATGAACAAATTCAAAGTCAAAAAAGGCGAAATATC 2919
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2920 CCCGTAAACAAGTTTCATTATTATAGTATAACGCTA 2955
RESULT 7
ID ADP75650 standard; DNA; 2979 BP.
XX AC ADP75650;
XX 12-AUG-2004 (first entry)
XX DE Pasteurella multocida chondroitin synthase coding sequence #1.
XX DE polymer production; hyaluronic acid polymer; chondroitin polymer;
XX DE chondroitin synthase; gene; ds; enzyme.
XX OS Pasteurella multocida.
XX PN WO2003029261-A2.
XX 10-APR-2003.
XX 12-JUL-2002; 2002WO-US022386.
XX 13-JUL-2001; 2001US-0305263P.
XX 22-JAN-2002; 2002US-0350642P.
XX 08-MAY-2002; 2002US-00142143.
XX (DEAN/) DEANGELIS P L.
XX Deangelis PL;
XX WPI; 2003-532558/50.
XX P-PSDB; ADP75651.
XX Producing polymer, e.g. hyaluronic acid or chondroitin polymer, by
XX providing a functional acceptor, a synthase capable of elongating the
XX acceptor and sugars such that that synthase elongates the acceptor to provide
XX polymer.
XX Claim 86; SEQ ID NO 3; 538pp; English.
PS
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XX The invention comprises a method for producing a polymer, especially a  
CC hyaluronic acid (HA) or chondroitin (CD) polymer composed of less than  
CC 150 sugars. The method involves providing a functional acceptor,  
CC providing a synthase capable of elongating the functional acceptor, and  
CC providing sugars such that the synthase elongates the functional acceptor  
CC to provide the polymer. The method of the invention is useful for  
CC producing a hyaluronic acid or chondroitin polymer composed of 1-150  
CC sugars. The present DNA sequence encodes a Pasteurella multocida  
CC chondroitin synthase of the invention.

XX  
SQ Sequence 2979 BP; 1130 A; 466 C; 495 G; 888 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 0 Length: 2979  
Score: 4502.50 Matches: 845  
Percent Similarity: 93.21% Conservations: 61  
Best Local Similarity: 86.93% Mismatches: 59  
Query Match: 88.15% Indels: 7  
DB: 11 Gaps: 2

US-10-642-248-2 (1-972) x ADP75650 (1-2979)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 61 ATGAATACATTTATCACAAGCAATAAAGCATATAACAGCAATGACTATGAATAGCACCTC 120  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 121 AAATTAATTTGAGAAGTCTGCTGAAACCTACGCGGCGAATAATCGTTGAATTCCAATATC 180  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 181 AAATGTAAGAAACATC-----TCGACCAATCT-----TATGTAAGT 219  
Qy 61 LysGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 220 GAAGATAAATAAACAAGTGTTCGATAGCTCATTAGATATCGCAACACAGCTCTTACTT 279  
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
Db 280 TCCAACGCTAAATAAATAAATTAACCTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG 339  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 340 AAATCTATCATCTGGGAAAAAATCGGAGAACCGCAAAATCAGAAAGGTGGAACTAGTACCC 399  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 400 AAAGATTTCTTAAGATCTTGCTCTGCTCCATTCGACGATCATGTTTAATGATTTTACA 459  
Qy 141 TrpTyrLysLysArgLysArgLysGluGlyLysProGluHisGlnHisValGlyLeu 160  
Db 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATATAAGCCTGTAAAGTAAAGATATCGGTCTT 519  
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 520 TCTATTATTATTCCTACATTTAATCGTAGCCGATATTTAGATATATACGTTAGCCCTGTG 579  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 580 GTCANTCAGAAAAACAACATCCCATTCGAGTCGTTGTTGCAGATGATGTTAGTAAGGAA 639  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 640 AACTTACTTACCATTGTGCAAAAAATACGAAACAAACCTTGACATAAAGTATGTAGACAA 699  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 700 AAAGATTATGGATATCAATTTGTCGACGTCAGAAACTTAGGTTTACGTACGACCAAGTAT 759  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260

Db 760 GATTTTGTCTCGATTCTAGACTCGGATATGGCACCACACAAATATATGGTTCATTCTTAT 819  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 820 CTTACAGAACCTATTAGAGACAATGATATGTTTAAATTTGGACCTAGAAAAATATGTGGAT 879  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 880 ACTCATAAATATTACCCGACAGAACAAATTCCTTAAACGATCCATATTTAAATAGAAATCACTACCT 939  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 940 GAAACCCCTACAAATACAAATCTTCGATTACATCAAAAGCAATAATATATCGTTGGATTGG 999  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 1000 AGATTAGAACATTTCAAAAAAACCAGATAATCTACGCTCTATGTGATTCCTCGCTTTTCGTTAT 1059  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
Db 1060 TTTAGTTGCGGTAAATGTTGCAATTTTCTAAAGAAATGGCTAAATAAAGTAGGTGGTTCGAT 1119  
Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1120 GAAGAATTTAATCATTCGGGGGGCGAAGATGTAGAAATTTGGTTACAGATTTATTTGCCCAA 1179  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1180 GGCTGTTTTTTCAGAGTAATTTGACGGCGGAATGGCATACCATCAAGAACCCACCTGGTAAA 1239  
Qy 401 GluAsnGluThrAspArgGluAlaGlyAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1240 GMAAATGAAACAGACCCGGAAGCTGGTAAAGTATTACGCTTAAATTTGTGAAGAAAG 1299  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAGATTCACATATTTATAGAAATACCT 1359  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1360 TTAGTTTCTATTATATCCCGCTTATACTGTGCAAAATATATTTCAAGATGTTGTAGAT 1419  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1420 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTGTTAAAGATGGTTCACA 1479  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1480 GATAATACCTTAGAAGTGAATCAATAGCTTTATGTTAAATATCTTAGGCTAGGCATCATG 1539  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1540 TCTAAACCAATGCGGAAATAGCTTCAGCATCAATGCAGCGGTTCCTTTTGTCTAAAGGT 1599  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1600 TATTATACCTGGCAGTTAGATTACAGATGATTCTTGAGCTGATGCAAGTTGCACTGTGT 1659  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
Db 1660 TTAAGAAGAAATTTTAAAGATATAACCGCTAGCTGTGTGTTTATACCCATTAATAGAACGTC 1719  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
Db 1720 AATCCGATGTTAGTCTTAATCGCTAATGTTTACAAATGGCCAGAAATTTTTCACGAGAAAA 1779  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1780 CTCACACGGCTATGATTGCTCACCATTTTAAATGTTTACGATTTAGAGCTTGGCATTTA 1839  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1840 ACCGATGGATTTAAACGAAAAATATTGAAACCGCGGGATTTATGACATGTTCTTAAACTC 1899

QY 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1900 AGTGAAGTTGGAAATTTAAACATCTTAATAAAAATCTGCTATTAACCGCGTATTACATGGT 1959  
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660  
Db 1960 GATAACACATCCATTAGAATCTCGGCATTCAAGAAGAAACCCATTTTGTGTAGTCAT 2019  
QY 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680  
Db 2020 CAGTCATTAATAGACAAGGCATCAATTAATTAATATGACAAATTTGATGATTTAGAT 2079  
QY 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
Db 2080 GAAAGTAGAAGTATATCTTTCAATAAAACCGCTGAATATCAAGAAAGAAATGGATATTTTA 2139  
QY 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2140 AAGAATCTTAACATCTCAATTAAGATGCCAAATCGCAGTCAGTATTTTCTATCCC 2199  
QY 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Db 2200 AATACATTAACCGCTTAGTGAAAAAACTAAACAATATTATTGAATATAATAAAATATA 2259  
QY 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Db 2260 TTCGTTATTATCTACATGTGTAAGAATCATCTTACACGACATCAAAAAAGAAATA 2319  
QY 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAspIleSerTyrTyr 780  
Db 2320 TTGGCTTTCTATCATAGCACCAGTGAATATTTTACTAATAATAGCATCTCATATTAC 2379  
QY 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2380 ACCAGTAATAGACTAATAAAAACTGAGGCACATTTAAGTAATATTAATAAATTAAGTCAG 2439  
QY 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
Db 2440 TTAATCTAAATTTGTGAATACATCATTTTGTGAATATCATGACAGCCCTATTTCGTTAAAAAT 2499  
QY 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Db 2500 GACAGCTATGCTTATATGAATAAATATGATGTCGGCATGAATTTCTCAGCATTTAACACAT 2559  
QY 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
Db 2560 GATTGGATCGAGAAATCAATGCGCATCCACCATTATAAAGCTGATTAAGAACTATTTT 2619  
QY 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2620 AATGACAAATGACTTAAGAGTATGAATGTGAAGGGGCATCACAGGTATGTTTATGAAG 2679  
QY 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 2680 TATGGCGTACCGATGAGCTTCTGACCATTTATTAAGAAGTCATCATCTCGCCATCA 2739  
QY 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
Db 2740 ATTGATAGTGTGCGAGAATATACACTGAGGATATTTGGTTCCCAATTTGACATTTTAATC 2799  
QY 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940  
Db 2800 TTAGAAAAAGAAACCGGCCATGTATTTAATAAAAAACATCGACCCCTGACTTATGCGCTTGG 2859  
QY 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Db 2860 GAAGGAAATTTACATCGACAAATGAACAAATTCAAAGTGCATAAAGGCGGAAATATC 2919  
QY 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Db 2920 CCGGTTAACAAGTTCTATTATTAATAGTATAACGCTA 2955

RESULT 8

AEA04966  
ID AEA04966 standard; DNA; 2979 BP.

XX AEA04966;

XX 11-AUG-2005 (first entry)

DT Chondroitin synthase, PmCS, coding sequence, SEQ ID 4.

XX Chondroitin synthase; polysaccharide; gene; ds.

XX Pasteurella multocida.

XX Key Location/Qualifiers

FT CDS 61..2958

FT /\*tag= a

FT /product= "PmCS"

PN US2005124046-A1.

XX 09-JUN-2005.

XX 16-JUL-2002; 2002US-00197153.

XX 10-NOV-1999; 99US-00437277.

XX (DEAN/) DEANGELIS P L.

XX Deangelis PL;

XX WPI; 2005-417007/42.

DR P-PSDB; AEA04965.

DR GENBANK; AF195517.

XX Elongating a functional acceptor (e.g. hyaluronic acid or chondroitin),  
PT useful in polysaccharide polymer grafting, comprises providing hyaluronic  
PT acid synthase, UDP-GlcUA and/or UDP-GlcNAc sugars to elongate the  
PT functional acceptor.

XX Disclosure; SEQ ID NO 4; 4lpp; English.

XX The present invention relates to a method for elongating a functional  
CC acceptor. The method comprises providing a hyaluronic acid (HA) synthase  
CC (PmHAS; AEA04963) capable of elongating the functional acceptor and  
CC providing UDP-GlcUA and UDP-GlcNAc sugars such that the hyaluronic acid  
CC synthase elongates the functional acceptor. PmHAS adds sugars to the  
CC nonreducing end of a growing polymer chain. The PmHAS sequence is  
CC significantly different from the other known HA synthases: there appears  
CC to be only two short potential sequence motifs (AEA04967 and AEA04968) in  
CC common between PmHAS and the other HA synthases. The method is useful in  
CC polysaccharide polymer grafting, which may be utilized in the development  
CC of biotechnological medical improvements. These may be used for producing  
CC hybrid polysaccharides or for forming polysaccharide coatings. Also  
CC disclosed is chondroitin synthase (PmCS; AEA04965) and its coding  
CC sequence (AEA04966) from Pasteurella multocida. Type A P. multocida  
CC produces a HA capsule [GlcUA-GlcNAc repeats] and possesses the PmHAS  
CC enzyme. On the other hand, Type F P. multocida produce a chondroitin or  
CC chondroitin-like polymer capsule [GlcUA-GalNAc repeats] using PmCS.  
CC Either HA or chondroitin chains can serve as acceptors for PmCS as both  
CC acceptors serve well for PmHAS.

XX SQ Sequence 2979 BP; 1130 A; 466 C; 495 G; 888 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 2979  
Score: 4502.50 Matches: 845  
Percent Similarity: 93.21% Conservative: 61  
Best Local Similarity: 86.93% Mismatches: 59  
Query Match: 88.15% Indels: 7  
DB: 14 Gaps: 2

US-10-642-248-2 (1-972) x AEA04966 (1-2979)

QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
DB 61 ATGAATACATATACAAAGCAATAAAGCAATATAACAGCAATGACTATGATTAAGTACACATC 120  
QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
DB 121 AAATTTTTCGAGAGTCTGCTGAAACCTACGGCGCAAAATCGTTGAATTCCTCAAAATATATC 180  
QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
DB 181 AAATGTAAGAAACATC-----TCGACCAATCT-----TATGTAAGT 219  
QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
DB 220 GAAGATAAATAAACAAGTGTTCGATAGCTCATAGATATCGCAACACAGCTCTTACTT 279  
QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100  
DB 280 TCCAACTGTAATAAATAAATTAACCTCTATCCGAATCGAATAAACAACAGTTTAAAAAATAAATGG 339  
QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
DB 340 AAATCTATCATCTCGGAAAAAATCGGAGAACGCAAGAAATCGAAAGGTGGAACTAGTACCC 399  
QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
DB 400 AAAGATTTCCTAAGATCTTGTCTTCCTCCATTCGAGATCAATGTTAATGATTTTACA 459  
QY 141 TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160  
DB 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATATAAGCCTGTAATAAGAAATATCGGTCTT 519  
QY 161 SerLeuLeuValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
DB 520 TCTATTATTCTTACATTTAATCGTAGCGGTATTTTAGATATAAAGCTTAGCTGTGTTG 579  
QY 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
DB 580 GTCAATCAGAAAAACAATACCTACCCATTTGNAAGCTGTGTTGAGATGATGGTAGTAAGAA 639  
QY 201 AspLeuSerProIleLeuArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
DB 640 AACTTACTTACCATGTGCAAAAATACGACAAACAACTTGACATAAAGTATGTAAGACAA 699  
QY 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
DB 700 AAAGATTATGGATATCAATTGTGTGAGTCAGAACCTTAGGTTTACGTACAGCAAAAGTAT 759  
QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
DB 760 GATTTGTCTCGATTCTAGATCGCATATGGCACCACCAAACTATATGCGGTTCATCTTAT 819  
QY 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
DB 820 CTTACAGAACTATTAGAGACAAATGATATTGTTTAAATGGACCTAGAAAATAATGTGGAT 879  
QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
DB 880 ACTCATATATATTACCGCAGAACAAATCTCTTAACGATCCATATTTAATAGAATCACTACCT 939  
QY 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
DB 940 GAAACCGCTACAAAATAACAAATCTCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 999  
QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
DB 1000 AGATTAGAACATTTCAAAAAACCGATTAATCTACGCTCTATGTGATCTCCGTTTCGTTAT 1059  
QY 341 PheAlaAlaGlyAsnValAlaPheAlaLysTyrTrpLeuAsnLysSerGlyPhePheAsp 360  
DB 1060 TTTAGTTCGGTAAATGTTGCAATTTCTAAAGAATGGCTAAATAAAGTAGGTGGTTCCGAT 1119

QY 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
DB 1120 GAAGAAATTTAAATCATTTGGGGGGCGAAGATGTAGAATTTGGTTACAGATTTATTTGCCAAA 1179  
QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
DB 1180 GGCTGTTTTTCAGAGTAATTGACGGGGAATGGCATACCATCAAGNACCACCTGGTAAA 1239  
QY 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
DB 1240 GAAAAAGAAACAGACCCGGAAGCTGGTAAAAAGTATTACGCTTAAAAATTTGTAAGAAAAAG 1299  
QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
DB 1300 GTACCTTACATCTATAGAAAGCTTTTACCCAATAGAAGATTCACATATTTCAATATACCT 1359  
QY 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
DB 1360 TTAGTTTCTATTTATATCCCGCTTATACTGTGCAAAATTTATTTCAAGATGTGTAGAT 1419  
QY 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
DB 1420 AGTCTCTTAATCAAACTGTGTGATCTCGAGTTTGTATTGTAAACGATGGTTCAACA 1479  
QY 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
DB 1480 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATAATCTTAGGGTACGCATATG 1539  
QY 501 SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
DB 1540 TCTAAACCAATGGCGGAATAGCCTCAGCATCAATGACGCCGTTTCTTTTGTAAAGGT 1599  
QY 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
DB 1600 TATTACATTGGCAGTTAGATTTCAGATGATTATCTTCAGCCTGATGCAGTTGAACCTGTGT 1659  
QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
DB 1660 TTAAGAAATTTTTTAAAGATATAAACCGTAGCTGTGTGTTTATACCACTTAATAGAAACGTC 1719  
QY 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
DB 1720 AATCCGAGTGTAGCTTAATCGCTTAATGGTTTACAAATTTGGCCAGAAATTTTCACGAGAAAA 1779  
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
DB 1780 CTCACACGGCTATGATTGCTCACCATTTTAGATGTTTACGATTAGAGCTTGGCATTTA 1839  
QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
DB 1840 ACGGATGGATTTAACGAAAAATATTGAAAAACCGCTGGATTATGACATGTTCTTTAAACCTC 1899  
QY 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysValTyrAsnArgValLeuHisGly 640  
DB 1900 AGTGAAGTTGGAAAATTTAAACATCTTAATAAATCTGCTATATAACCGGCTATTACATGGT 1959  
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
DB 1960 GATTAACATCCATTAGAAAACCTCGCATTCAAAAGAAAAAACCACTTTTGTGTAGTCAAT 2019  
QY 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
DB 2020 CAGTCATTTAAATAGCAAGGCATCAATTTATTAATATATGACAAATTTGTGATTTAGAT 2079  
QY 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
DB 2080 GAAAGTAGAAAAGTATATCTTCAATAAACCCTGAAATATCAAGAAAGAAATGGATATTTTA 2139  
QY 701 LysAspIleValIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
DB 2140 AAAGATCTTAACATCTTCAAAAATTAAGATGCCAAATGCGCAGTCAGTATTTTCTATCCC 2199  
QY 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740

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Db 2200 AATACATTAACGGCTAGTGAAGAAACCTAAACATATTTTGAATATATAAATAATA 2259
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2260 TTGGTTATTATTCATCATGTTGATAAGAAATCATCTTACACAGACATCAAAAAAGAAATA 2319
Qy 761 LeuAlaPheThrHisLysHisGlnValAsnIleLeuLeuAsnAspIleSerTyrTyr 780
Db 2320 TTGGCTTTCTATCATAGACCAAGTGAATATTTTACTAAATATGACATCTCATATATC 2379
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2380 ACGGTATATGACTATATAAATACTAGGCACATTTAAGTAAATATAATAATTAAGTCAG 2439
Qy 801 LeuAsnLeuAsnCysGluTyrIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2440 TTTAAATCTAAATGTGAATCATCATTTTGTGATAATCATGACAGCCTATTCGTTAAAAAT 2499
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2500 GACAGCTATGCTTATATGAAGAAATATGATGTCGCATGAATTTCTCAGCATTAACACAT 2559
Qy 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2560 GATTGGATCGAAGAAATCAATGCGCATCCACCATTTTAAAGCTGATTAAACCTATTTT 2619
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2620 AATGACAATGACTTAAAGAAGTATGAATGTGAAGGGGCATCACAAGGTATGTTTATGAAG 2679
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2680 TATCGCTTACGCGATGAGCTTCTGACGATTTATTAAGAAGTCATCACAATCCTCGCAATCA 2739
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuIle 920
Db 2740 ATTGATAGTGGCCAGAAATATAACACTGAGGATATTTGGTCCAAATTTGCATTTTAATC 2799
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db 2800 TTAGAAAGAAACCGGCGCATGTATTTAATAAACAATCGACCTGACTTATATGCTTGG 2859
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2860 GAACGAAATTTACAAATGGACAAATGAACAAATTCAAAGTGCAGAAAGGCGGAAATATC 2919
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2920 CCCGTTAACAAAGTTCATTTAATAGTATATACGCTA 2955

RESULT 9
AAA27449
ID AAA27449 standard; cDNA; 2979 BP.
XX
AC AAA27449;
XX
XX
DT 17-AUG-2000 (first entry)
XX
DE P. multocida chondroitin synthase coding sequence.
XX
KW Chondroitin synthase; CS; enzyme; hyaluronic acid; ulcer;
KW tissue abrasion; viscoelastic replacement; bioadhesive; ss.
XX
OS Pasteurella multocida.
XX
FH Key Location/Qualifiers
FT CDS 61..2958
FT /*tag= a
FT /product= "PmCS"
XX
XX
XX WO200027437-A2.
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PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-US026501.
XX
PR 11-NOV-1998; 98US-01079229P.
PR 01-APR-1999; 99US-00283402.
XX
PA (OKLA ) UNIV OKLAHOMA STATE.
XX
XX Deangelis PL;
XX
XX WPI; 2000-376319/32.
DR P-PSDB; AAY96213.
XX
PT Novel method for the enzymatic transfer of sugar molecules to an
PT acceptor, useful for synthesis of e.g. polysaccharide bioadhesives or
PT drug delivery systems, including hybrid molecules.
XX
PS Claim 16; Page 86; 86pp; English.
XX
CC The present sequence is the coding sequence of the Pasteurella multocida
CC chondroitin synthase PmCS. PmCS catalyses glycosaminoglycan
CC polymerisation to produce chondroitin: a linear polysaccharide which has
CC viscoelastic properties which makes it useful for a number of
CC applications. Chondroitin can be used with hyaluronic acid (HA) to coat
CC medical devices e.g. catheters and sensors to reduce tissue abrasion. In
CC addition, they can be used as bioadhesives for haemostatic sealing and
CC healing of wounds and surgical incisions; and as biomaterials that
CC provide sustained delivery of encapsulated drugs, to wounds, ulcers,
CC injuries or surgical sites
XX
SQ Sequence 2979 BP; 1129 A; 466 C; 497 G; 887 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2979
Score: 4490.50 Matches: 843
Percent Similarity: 93.11% Conservative: 62
Best Local Similarity: 86.73% Mismatches: 60
Query Match: 87.91% Indels: 7
DB: 3 Gaps: 2

US-10-642-248-2 (1-972) x AAA27449 (1-2979)
Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 61 ATGAATACATTATCACAGCAATAAAGCATATACAGCAATGACTATGAAATTTAGACTC 120
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 121 AAATTATTTGAGAAGTCTGCTGAACCTACGGCGGAAATAATCGTTGAATTTCCAAATATC 180
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 181 AAATGTAAGAAAAAATCTC-----TCGACCAATTTCT-----TATGTAAGT 219
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 220 GAAGATAAAAAAACAAGTGTTCGATAGCTATGATATCGAACACACAGCTCTTACTT 279
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db 280 TCCAAAGTAAAAAATTAATCTCTATCCGAATCAGAAAAAACAAGTTAAAAAATAAATGG 339
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 340 AAATCTCATCTCGGAAAAAATCGAGAACGAGAAATCAGAAAGGTGGAACTAGTAGTACC 399
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 400 AAAGATTTTCTTAAGATCTTGTTCCTGCTCCATTCGACATCATGTTAATGATTTTACA 459
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
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Db 460 TGGTACAAAAATCGAAAAAAGGCTTAGGTATATAAGCCGTGTAATAAGAAATATACGGTCTT 519
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 520 TCTATTATTATCTTACATTTAACTCGTAGCCGTATTTTAGATATAACGTTAGCCGTGTTG 579
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 580 GTCAATCAGAAAAACAACTACCCATTTGAAGTCGTGTTGTCAGATGATGGTAGTAAGGAA 639
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 640 AACTTACTTACCATTTGTCAAAAATACCAACAAAACTTGACATAAAGATATGTAAAGCAA 699
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 700 AAAGATTATGATATCAATTTGTGTCAGCTCAGAACTTAGGTTTACGTACAGCAAAAGTAT 759
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrIleHisSerTyr 260
Db 760 GATTTGTCTCGATTCAGATCGCATATGGCATATGGCACCACCAACAATATATGGTTCATCTTAT 819
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db 820 CTTACAGAACTATTAGAAGACAATGATATTTGTTTAAATTTGGACCTAGAAAAATATGTGGAT 879
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 880 ACTCATATATATACCGCAGAAACAATTCCTTTAACGATTCATATTTAATAGAATCACTACCT 939
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320
Db 940 GAAACCGCTCACAATAACAAATCCTTCGATATACATCAAAAGGAAATATATCGTTGGATTGG 999
Qy 321 ArgLeuGluGlnPheGlyThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 1000 AGATTAGAACATTTCAAAAAAACCGATAATCTACGCTATGTGATCTCCGTTTCGTTTAT 1059
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysTyrProLeuAsnLysSerGlyPhePheAsp 360
Db 1060 TTTTGTTCGGGGTAATGTTCATTTCTAAAGAAATCGCTAAATAAGTAGTGGTTGGTTCCGAT 1119
Qy 361 GluGluPheAsnHisTyrGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1120 GAAGAAATTTAATCATTGGGGGGCGAGAGATGTAGAAATTTGGTTACAGATTTATTCGCCAAA 1179
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1180 GCCTGTTTTTTCAGAGTAATTCAGCGCGGAATGGCCATCCATCAAGAACCACCTGGTAAA 1239
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db 1240 GAAAAATGAAACAGAACCGCAAGCTGGTAAAGATTTACGCTTTAAATTTGTGAAAGAAAAG 1299
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1300 GTACCTTACATCTATAGAAGCTTTTACCAATAGAAGATTCACATATTCATAGATACCT 1359
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1360 TTAGTTTCTATTATATCCCGCTTATTAATCTGTGCAAAATATATTTCAAAAGATGTGTAGAT 1419
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1420 AGTGCTCTTAAATCAAACTGTTGTGATCTCGAGGTTGTATTGTAAACGATGGTTCAACA 1479
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1480 GATAATACCTTAGAAGTGAATCAATAAGCTTTATGTGTAATTAATCTTAGGTAGCATCATG 1539
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 1540 TCTNAACCAAAATGGCGGATAGCCTCAGCATCAATGACGACCGCTTCTTTTGTCTAAAGGT 1599
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Db 880 ACTCATAATATTACCGCAGACAAATTCCTTAACGATCCATATTTAATAGAAATCACTACCT 939  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 940 GAAACCGCTACAAATAACAAATCCCTTCGATTAACATAAAGGAATAATATCTGTAATGG 999  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 1000 AGATTAGAACATTTCAAAACCAACCGATTAATCTACGCTCTATGATTCCTCCGTTCCGTTAT 1059  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysIleThrLeuAsnLysSerGlyPhePheAsp 360  
Db 1060 TTTGTTCGGGTAAATGTTGCATTTTCTAAAGAAATGGCTAAATAAAGTAGGTGGTTCGAT 1119  
Qy 361 GluGluPheAsnHisTrpGlyGluAspValGluPheGlyIleThrArgLeuPheArgTyr 380  
Db 1120 GAAGAATTTAATCATTTGGGGGGCGGAAGATGTAGAAATTTGGTTACAGATTATTTGCCAAA 1179  
Qy 381 GlySerPhePheLeuThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1180 GGCTGTTTTTCAGAGTAATTGACCGCGGAATGGCCATCCATCAAGAACCCCTGGTAAA 1239  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGlyLys 420  
Db 1240 GAAATGAACACAGACGCGAGCTGGTAAAGTATTACGCTTAAATAATTGTGAAGAAAG 1299  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1300 GTACCTTTACATCATAGAAAGCTTTTACCANATAGAAGATTACATATTTCATAGAAATCCT 1359  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1360 TTAGTTTCTATTATATCCCCCTTATTAACCTGTCGAAATATTATTCANAGATGTGTAGAT 1419  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1420 AGTGCTTTAATCAAACTGTTGTCGATCTCGAGGTTGTATTGTAAACGATGGTTCAACA 1479  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1480 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATTAATCCCTAGGGTACGCAATCG 1539  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1540 TCTAAACCAAAATGCGCGAATAGCTCAGCATCAATGCGAGCGGTTCTTTCTCTAAAGGT 1599  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1600 TATTACATTTGGCAGTTAGATTACAGATGATTATCTTGAGCCTGATGTCAGTTGAACCTGTGT 1659  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560  
Db 1660 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTGTGTGTTATATACCACTAATAGAAACGTC 1719  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
Db 1720 AATCCGGATGGTAGCTTAATCGCTAATGGTTACATTTGCCAGAAATTTTTCACGAGAAA 1779  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1780 CTCACAAACGGCTATGATGCTCACCACTTTTAGAATGTTTACGATTAGAGCTTGGCATTTA 1839  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1840 ACGGATGGATTTTAAACGAAATAATTGAAAACGCGCTGGATTTATGACATGTTCTCTTAAACTC 1899  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1900 AGTGAAGTTGGAATAATTTAAACATCTTAATAAAATCTGCTATTAACCGCGTATTACATGGT 1959  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1960 GATACACATCCATTAAAGAACTCGGCATTCAAAAGAAAACCACTTTTGTGTGTAGTCAAT 2019

Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Db 2020 CAGTCATTAAATAGACAAGGCATCAATATTATTAATATGACAAATTTGATGATTAGAT 2079  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
Db 2080 GAAAGTAGAAGTATATCTTCAATAAACCCTCGAATATCAAGAAGAAATCGATATGTTA 2139  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2140 AAAAGTCTTAAACTCATTTCAAAATAAGATGCCAAATCGCAGTCAGTATTTCTATCCC 2199  
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Db 2200 AATACATTTAAACGGCTAGTGAATAAATAATATTTATTTGAATATAATAAATAATA 2259  
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Db 2260 TTCGTTATTATTCTACATGTTGTAAGAATCATCTTACACCAGACATCNAANAAGAAATA 2319  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
Db 2320 TTGGCTTTCTATCATTAAGCACAAGTGNATATTTTACTAATAATATGACATCTCATATTAC 2379  
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2380 ACGAGTAATAGACTAATAAATACTGAGGCACATTTAAGTAATATTAATAAATAAAGTCA 2439  
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
Db 2440 TTAATCTTAAATTTGTGAATACATCATCTTTTGTGAATATGACAGCTATTCGTTAAATAAT 2499  
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Db 2500 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTAAACAT 2559  
Qy 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
Db 2560 GATTGGATCGAGAAATCAATCGCATCCACCATTTAAAGAGCTGATTTAAACCTATTTT 2619  
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2620 AATGCAATGACTTAAAGAGTATGAATGTGAAGGGGCATCAAGGATGTTTATGAAG 2679  
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 2680 TATGCGCTACCGCATGAGCTTCTGACGATTATTAAGAAGTCATCACATCTCTGCCAATCA 2739  
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
Db 2740 ATTGATAGTGTGCCAGAAATATAACACTGAGGATAATTTGGTTCCAATTTTGAATC 2799  
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940  
Db 2800 TTAGAAAAGAAAACCGGCATCTGATTTAATAAACAATCGACCTGACCTTATATGCTTGG 2859  
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Db 2860 GAACGAAATTTACAATGGACAATTAACAAATTCAAAGTGCANAAAAAGCGGAAATAATC 2919  
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Db 2920 CCGCTTAACAAGTTTCATTATTATTAATAGTATAACGCTA 2955

## RESULT 11

ADP75648

ID ADP75648 standard; DNA; 2979 BP.

XX ADP75648;

AC ADP75648;

XX 12-AUG-2004 (first entry)

XX



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|||||
1420 AGTGCTCTTAATCAACCTGTTGTCGATCTCGAGGTGGTATTTCTTAACGATGGTTCAACA 1479
Qy AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db GATAATACCTTTAGAAAGTGATCAATAAGCTTTTATGGTAATAATCTCTAGGGTAGCGATCATG 1539
Qy SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGly 520
Db TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAATATGACGCCGTTCTTTTGGCTAAAGGT 1599
Qy TyrTrpIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540
Db TATTACATTTGGCAGCTAGATTACAGATGATTATCTTTGAGCCTGATGCACTTGAACCTGTGT 1659
Qy LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTGTTTATACCATTAATAGAAACGTC 1719
Qy AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580
Db AATCGGATGGTAGCTTAATCGCTAATGTTTACAAATGGCCAGAAATTTTCACGAGAAAAA 1779
Qy LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db CTCACACGGCTATGATTTGCTCACCATTTTACGATTTTACGATTTAGAGCTTGGCATTTA 1839
Qy ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db ACGGATGGATTAAACGAAATATTGAAACCGCGTGGATTATGACATGCTTCTTTAAACCTC 1899
Qy SerGluValGlyIlePheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGCGTATTACATGGT 1959
Qy AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660
Db GATAACACATCCATTAAAGAACTCGGCATTCAAAGAGAAACCACTTTTGTGTAGTCAAT 2019
Qy GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db CAGTCATTAAATAGACAGGCATCAATATTATATAATTATGACAAATTTTGATGATTTAGAT 2079
Qy GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db GAAAGTAGAAGATATATCTTCAATAAAACCGCTGAATATCAAGAGAAATGGATATGTTA 2139
Qy LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db AAAGATCTTAAACTCATTCAAATAAAGATGCGAAATCGCAATCGAGTCAGTATTTCTATCCC 2199
Qy AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740
Db AATACATTAAACCGCTTAGTGAATAAACTTAAACAATATTATTGAATAATAAAAAATATA 2259
Qy PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db TTCTGTTATTATTCTCATCTGATAGAAATCATCTTTACACCAAGCATCAAAAAAGAAATA 2319
Qy LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780
Db TTGGCTTTCTATCATAGACCAAGCAAGTAATATTTTACTTAAATAATGACATCTCATATTAC 2379
Qy ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db ACGAGTAATAGACTAATAAAAACTGAGGCACATTTTAAAGTAATATTAAATAATTAAGTCAG 2439
Qy LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db TTTAAATCTAAATTTGTAATACATCATCTTTTGTGTAATCATGACGCGCTATTCGTAAAAAT 2499
Qy AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
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Db 2500 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTTCTCAGCATTAACACAT 2559
Qy AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db GATTGGATCGAGAAATCAATCGCATCCACCATTTTAAAAAGCTGATTTAAACCTATTTT 2619
Qy AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db AATGACAATGACTTAAAGAGTATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGAAG 2679
Qy TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db TATGCGCTACCGCATGAGCTTCTGACGATTATTAAAGAAGTCATCACATCTCGCAATCA 2739
Qy IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db ATTGATAGTGTGCCAGAAATATACACTGAGGATATTTGGTTCCAATTTGCACCTTTAATC 2799
Qy LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db TTGAAAAAGAAACCGGCCATGTATTTAATAAAAAACATCGACCTGACTTATATGCTTTGG 2859
Qy GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db GAACGNAATTTACAAATGACAAATGAACAATTCAAAGTGCNAAGGCGGCAAAATATC 2919
Qy ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db CCGGTTAAACAGTTTCATTTATATAGTATAACGCTA 2955

RESULT 12
ADP75667
ID ADP75667 standard; DNA; 2271 BP.
XX
AC ADP75667;
XX
DT 12-AUG-2004 (first entry)
XX
DE Pasteurella multocida truncated hyaluronidic acid synthase gene #11.
XX polymer production; hyaluronidic acid polymer; chondroitin polymer;
KW hyaluronidic acid synthase; gene; db; enzyme.
XX
OS Pasteurella multocida.
XX
FN WO2003029261-A2.
XX
PD 10-APR-2003.
XX
PF 12-JUL-2002; 2002WO-US022386.
XX
PR 13-JUL-2001; 2001US-0305263P.
PR 22-JAN-2002; 2002US-0350642P.
PR 08-MAY-2002; 2002US-00142143.
XX
PA (DEAN/) DEANGELIS P L.
XX
PI Deangelis PL;
XX
XX WPI; 2003-532559/50.
XX
DR Producing polymer, e.g. hyaluronidic acid or chondroitin polymer, by
PT providing a functional acceptor, a synthase capable of elongating the
PT acceptor and sugars such that synthase elongates the acceptor to provide
PT polymer.
XX
PS Disclosure; SEQ ID NO 20; 538pp; English.
XX
SS The invention comprises a method for producing a polymer, especially a
CC hyaluronidic acid (HA) or chondroitin (CD) polymer composed of less than
CC 150 sugars. The method involves providing a functional acceptor,
CC providing a synthase capable of elongating the functional acceptor, and
CC providing sugars such that the synthase elongates the functional acceptor
```

CC to provide the polymer. The method of the invention is useful for  
CC producing a hyaluronic acid or chondroitin polymer composed of 1-150  
CC sugars. The present DNA sequence encodes a truncated Pasteurella  
CC multocida hyaluronic acid synthase of the invention.

XX  
SQ Sequence 2271 BP; 812 A; 384 C; 404 G; 671 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 0 Length: 2271  
Score: 3964.00 Matches: 755  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.87% Mismatches: 0  
Query Match: 77.60% Indels: 0  
DB: 11 Gaps: 0

US-10-642-248-2 (1-972) x ADP75667 (1-2271)

QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
DB 1 ATGNATACATTATCACAGGCNATTAAGCATATTAACAGCAATGACTATCAATTAGCACTC 60  
QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
DB 61 AAATTATTGAAAAGTCGGCGGAATCTATGGACGGAAAATTGTTGAATTTCAAAATTACC 120  
QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
DB 121 AAATGCCAAGAAAACCTCAGCACATCTTCTGTTAAATTCAGCACATCTTCTGTAAAT 180  
QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
DB 181 AAGAAGAAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCACACAACTGTTACTT 240  
QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100  
DB 241 TCCAACTGAAAAAATTAGTACTTCTGACTCGGAAAAAACACGTTAAAAAATAAATGG 300  
QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
DB 301 AAATTGCTCATGAGAGAATACTGAAAATCGGAGGTAAGAGCGGTGCGCCCTTGTACCA 360  
QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
DB 361 AAAGATTTTCCAAAGATCTGGTTTTAGCGCCTTTACTGATCAATGTTAATGATTTTACA 420  
QY 141 TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160  
DB 421 TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAAACATCAACATGTTGGTCTT 480  
QY 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
DB 481 TCTATTATCGTTACAACATTCAAATCGACCACAAATTTTATCGATTACATTAGCCCTGTTA 540  
QY 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
DB 541 GTAAACCAAAAACACATTACCCTTTGAAAGTTATCGTGACAGATGATGGTAGTCAGAA 600  
QY 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
DB 601 GATCTATCACCGATCATTCGCCAATATGAAAATAAAATTTGGATATTCGCTACGTCAGACAA 660  
QY 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
DB 661 AAAGATAACGGTTTTCAAGCCAGTCCCGCTCGGAATATGGGATTACGCTTAGCAAAAATAT 720  
QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
DB 721 GACTTTATGGCTTACTCGACTGATATGGCGCAATCCATTTATGGTTTCATCTTAT 780  
QY 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
DB 781 GTTCAGAGCTATTAGAAGATGATGATTTAAACATCATTTGTTCCAGAAAATAATACATCAT 840

QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
DB 841 ACACAACATATTGACCCAAAGACTCTTTAAATTAACGCGAGTTTGCTTGAATCATTTACCA 900  
QY 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
DB 901 GAAAGTGAACCAATAATAGTGTTCGCGCAAAAGGGAAGGAACAGTTTCTCTGGATTGG 960  
QY 321 ArgLeuGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
DB 961 CGCTTAGAACCAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCCCTTTCCGTTTT 1020  
QY 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPhePheAsp 360  
DB 1021 TTTGCGCGGGTAATGTTGCTTTCGCTTAAATAATGGCTAATAATCCCGTTTCTTTGAT 1080  
QY 361 GluGluPheAsnHisTyrGlyGlyAspValGluPheGlyTyrArgLeuPheArgTyr 380  
DB 1081 GAGGAATTTAATCACTGGGTGGAGAAGATGCGAATTTGGATATCGCTTATTTCCGTTAC 1140  
QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
DB 1141 GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCCTACCATCAAGAGCCACCAGGTAAA 1200  
QY 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
DB 1201 GAAATGAACCCGATCGTGANGCGGGAANAATATTACGCTCGATATTATGAGAGAAAAG 1260  
QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
DB 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAGATTCGCATATCAATAGATGACCT 1320  
QY 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
DB 1321 TTAGTTTTCRAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACGTTCGCTAGAT 1380  
QY 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
DB 1381 AGTGCACTGAATCAGACTGTTGTGTGATCTCGAGGTTTGTATTGTAAACATGGTTCAACA 1440  
QY 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
DB 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATAATCCTAGGGTAGCATCATG 1500  
QY 501 SerLysProAsnGlyLysIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
DB 1501 TCTAAACCAAAATGCGGAATAGCCTCAGCATCAAAATGCAGCCGTTTCTTTTGTAAAGGT 1560  
QY 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
DB 1561 TATTACATGGCGAGTTAGATTGAGATGATTATCTTGAGCCTGATGCGATTTGAAGCTGTGT 1620  
QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560  
DB 1621 TTAAGAAGATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCCTAATAAGAAACGTC 1680  
QY 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580  
DB 1681 AATCCGAGTGGTAGCTTAATCGCTAATGTTGTGTACAAATTTGGCCAGAAATTTTCCAGGAGAAAA 1740  
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrHisLeu 600  
DB 1741 CTCACAAACGGCTATGATTGCTCACCACTTTAGAAATGTTTACGATTAGAGCTTGGCATTTA 1800  
QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
DB 1801 ACTGATGATTCATGAAGAAAATTTGAAATTTGCCGTAGACTATGACATGTTTCTCAAACTC 1860  
QY 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
DB 1861 AGTGAAGTTGGAATAATTAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1920  
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660

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Db 1921 GATAACACATCAATTAAGAACTTGGCATTCAAAGAAAAACCAATTTTGTGTAGTCAAT 1980
Qy 661 GlnSerLeuAenArgGlnGlyIleThrTyTrpSerLeuPheAspLeuAsp 680
Db 1981 CAGTCATTAAATAGACAAGGCATCACTATTATTAATATGACGAAATTTGATGATTTAGAT 2040
Qy 681 GluSerArgLysTyTrpIlePheAsnLysThrAlaGluTyTrpGlnGluGluIleAspIleLeu 700
Db 2041 GAAAGTGAAGAGTATATTTTCAATAAACCCTGATATCAAGAGAGATTTGATATCTTA 2100
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyPro 720
Db 2101 AAAGATATTAATATCAATCCAGATAAAGATGCCAAATCGCAGTCAGTATTTTATATCCC 2160
Qy 721 AsnThrLeuAenGlyLeuValLysLysLeuAsnAsnIleIleGluTyTrpAsnLysAsnIle 740
Db 2161 AATACATTAACCGCTTAGTGTAAAAAACTAAACCAATATTATTTGAATATATAAAAAATATA 2220
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIle 756
Db 2221 TTCGTTATTGTTTACATGTTGATAAGAAATCATCTTACACCGATATC 2268

RESULT 13
ID ADP75698 standard; DNA; 2136 BP.
XX
AC ADP75698;
XX
DT 12-AUG-2004 (first entry)
XX
DE Pasteurella multocida truncated hyaluronidic acid synthase gene #20.
XX
KW polymer production; hyaluronidic acid polymer; chondroitin polymer;
XX
KW hyaluronidic acid synthase; gene; da; enzyme.
XX
OS Pasteurella multocida.
XX
FN WO2003029261-A2.
XX
PD 10-APR-2003.
XX
PF 12-JUL-2002; 2002WO-US022386.
XX
PR 13-JUL-2001; 2001US-0305263P.
XX
PR 22-JAN-2002; 2002US-0350642P.
XX
PR 08-MAY-2002; 2002US-00142143.
XX
PA (DEAN/) DEANGELIS P L.
XX
PI Deangelis PL;
XX
DR WPI; 2003-532558/50.
XX
PT Producing polymer, e.g. hyaluronidic acid or chondroitin polymer, by
PT providing a functional acceptor, a synthase capable of elongating the
PT acceptor and sugars such that the synthase elongates the acceptor to provide
PT polymer.
XX
PS Disclosure; SEQ ID NO 51; 538pp; English.
XX
CC The invention comprises a method for producing a polymer, especially a
CC hyaluronidic acid (HA) or chondroitin (CD) polymer composed of less than
CC 150 sugars. The method involves providing a functional acceptor,
CC providing a synthase capable of elongating the functional acceptor, and
CC providing sugars such that the synthase elongates the functional acceptor
CC to provide the polymer. The method of the invention is useful for
CC producing a hyaluronidic acid or chondroitin polymer composed of 1-150
CC sugars. The present DNA sequence encodes a truncated Pasteurella
CC multocida hyaluronidic acid synthase of the invention.
XX
SQ Sequence 2136 BP; 754 A; 365 C; 388 G; 629 T; 0 U; 0 Other;
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Alignment Scores: 3.96e-311 Length: 2136
Pred. No.: 3705.00 Matches: 702
Percent Similarity: 99.72% Conservative: 7
Best Local Similarity: 98.73% Mismatches: 2
Query Match: 72.53% Indels: 0
DB: 11 Gaps: 0

US-10-642-248-2 (1-972) x ADP75698 (1-2136)
Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyAsnSerAsnAspTyTrpGlnLeuAlaLeu 20
Db 1 ATGAACACATATACACAGCAATATAAGCATATATAACAGCAATGACATATCAATAGCACTC 60
Qy 21 LysLeuPheGluLysSerAlaGluIleTyTrpGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AAATTAATTTTCAAAAGTCGGCGGAAATCTATGGACGGAAAAATTTGTTGAATTTCAAAATACC 120
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 121 AAATGCCAAGAAAAAATCTTCAGCACATCTCTGTTAAATTCAGCACATCTTCTGTAAT 180
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 181 AAGAAGAAAAAAGTCAATGTTTGGCATAGTCCGTTAGATATTCGCAACACAACTGTTACTT 240
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db 241 TCCAACTGAAAAAATTTAGTACTTTCTGACTCGCGAAAAAACACGCTTAAAAAATAAATGG 300
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 301 AAATTTGCTCACTGAGAAGAAAAATCTGAAATCGCGAGGTAAAGAGCGGCGCCCTTGTATCCA 360
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 361 AAAGATTTTCCCAAGATCTGGTTTTTAGCGCTTTTACCTGATCATGTGTAATGATTTTACA 420
Qy 141 TrpTyTrpLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 421 TGGTACAAAAAAGCGAAGAAAAAGACTTTGGCATAAAACCTGAAACATCAACATGTTGGTCTT 480
Qy 161 SerIleLeuValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 481 TCTATTATCGTTACAACATTCATCGACAGCAATTTTATCGATTTACATTTAGCCCTGTTTA 540
Qy 181 ValAsnGlnLysThrHisTyTrpPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTCACAGATGATGGTAGTCAGGAA 600
Qy 201 AspLeuSerProIleIleArgGlnTyTrpGluAsnLysLeuAspIleArgTyValArgGln 220
Db 601 GATCTATACCGATCATTCGCCAATATGAAATAAATTTGGATATTCGCTAGCTCAGACAA 660
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyTrp 240
Db 661 AAAGATACCGTTTTTCAAGCCAGTCCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 720
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyTrp 260
Db 721 GACTTTATTTGGCTTACTCGATGATGCGCCAAATCCATTTATGGTTTCATCTTAT 780
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyTrpIleAsp 280
Db 781 GTTGCAAGACTATTAGAGATGATGATTTTAAACATCATTTGGTCCCAAGAAAAATACATCAT 840
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 841 ACACACATATTTGACCCCAAAAGACTTCTTAAATAACGCGAGTTTCTTGAATTCATTACCA 900
Qy 301 GluValLysThrAsnAsnSerValAlaLysGlyGluGlyThrValSerLeuAspTrp 320
Db 901 GAAGTGAAAAACCAATTAATAGTGTTCGCCGAAAAAGGGAGGAAACAGTTTCTCTGGATTGG 960
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QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 961 CGCTTTAGAACAAATTCGAAATAAAACAGAAATCTCCGCTTATCCGATTCGCCCTTTCCGTTTT 1020
QY 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360
Db 1021 TTTGCGGGGGTAATGTTGCTTTTCGCTTAAAAATGGCTAAATAATCCGGTTCCTTTTGAT 1080
QY 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1081 GAGCAATTTAATCACTCGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCCGTTAC 1140
QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1141 GGTAGTTTCTTTAAACATTTGATGGCATTTATGGCTTACCATTCAAGAGCCACCCAGGTAAA 1200
QY 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db 1201 GAAATGAAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAG 1260
QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1261 GTCCCTTATATCTATAGAAAACCTTTTACCATAGAGATTCCGATATTCATAGAAATACCT 1320
QY 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1321 TTAGTTTCTATTTATATCCCGCTTTATAACTGTGCAATATATATTCAAAGATGTGTAGAT 1380
QY 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1381 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTGTACGATGGTTCACA 1440
QY 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGCTTAATAATCTTAGGGTACGCATCATG 1500
QY 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGly 520
Db 1501 TCTAAACCAATGGCGAATAGCCTCAGCATCAATAGCCGCTTCTTTTGCTTAAAGGT 1560
QY 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1561 TATTACATGGCGAGTTAGATTGAGATGATTATCTTGAGCTGTAGCTGATGAGTTGACTGTGT 1620
QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTATACCACTAATAGAAACGTC 1680
QY 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580
Db 1681 AATCCGATGGTAGCTTAATCGCTTAATGGTTACAAATGGCCAGAAATTTTCACGAGAAAAA 1740
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1741 CTCAACACGGCTATGTTGCTCACATTTTAGAATGTTTACGATTAGAGCTTGGCATTTA 1800
QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1801 ACGGATGGATTTAACGAAAAATATTGAAACCGCCGCTGGGATTATGACATGTTCTTTAAACTC 1860
QY 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAAAATCTGTATATAACCCGCTATTACATGGT 1920
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660
Db 1921 GATTAACATCTCATTAAGAACTCGGCATTCAAAGGAAAAACCAATTTTGTGTAGTCAAT 1980
QY 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 1981 CAGTCATTAATAGACAAGGCATCAATTTATTAATATTATGACAAATTTGATGATTTAGAT 2040
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QY 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeu 700
Db 2041 GAAAGTAGAAGTATATCTTCAATAAACCCTGAATATCAGAGAAATGGATATTTA 2100
QY 701 LysAspIleLysIleIleGlnAsnLysAspAla 711
Db 2101 AAAGATCTTAAACTCATTTCAGAATAAAGATGCC 2133
RESULT 14
AEA04964
ID AEA04964 standard; DNA; 2112 BP.
XX
AC AEA04964;
XX
DT 11-AUG-2005 (first entry)
XX
DE Hyaluronic acid synthase, PmHAS, coding sequence, SEQ ID 2.
XX
KW Hyaluronic acid synthase; polysaccharide; gene; ds.
XX
OS Pasteurella multocida.
XX
FH Key Location/Qualifiers
FT CDS 1..2112
FT /*tag= a
FT /product= "PmHAS"
XX
PN US2005124046-A1.
XX
OS 09-JUN-2005.
XX
PF 16-JUL-2002; 2002US-00197153.
XX
PR 10-NOV-1999; 99US-00437277.
XX
PA (DEAN/) DEANGELIS P L.
XX
PI Deangelis PL;
XX
DR WPI; 2005-417007/42.
DR P-PSDB; AEA04963.
DR GENBANK; AF036004.
XX
PT Elongating a functional acceptor (e.g. hyaluronic acid or chondroitin),
PT useful in polysaccharide polymer grafting, comprises providing hyaluronic
PT acid synthase, UDP-GlcUA and/or UDP-GlcNAc sugars to elongate the
PT functional acceptor.
XX
PS Claim 4; SEQ ID NO 2; 41pp; English.
XX
CC The present invention relates to a method for elongating a functional
CC acceptor. The method comprises providing a hyaluronic acid (HA) synthase
CC (PmHAS; AEA04963) capable of elongating the functional acceptor and
CC providing UDP-GlcUA and UDP-GlcNAc sugars such that the hyaluronic acid
CC synthase elongates the functional acceptor. PmHAS adds sugars to the
CC nonreducing end of a growing polymer chain. The PmHAS sequence is
CC significantly different from the other known HA synthases: there appears
CC to be only two short potential sequence motifs (AEA04967 and AEA04968) in
CC common between PmHAS and the other HA synthases. The method is useful in
CC polysaccharide polymer grafting, which may be utilized in the development
CC of biotechnological medical improvements. These may be used for producing
CC hybrid polysaccharides or for forming polysaccharide coatings. The
CC present sequence is the coding sequence for PmHAS.
XX
SQ Sequence 2112 BP; 746 A; 358 C; 387 G; 621 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1,93e-310 Length: 2112
Score: 3637.00 Matches: 703
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 72.38% Indels: 0
DB: 14 Gaps: 0
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US-10-642-248-2 (1-972) x ABA04964 (1-2112)

Qy 1 MetAsnThrLeuSerGlnAlaIleValAlaTyrrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 1 ATGAATACATTTATCACAGCAATTAAGCAATATACAGCAATGATCATCAATATGACACTC 60  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 61 AAATATTTGAAAGTCGGCGGAATCTATGGACGGAAATTTGTGAATTTCAAAATACC 120  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 121 AAATGCAAGAAAGAACTCTCAGCACATCTCTCTGTTAAATTCAGCACATCTTCTGTAAAT 180  
Qy 61 LysGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 181 AAAGAAGAAAGCAATGTTTGGGATAGTCCGTTAGATATTTGCAACAACTGTTACTT 240  
Qy 81 SerAsnValLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
Db 241 TCCAACTGTAAGAAATTTAGTACTTCTGACTCGGAAAGAAACACGTTAAAGAAATTAATGG 300  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValAlaAlaValAlaLeuValPro 120  
Db 301 AAATTTGCTCACTGAGAGAAATCTGAAATCGCGAGGTTAAGAGCGGTGCGCCCTTGTACCA 360  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 361 AAAGATTTTCCCAAGATCTGTTTGGGCTTTTACCTGATCATGTTTAATGATTTTACA 420  
Qy 141 TrpTyrLysLysArgLysLysArgLysGlyLysProGluHisGlnHisValGlyLeu 160  
Db 421 TGGTACAAAGCGGAAAGAAAGACTTGGCAATAAACCCTGAACATCAACATGTTGGTCTT 480  
Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 481 TCTATTATCGTTACAACTCAATCGACCAGCAATTTTATCGATTACATTAGCCCTGTTTA 540  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 541 GTAAACCAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 601 GATCTATCACCGCATCATTCGCCCAATATGAATAAATTTGGATATTTCCGTACTGTCAGCAA 660  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 661 AAAGATAACGGTTTTCAAGCCAGTCCCGTCCGAATATGGGATTACGCTTAGCAAAATAT 720  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
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Qy 261 ValAlaGluLeuLeuGluAspAspPheThrIleIleGlyProArgLysTyrIleAsp 280  
Db 781 GTTCAGAGACTATTAGAAGATGATGATTTAAACAATCATTTGGTCCCAAGAAATATACATCGAT 840  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 841 ACACAACATATTTGACCAAAAGACTTCTTAATATACCGGAGTTTGGTGAATCATTTACCA 900  
Qy 301 GluValLysThrAsnAsnSerValAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
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Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
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Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
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Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
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Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
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Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
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Qy 701 LysAspIle 703  
Db 2101 AAAGATATTT 2109

## RESULT 15

AAA27448  
ID AAA27448 standard; cDNA; 2112 BP.

XX AC  
XX AAA27448;

XX DT 17-AUG-2000 (first entry)

XX XX P.multocida hyaluronic acid synthase-D coding sequence.

XX XX Hyaluronic acid synthase-D; HAS-D; enzyme; ophthalmic surgery; cataract;  
KW arthritis; ulcer; tissue abrasion; viscoelastic replacement;  
KW hyaluronic acid production; bioadhesive; ss.

XX OS Pasteurella multocida.

XX FH Key Location/Qualifiers

XX CD 1. .2112

XX FT /\*tag= a

XX FT /product= "PmHAS-D"

XX FT /transl\_except= (pos:1348..1353,aa:Asn)

XX PN WO200027437-A2.

XX XX 18-MAY-2000.

XX PF 10-NOV-1999; 99WO-US026501.

XX PR 11-NOV-1998; 98US-0107929P.

XX PR 01-APR-1999; 99US-00283402.

XX PA (OKLA ) UNIV OKLAHOMA STATE.

XX XX Deangelis PL;

XX XX WPI; 2000-376319/32.

XX DR P-PSDB; AAY96212.

XX PT Novel method for the enzymatic transfer of sugar molecules to an  
PT acceptor, useful for synthesis of e.g. polysaccharide bioadhesives or  
PT drug delivery systems, including hybrid molecules.

XX PS Claim 20; Page 84; 86pp; English.

XX CC The present sequence is the coding sequence of the soluble recombinant  
CC form of Pasteurella multocida hyaluronic acid synthase-D, PmHAS-D. This  
CC sequence encodes residues 1 to 703 of the 972 residues of the native  
CC PmHAS enzyme. PmHAS-D catalyses glycosaminoglycan polymerisation to  
CC produce hyaluronic acid. HA: a linear polysaccharide. HA has viscoelastic  
CC properties which makes it useful for a number of applications. HA can be  
CC used during ophthalmic surgery as a viscoelastic replacement for the  
CC vitreous humour e.g. during implantation of intraocular lenses in  
CC cataract patients. HA injections directly into joints is also used to  
CC alleviate pain associated with arthritis. HA can also be used to coat  
CC medical devices e.g. catheters and sensors to reduce tissue abrasion. HA  
CC can also be used as bioadhesives for haemostatic sealing and healing of  
CC wounds and surgical incisions; and as biomaterials that provide sustained  
CC delivery of encapsulated drugs, to wounds, ulcers, injuries or surgical  
CC sites. The present sequence can therefore be used to produce HA

SQ Sequence 2112 BP; 745 A; 359 C; 387 G; 621 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 4.29e-310 Length: 2112  
Score: 3693.00 Matches: 702  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.86% Mismatches: 0  
Query Match: 72.30% Indels: 0  
DB: 3 Gaps: 0

US-10-642-248-2 (1-972) x AAA27448 (1-2112)

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QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
DB |||||  
DB 61 AAATTTATTTGAAAAGTCGGCGGAAATCTATGACGCGAAATTTGTTGAAATTTCAAATTACC 120  
QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
DB |||||  
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QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
DB |||||  
DB 181 AAAGAAGAAAAGTCAATGTTTCGGATAGTCGTTAGATATTGCAACACACACTGTACTT 240  
QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100  
DB |||||  
DB 241 TCCACAGTAAATAAATTTAGTACTTTCTGACTCGGAAAAAACAACACGTTAAAAATAAATGG 300  
QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
DB |||||  
DB 301 AAATTCCTCAGTGAAGAAATCTGAAAATGCGGAGGTAAAGACGCTGCCCTTGTACCA 360  
QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
DB |||||  
DB 361 AAAGATTTTCCCAAGATCTGGTTTTCAGCGCTTTACCTGATCATGTTAATGATTTTACA 420  
QY 141 TrpTyrLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160  
DB |||||  
DB 421 TGGTACAAAAAGCGAAAGAAAGACCTTGGCATATAAAACCTGAACATCAACATGTGTGCTTT 480  
QY 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
DB |||||  
DB 481 TCTATTATCGTTACAAACATTTCAATCACCAGCAATTTTATCGAATTACATTTAGCTGTTTA 540  
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DB |||||  
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DB |||||  
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DB |||||  
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QY 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
DB |||||  
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DB |||||  
DB 1021 TTTTCGCGCGGTAAATGTGCTTTTCGCTAAAAAATGGCTAAATAATCCCGGTTCTTTTGAT 1080  
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Job time : 1299 secs

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Db 1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380
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Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrHisLeu 600
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Qy 701 LysAspIle 703
Db 2101 AAAGATATT 2109
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame plus p2n model

Run on: January 8, 2006, 16:49:54 ; Search time 10619 Seconds  
(without alignments)  
5203.111 Million cell updates/sec

Title: US-10-642-248-2  
Perfect score: 5108  
Sequence: 1 MNTLSQAIKAYNSNDYQLA.....SARGENIPVKNKFIINSITL 972

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb.ba.\*  
2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	5108	100.0	2920 1	AF036004 Pasteurel
2	5108	100.0	2937 6	AR616925 Sequence
3	5105	99.9	16727 1	AF067175 Pasteurel

4	5104	99.9	2919	1	AF237926	Pasteurel
5	5104	99.9	2937	6	BD087261	BD087261 Hyaluro
6	5104	99.9	2937	6	BD205371	BD205371 Nucleic a
7	4502.5	88.1	2979	1	AF195517	AF195517 Pasteurel
8	4490.5	87.9	2979	6	BD228712	BD228712 Polymer g
9	4490.5	87.9	2979	6	AR225814	AR225814 Sequence
10	4310.5	84.4	11885	1	AE006116	AE006116 Pasteurel
11	4306.5	84.3	3156	1	AF604234	AF604234 Pasteurel
12	4301.5	84.2	8838	1	AF302467	AF302467 Pasteurel
13	3693	72.3	2112	6	BD228711	BD228711 Polymer g
14	3693	72.3	2112	6	AR225813	AR225813 Sequence
15	2209	43.2	2058	6	AX698176	AX698176 Sequence
16	2209	43.2	14483	6	AB079602	AB079602 Escherich
17	2209	43.2	14483	6	AX698178	AX698178 Sequence
18	1306	25.6	998	1	AY225345	AY225345 Pasteurel
19	1303	25.5	907	1	AY225347	AY225347 Pasteurel
20	1148.5	22.5	864	1	AY225346	AY225346 Pasteurel
21	432.5	8.5	11455	1	AY044868	AY044868 Campyloba
22	418	8.2	12370	1	AY422196	AY422196 Campyloba
23	417	8.2	12388	1	AF401529	AF401529 Campyloba
24	410	8.0	11442	1	AF400048	AF400048 Campyloba
25	404	7.9	13484	1	AF400047	AF400047 Campyloba
26	404	7.9	13484	1	AY044156	AY044156 Campyloba
27	404	7.9	282183	1	CJ11168X4	AL139077 Campyloba
28	398.5	7.8	110000	1	AE017180_21	Continuation (22 o
29	388.5	7.6	12390	1	AF401528	AF401528 Campyloba
30	384.5	7.5	6047	1	AY644679	AY644679 Campyloba
31	384.5	7.5	11474	1	AF130984	AF130984 Campyloba
32	384.5	7.5	11474	1	AF215659	AF215659 Campyloba
33	384.5	7.5	11474	6	BD249790	BD249790 Campyloba
34	384.5	7.5	11474	6	AR271699	AR271699 Sequence
35	384.5	7.5	11474	6	AR481781	AR481781 Sequence
36	384.5	7.5	11474	6	AR527380	AR527380 Sequence
37	384.5	7.5	11474	6	AR609659	AR609659 Sequence
38	384.5	7.5	11474	6	AX934424	AX934424 Sequence
39	384.5	7.5	24437	1	AF167344	AF167344 Campyloba
40	382.5	7.5	12576	1	AY297047	AY297047 Campyloba
41	379	7.4	24425	1	AY422197	AY422197 Campyloba
42	376	7.4	270050	1	AL591977	AL591977 Listeria
43	376	7.4	349980	6	AX641667	AX641667 Sequence
44	371	7.3	14157	1	AE007717	AE007717 Clostridi
45	357	7.0	17250	1	CR931720	CR931720 Streptoco

#### ALIGNMENTS

RESULT 1	AF036004	Pasteurella multocida hyaluronan synthase (PmHAS) gene, complete cds.	2920 bp	DNA	linear	BCT 04-MAR-2004
LOCUS	AF036004	Pasteurella multocida				
DEFINITION	AF036004.2	GI:44986831				
ACCESSION	AF036004	Pasteurella multocida				
VERSION	AF036004.2	GI:44986831				
KEYWORDS		Pasteurella multocida				
SOURCE		Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella.				
ORGANISM		1 (bases 1 to 2920)				
REFERENCE		DeAngelis, P.L., Jing, W. and Achyuthan, A.M.				
AUTHORS		Identification and molecular cloning of a unique hyaluronan synthase from Pasteurella multocida				
TITLE		J. Biol. Chem. 273 (14), 8454-8458 (1998)				
JOURNAL		9525958				
PUBMED		2 (bases 1 to 2920)				
REFERENCE		DeAngelis, P.L., Jing, W. and Achyuthan, A.M.				
AUTHORS		Direct Submission				
TITLE		Submitted (26-NOV-1997) Biochem. & Molec. Biol., Univ. of Oklahoma				
JOURNAL		Health Sciences Center, 940 Stanton L. Young Blvd., Oklahoma City, OK 73104, USA				
REFERENCE		3 (bases 1 to 2920)				
AUTHORS		DeAngelis, P.L., Jing, W. and Achyuthan, A.M.				
TITLE		Direct Submission				



Db 1261 GTCCCTTATCTATAGAAAACCTTTTACCAATAGAGATTGCGATATCAATAGAGTACCT 1320  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCyshAlaSerTyrIleGlnArgCysValAsp 460  
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## RESULT 2

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ACCESSION AR616925  
VERSION AR616925.1 GI:59720260  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2937)  
AUTHORS Weigel,P.H., Kumari,K. and DeAngelis,P.  
TITLE Hyaluronan synthase gene and uses thereof  
JOURNAL Patent: US 6833264-A 8 21-DEC-2004;  
The Board of Regents of the University of Oklahoma, Norman, OK  
FEATURES  
source Location/Qualifiers  
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US-10-642-248-2 (1-972) x AR616925 (1-2937)

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VERSION AF237926.1 GI:7716512
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SOURCE Pasteurella multocida
ORGANISM Pasteurella multocida
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
REFERENCE
AUTHORS Fuller,T.E., Kennedy,M.J. and Lowery,D.E.
TITLE Identification of Pasteurella multocida virulence genes in a
septiceemic mouse model using signature-tagged mutagenesis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2919)
AUTHORS Fuller,T.E., Kennedy,M.J. and Lowery,D.E.
TITLE Direct Submission.
JOURNAL Submitted (24-FEB-2000) Discovery Research, Pharmacia & Upjohn
Animal Health, 7923-25-43*, 7000 Portage Road, Kalamazoo, MI
49001-0199, USA

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ORIGIN

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Hyaluronan synthase gene and utilization thereof.  
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Weigel,P.H., Kumari,K. and Deangelis,P.  
Hyaluronan synthase gene and utilization thereof

JOURNAL Patent: JP 2001521741-A 13 13-NOV-2001;  
THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA  
OS Pasturella multocida  
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PD 13-NOV-2001  
PF 30-OCT-1998 JP 2000519083  
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LOCUS Nucleic acid encoding hyaluronan synthase and method of using the
DEFINITION same.
ACCESSION BD205371
VERSION BD205371.1 GI:33015141
KEYWORDS JP 2002510648-A/1.
SOURCE Pasteurella multocida
ORGANISM Pasteurella multocida
REFERENCE Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
1 (bases 1 to 2937) Pasteurellaceae; Pasteurella.
AUTHORS Deangelis, P.
TITLE Nucleic acid encoding hyaluronan synthase and method of using the
JOURNAL Patent: JP 2002510648-A 1 09-APR-2002;
COMMENT BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
OS Pasteurella multocida
PN JP 2002510648-A/1
PD 09-APR-2002
PF 01-APR-1999 JP 2000542035
PR 02-APR-1998 US 60/080414, 26-OCT-1998 US 09/178851 PI
PAUL DEANGELIS
PC A61K39/102, A61K39/00, A61K47/36, A61P31/04, C12N1/15, C12N1/19, PC
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VERSION AF195517.2 GI:44985817
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1 (bases 1 to 2979)
DeAngelis,P.L. and Padgett-McCue,A.J.
IDENTIFICATION AND MOLECULAR CLONING OF A CHONDROITIN SYNTHASE FROM
PASTEURELLA MULTOCIDA TYPE F
J. Biol. Chem. 275 (31), 24124-24129 (2000)
10818104
2 (bases 1 to 2979)
DeAngelis,P.L. and Padgett-McCue,A.J.
DIRECT SUBMISSION
Submitted (15-OCT-1999) Biochem. & Molec. Biol., Univ. of Oklahoma
Health Sciences Center, 940 Stanton L. Young Blvd., Oklahoma City,
OK 73104, USA
3 (bases 1 to 2979)
DeAngelis,P.L. and Padgett-McCue,A.J.
DIRECT SUBMISSION
Submitted (04-MAR-2004) Biochem. & Molec. Biol., Univ. of Oklahoma
Health Sciences Center, 940 Stanton L. Young Blvd., Oklahoma City,
OK 73104, USA
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COMMENT On Mar 4, 2004 this sequence version replaced gi:9716369.
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580	GTCAAATCAGAAAAACAACTACCCATTTGAAAGTCGTTGTCAGATGATGGTAGTAGGAA	639
201	AspLeuSerProIlelleAqGlnTyrrGluAsnLysLeuAspIleAqTyrrValAqGln	220
640	AACCTTACTTACCATTGCAAAAATACGAACAAAACCTTGACATAAAGTATGTAAACAA	699
221	LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyrr	240
700	AAACATTATGATATCAATTGTGTGAGTCAGAAACCTTAGGTTTACGTACAGCAAAAGTAT	759
241	AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrrValHisSerTyrr	260
760	GATTTTGTCTGATCTTAGAGTCGGATATGGCACCAACAATTTATGGGTTTCATCTTAT	819
261	ValAlaGluLeuLeuGluAspAspLeuThrIlelleGlyProAqLysTyrrIleAsp	280
820	CTTACAGAACATTAGAGAACATGATATGTTTAAATGGACCTAGAAAATATGTGGAT	879
281	ThrGlnHisIleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro	300
880	ACTCATAATATTACCGCAGACAATTCCTTAAACGATCCATATTTAATAGAATCACTACCT	939
301	GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyrr	320
940	GAACCCGCTACAAATAACAATCTTCGATTACATCAAAAGGAAATATATCGTTGGATGG	999
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341	PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrrLeuAsnLysSerGlyPheAsp	360
1060	TTTAGTTCCGGTAATGTTGCATTTCTTAAAGAATGGCTAAATAAAGTAGGTTCGAT	1119
361	GluGluPheAsnHisTyrrGlyGlyGluAspValGluPheGlyTyrrArgLeuPheArgTyrr	380
1120	GAAGAAATTTAATCAATGGGGGGGCGAAGATGAGAAATTTGGTTACAGATTATTTGCCAAA	1179
381	GlySerPhePheLysThrIleAspGlyIleMetAlaTyrrHisGlnGluProGlyLys	400
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401	GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGlyLys	420
1240	GAAATGAAACAGACCGCGAAGCTGTAAAAGTATTACGCTTAAATTTGCAAGAGAAAG	1299
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441	LeuValSerIleTyrrIleProAlaTyrrAsnCysAlaAsnTyrrIleGlnAqGlyValAsp	460
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461	SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr	480
1420	AGTGCTCTTAAATCAACTGTTGTGCACTCGAGGTTTGATTTTGTAACGATGGTTCACCA	1479
481	AspAsnThrLeuGluValIleAsnLysLeuTyrrGlyAsnAsnProAqValArgIleMet	500
1480	GATAATACTTAGAAGTGCATCAATAAGCTTTATGGTAAATATCTAGGTACGATCATG	1539

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Qy	601	ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu	620
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Qy	661	GlnSerLeuAsnArgGlnGlyIleThrTyrAsnTyrAspGluPheAspAspLeuAsp	680
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Qy	781	ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln	800
Db	2380	ACGAGTAAATAGACTAATAAAACCTGAGGCACATTTAAGTAAATATTAATAAATTAAGTCAG	2439
Qy	801	LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn	820
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Qy	821	AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis	840
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Qy	841	AspTrpIleGluLysIleAsnAlaHisProPheLysLysLysLeuIleLysThrTyrPhe	860
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Db 2680 TATGGCTACCGCATGAGCTTCTGACGATTATTAAAGAAGTCATCACATCTGCGCAATCA 2739
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuIle 920
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Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940
Db 2800 TTAGAAAAGAAAACCGGCATGATTATTAAACATCGACCTGACTTATATGCTTGG 2859
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LOCUS Polymer grafting by polysaccharide synthases.
DEFINITION BD228712
ACCESSION BD228712.1 GI:33038482
VERSION JP 2002529064-A/2.
KEYWORDS Pasteurella multocida
SOURCE Pasteurella multocida
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
REFERENCE 1 (bases 1 to 2979)
AUTHORS Deangelis,P.L.
TITLE Polymer grafting by polysaccharide synthases
JOURNAL Patent: JP 2002529064-A 2 10-SEP-2002;
THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
COMMENT OS Pasteurella multocida
PN JP 2002529064-A/2
PD 10-SEP-2002
PF 10-NOV-1999 JP 2000580666
PR 11-NOV-1998 US 60/107929, 01-APR-1999 US 09/283402 PI
PAUL L DEANGELIS
PC C12N15/09, A61K47/36, C12N1/21, C12P19/26//C12N9/26, C12N15/00 CC
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Best Local Similarity: 86.73% Mismatches: 60
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US-10-642-248-2 (1-972) x BD228712 (1-2979)

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Db 61 ATGAATACATTATCACAGCAATAAAGCATATAACAGCAATGACTATGAATAGCACTC 120
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Qy 61 LysGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 220 GAAGATAAAAAAACACAGTGTTCGATAGCTCATTAGATATCGCAACACACAGCTCTTACTT 279
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerCysLysAsnThrLeuLysAsnLysTyr 100
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Db 340 AAATCTATCTACTCGGAANAANAATCGCAGAACCGCAGAAATCAGAAAGGTGGAACCTAGTACCC 399
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Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnAtqValPro 440
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US-10-642-248-2 (1-972) x AR225814 (1-2979)

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AUTHORS	May,B.J., Zhang,Q., Li,L.L., Paustian,M.L., Whittam,T.S. and Kapur,V.		
TITLE	Complete genomic sequence of Pasteurella multocida, Pm70		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)		
PUBMED	11248100		
REFERENCE	2 (bases 1 to 11885)		
AUTHORS	Zhang,Q. and Kapur,V.		

TITLE  
JOURNALFEATURES  
source

Direct Submission  
Submitted (24-Oct-2000) Department of Veterinary Pathobiology,  
University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN  
55108, USA

## Location/Qualifiers

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RESULT 11
LOCUS AY604234 3156 bp DNA linear BCT 12-MAY-2004
DEFINITION Pasteurella multocida strain J-4103 glycosyltransferase Fcbb (fcbb)
gene, complete cds.
ACCESSION AY604234
VERSION AY604234.1 GI:47080018
KEYWORDS Pasteurella multocida
SOURCE Pasteurella multocida
ORGANISM Pasteurella multocida
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
1 (bases 1 to 3156)
Jaglic,Z. and Bartos,M.
The first detection of Pasteurella multocida serogroup F in
rabbits: analysis of serogroup F specific fcbb gene
Unpublished
REFERENCE 1 (bases 1 to 3156)
Jaglic,Z. and Bartos,M.
Direct Submission
AUTHORS Jaglic,Z. and Bartos,M.
TITLE Direct Submission
JOURNAL Submitted (22-APR-2004) Bacteriology, Veterinary Research
Institute, Hudcova 70, Brno 62132, Czech Republic
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ORIGIN

Alignment Scores:

Pred. No.: 1.25e-259 Length: 3156

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LOCUS Pasteurella multocida P4218 region 2 capsule biosynthesis gene
DEFINITION cluster, partial sequence.
ACCESSION AF302467
VERSION AF302467.1 GI:13274373
KEYWORDS Pasteurella multocida
SOURCE Pasteurella multocida
ORGANISM Pasteurella multocida
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
REFERENCE 1 (bases 1 to 8838)
AUTHORS Townsend, K.M., Boyce, J.D., Chung, J.Y., Frost, A.J. and Adler, B.
TITLE Genetic organization of Pasteurella multocida cap loci and
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development of a multiplex capsular PCR typing system  
J. Clin. Microbiol. 39 (3), 924-929 (2001)

11230405  
JOURNAL PUBLISHED  
REFERENCE 2 (bases 1 to 8838)  
Townsend,K.M., Boyce,J.D., Chung,J.Y., Frost,A.J. and Adler,B.  
AUTHORS Direct Submission  
TITLE Submitted (03-SEP-2000) Veterinary Pathology and Anatomy, The  
JOURNAL University of Queensland, School of Veterinary Science, Brisbane,  
QLD 4073, Australia  
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ORIGIN

Alignment Scores:  
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Score: 4301.50 Matches: 802  
Percent Similarity: 91.15% Conservative: 84  
Best Local Similarity: 82.51% Mismatches: 79  
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DB: 1 Gaps: 2

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VERSION AR225813.1 GI:27263928
KEYWORDS SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2112)
DeAngelis,P.L.
TITLE Polymer grafting by polysaccharide syntheses
JOURNAL Patent: US 644447-A 2 03-SEP-2002;
The Board of Regents of the University of Oklahoma; Norman, OK
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KEYWORDS Escherichia coli
SOURCE Escherichia coli
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1
AUTHORS Ninomiya, T., Sugiyama, N. and Kimata, K.
TITLE Chondroitin polymerase and DNA encoding the same
JOURNAL Patent: EP 1283259-A 1 12-FEB-2003;
Seikagaku Corporation (JP)
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## ORIGIN

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US-10-642-248-2 (1-972) x AK698176 (1-2058)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 8, 2006, 17:28:01 ; Search time 400 Seconds  
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4319.475 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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SUMMARIES

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2	5104	99.9	2937	US-10-172-527A-9	Sequence 9, Appli
3	4490.5	87.9	2979	US-09-437-277-4	Sequence 4, Appli
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6	384.5	7.5	11474	US-09-816-028A-1	Sequence 1, Appli
7	384.5	7.5	11474	US-10-303-162-1	Sequence 1, Appli
8	384.5	7.5	11474	US-10-303-134-1	Sequence 1, Appli
9	384.5	7.5	11474	US-10-303-118-1	Sequence 1, Appli

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12	302.5	5.9	6865	3	US-09-900-038A-3	Sequence 3, Appli
13	301.5	5.9	2166	3	US-09-107-532A-3235	Sequence 3235, Ap
14	287.5	5.6	2529	3	US-09-134-000C-2344	Sequence 2344, Ap
15	281.5	5.5	32768	3	US-08-961-527-71	Sequence 71, Appli
16	264.5	5.2	1002	3	US-09-107-532A-1469	Sequence 1469, Ap
17	252	4.9	1602	3	US-09-134-000C-1682	Sequence 1682, Ap
18	251.5	4.9	14602	2	US-08-597-236-1	Sequence 1, Appli
19	245.5	4.9	984	3	US-08-746-682A-1	Sequence 2537, Ap
20	245.5	4.8	536165	3	US-09-107-532A-2527	Sequence 1, Appli
21	245	4.8	1830121	3	US-09-214-808-1	Sequence 1, Appli
22	244	4.8	1830121	3	US-09-557-884-1	Sequence 1, Appli
23	244	4.8	1830121	3	US-09-643-990A-1	Sequence 1, Appli
24	244	4.8	1830121	3	US-10-158-865-1	Sequence 1, Appli
25	241.5	4.7	993	3	US-09-134-000C-2987	Sequence 2987, Ap
26	236.5	4.6	3171	3	US-09-134-000C-1681	Sequence 1681, Ap
27	235	4.6	1035	3	US-08-891-641-40	Sequence 40, Appli
28	231.5	4.5	2023	3	US-08-961-083-199	Sequence 199, App
29	231.5	4.5	2023	3	US-09-536-784-199	Sequence 199, App
30	231.5	4.5	2023	3	US-09-765-271-199	Sequence 199, App
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43	210.5	4.1	5859	2	US-08-683-426-7	Sequence 7, Appli
44	210.5	4.1	5859	2	US-08-683-458-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1  
US-09-469-2008-8  
; Sequence 8, Application US/09469200E  
; Patent No. 6833264  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Kumari, Kshama  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/09/469,200E  
; CURRENT FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: Pastuerella Multocida  
US-09-469-2008-8

Alignment Scores:				
Pred. No.:	0	Length:	2937	
Score:	5108.00	Matches:	972	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	3	Gaps:	0	
US-10-642-248-2 (1-972) x US-09-469-2008-8 (1-2937)				

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Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
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Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1939 GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAAACCACTTTTGTGTAGTCAT 1998  
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; SEQ ID NO 9
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: pasteurella multocida
US-10-172-527A-9

Alignment Scores:
Pred. No.: 0 Length: 2937
Score: 5104.00 Matches: 971
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.92% Indels: 0
DB: 3 Gaps: 0

US-10-642-248-2 (1-972) x US-10-172-527A-9 (1-2937)

QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
DB 19 ATGAATACATTATCACAGGCANTAAAGCATATTAACAGCATGACTATCAATTAGCACATC 78
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RESULT 2
US-10-172-527A-9
; Sequence 9, Application US/10172527A
; Patent No. 6951743
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H
; APPLICANT: Kumari, Kshama
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: HYALURONAN SYNTHASE GENES AND EXPRESSION THEREOF IN BACILLUS HOST
; FILE REFERENCE: 3554.048
; CURRENT APPLICATION NUMBER: US/10/172,527A
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/297,788
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/297,744
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 09/469,200
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
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Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Db 2179 AATACATATTAAACGGCTTAGTGAAAAAATAAACAAATATTATTGAATATATAAAAAATATA 2238  
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Db 2239 TTCGTTATTGTTCTACATGTTGATAAGAAATCATCTTACACCAAGATATCAAAAAAGAAATA 2298  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2358  
Qy 781 ThrSerAsnArgLeuLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2359 ACAGTAATAGATAATAAAAACTGAGCGCATTTAAGTAATAATTAATAAATTAAGTCAG 2418  
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
Db 2419 TTAATCTTAATGTGAATACATCATTTTGTGAATAATCATGACAGCCTTATTCGTTAAAAAT 2478  
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Db 2479 GACAGCTATGCTTATGAAAAAATATGATGTCGCGCATGAAATTTCTCAGCATTAACACAT 2538  
Qy 841 AspTrpIleGluLysIleAsnAlaHisProProPheLysLysLeuLysLysThrPhe 860  
Db 2539 GATTGGATCGAGAAAAATCAATGCGCATCCACCATTAAAAAGCTCATTAATAACCTTATTTT 2598  
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyValaSerGlnGlyMetPheMetThr 880  
Db 2599 AATGACAACTGACTTAAAAAGTATGAATGTGAAGGGGCATCACAGGTATGTTATGACG 2658  
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTATTAAAGAGTCATCATCTTCCAGTCA 2718  
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
Db 2719 ATTGATAGTGTGCGAGAATAATACACTGAGGATATTTGGTTCCCAATTTGCACCTTTAATC 2778  
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940  
Db 2779 TTAGAAAAAGAAAAACCGGCCCATGTATTATAAATAACATCGACCTGACTTATATAGCCTTGG 2838  
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Db 2839 GAACGAAAAATTACAAATGGCAAAATGAACAAATTTGAAAGTGCNAAGAGAGAGAGAAATATA 2898  
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Db 2899 CCTGTTAAACAAGTTTCATTATTATAATAGTATAACTCTA 2934

## RESULT 3

US-09-437-277-4

; Sequence 4, Application US/09437277

; Patent No. 644447

; GENERAL INFORMATION:

; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA

; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES

FILE REFERENCE: 5820.551  
CURRENT APPLICATION NUMBER: US/09/437,277  
CURRENT FILING DATE: 1999-11-10  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: WordPerfect 8.0 (saved in ASCII format)  
SEQ ID NO 4  
LENGTH: 2979  
TYPE: DNA  
ORGANISM: Pasteurella multocida  
US-09-437-277-4

Alignment Scores:  
Pred. No.: 0 Length: 2979  
Score: 4490.50 Matches: 843  
Percent Similarity: 93.11% Conservative: 62  
Best Local Similarity: 86.73% Mismatches: 60  
Query Match: 87.91% Indels: 7  
DB: 2 Gaps: 2

US-10-642-248-2 (1-972) x US-09-437-277-4 (1-2979)

```
Qy      1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db      61 ATGAATACATTATCACAGCAATAAAGCATATATAACAGCAATGACTATGAATTAGCACTC 120

Qy      21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db      121 AAATTTATTGAGAGTCTGCTGAAACCTTACCGGGCGAANAATCGTTGAATTCCAATATATC 180

Qy      41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db      181 AAATGTAAGAAAGAACTC-----TCGACCAATTCT-----TATGTAAGT 219

Qy      61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db      220 GAAGATAAAAAACAGTGTTCGATAGCTCATTTAGATATCGCAACACAGCTCTTACTT 279

Qy      81 SerAsnValLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100
Db      280 TCCACGCTAAATAAATAAATTAACCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG 339

Qy      101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db      340 AAATCTATCACTGGGAAAAAATCGAGAACCGAGAAATCAGAAAGGTGGAACCTAGTACCC 399

Qy      121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db      400 AAAGATTTTCTTAAAGATCTTGTCTCTCCATTCATTCGCCAGATCATGTTTAATGATTTTACA 459

Qy      141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db      460 TGGTACAAAATTCGAAAAAAGCTTAGGTATAAAGCCTGTAAAGATTAAGAAATTCGGTCTT 519

Qy      161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db      520 TCTATTATTTCCTACATTTTAATCGTACCGCTATTTTAGATATTAACGTTAGCCTGTTG 579

Qy      181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db      580 GTCAATCAGAAAAACAACATACCATTGGAAGTCGTTGTTGTCAGATGATGTTAGTAGGAA 639

Qy      201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db      640 AAATCTACTTACCATTTGTGCAAAATACGAAACAAAACCTTGACATAAAGATGATGAGACAA 699

Qy      221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db      700 AAAGATTATGGATATCAATGTGTGAGTCAGAGTCAGAAACTTAGTTTACGTACACCAAGTAT 759

Qy      241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260
Db      760 GATTGTGCTCGATCTAGATGCGATATGGCACCACCAACAATTTATGGGTTTCATCTTAT 819
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Qy      261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db      820 CTTACAGAACTATTAGAACAAATGATATTGTTTAAATTTGGACCTAGAAAAATATGTGGAT 879

Qy      281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db      880 ACTATAAATATTACCGCAGAACCAATTCCTTAACGATCCATATTATTAAGAAATCACTACCT 939

Qy      301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320
Db      940 GAAACCCCTACAAATAACAATCTTCGATTACAAAGGAAATATATCGTTGGATTGG 999

Qy      321 ArgLeuGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db      1000 AGATTAGAACATTTCAAAAAAACCGATAATCTACGTCTATGTGATTCTCCGTTTCGTTAT 1059

Qy      341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPhePheAsp 360
Db      1060 TTTGTTGCGGGTAATGTTGCAATTTCTTAAGAAATGGCTAATAAAGTAGGTGGTTCGAT 1119

Qy      361 GluGluPheAsnHisTyrGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db      1120 GAAGAATTTAATCATTTGGGGGGCGAAGATGTAGAAATTTGGTTACAGATTATTTGCCAAA 1179

Qy      381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db      1180 GGCTGTTTTTTCAGAGTAATTCACGGCGGAATTCGCATCAAGAACCCACCTGGGTAAA 1239

Qy      401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db      1240 GAAATCAAAACAGAACCGAAGCTGGTAAAGATTAATACGCTTAAATTTGGAAGAAAAG 1299

Qy      421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db      1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAACATTCACATATTTCATAGAATACCT 1359

Qy      441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db      1360 TTAGTTTCTATTATATATCCCGCTTATAACTGTGCAAAATATATATTCAAAGATGTGTAGAT 1419

Qy      461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db      1420 AGTCCTCTTAATCAAACTGTTGTCGATCTCGAGTTTGTATTGTTGTAACGATGGTTCAACA 1479

Qy      481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db      1480 GATTAATACCTTAGAAGTGATCAATAAGCTTTATGTAATAATCTAGGTCAGCATCATG 1539

Qy      501 SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db      1540 TCTAAACCAATTCGCGAATAGCCTCAGCATCAAAATGCAGCGTTTCTTTTGTCTAAAGGT 1599

Qy      521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrIleGluProAspAlaValGluLeuCys 540
Db      1600 TATTACATTCGCGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCGAGTTGAACGTGT 1659

Qy      541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560
Db      1660 TTAAGAAGAAATTTTAAAGATAAACCGTAGCTGTGTGTTTATACCATTAATAGAAACGTC 1719

Qy      561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580
Db      1720 AATCCGGATGTAGCTTAATCGCTAAATGGTTACAATTCGCGAGAATTTTTCACGAGAAAAA 1779

Qy      581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTyrHisLeu 600
Db      1780 CTCACACGCGTATGATTCCTCACCATTATTAGAATGTTTACGATTAGAGCTTGGCATTTA 1839

Qy      601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db      1840 ACGGATGATTTTACGAAAAAATATTGAAACCGCGGTGATATGACATGTTCTCTTAAATCTC 1899

Qy      621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
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Db 1900 AGTGAAGTGGAAAAATTAACATCTTAATAAATAATCTGCTATAACCGGTATTACATGGT 1959
Qy 641 AsnAsnThrSerLeuLysLysLeuGlyLeuGlnLysLysAsnHisPheValValAsn 660
Db 1960 GATAACACATCCATTAGAAATCGGCATTCAAAAGAAAAACCACTTTTGTGTAGTCAAT 2019
Qy 661 GlnSerLeuAsnArgGlnGlyLeuThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 2020 CAGTCATTAATAAGACAAAGGCATCAATATTATTAATATTATGACAAATTTGATGATTTAGAT 2079
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2080 GAAAGTAGAAGATATATCTTCATATAAACCGCTGAATATCAAGAGAAATGGATATGTTA 2139
Qy 701 LysAspLeuLysIleLeuGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2140 AAAGATCTTAATAACTCAATCAAAATAAAGATGCCAAATCGCAGTCAGTATTTCTATCCC 2199
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740
Db 2200 AATACATTAACCGCTTAGTGAAAAAATAAACAATATTATTGAATATATAATAAAAAATATA 2259
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2260 TTCGTTATTAATCTACATGTTGATAGAAATCACTTACACGACATCAAAAAGAAATA 2319
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780
Db 2320 TTGGCTTCTATCATAGACCAAGTGAATATTATTACTAATAATAGCATCTCATATTAC 2379
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2380 ACGAGTAAATAGCAATAAATAAAGTGGAGCAATTTAAGTAAATATAATAAATTAAGTCAG 2439
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2440 TTAATCTAATGTTGAATACATCATCTTTTGTATTAATCATGACGCCATTCGTTAAANAT 2499
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2500 GACAGCTATGCTTATATGAAAAAATATGATGTCGCATGAATTTCTCAGCATTAACACAT 2559
Qy 841 AspTyrIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2560 GATTGGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAAAGCTGATTAACACCTATTTT 2619
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2620 AATGACAAATGACTTAAGAAATGATGAATGTGAAAGGGGCATCACAAAGTATGTTTGAAG 2679
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2680 TATCGCTACCGCATGAGCTTCTGACGATTAATAAGAAATGATCATCATCTCGCAATCA 2739
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleThrPheGlnPheAlaLeuLeuIle 920
Db 2740 ATTGATAGTGGCAGAAATAAACAATGAGGATATTTGGTTCCAAATTTGCACATTTTAATC 2799
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940
Db 2800 TTAGAAAGAAACCGGCATGATATTTAATAAACATCGACCCCTGACTTATATGCCCTGG 2859
Qy 941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaTyrArgGlyGluAsnIle 960
Db 2860 GAACGAAAAATTACAAATGGACAAATGAACAAATTCAAAGTGCAAAAAAGGCGAAAAATATC 2919
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2920 CCGGTTAACAGATTCATTTAATAGTATATACGCTA 2955
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RESULT 4

US-09-437-277-2

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; Sequence 2, Application US/09437277
; Patent No. 644447
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
; FILE REFERENCES: 5820.551
; CURRENT APPLICATION NUMBER: US/09/437,277
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
; SEQ ID NO 2
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Pasteurella multocida
; US-09-437-277-2
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Alignment Scores:
Pred. No.: 0 Length: 2112
Score: 3693.00 Matches: 702
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.86% Mismatches: 0
Query Match: 72.30% Indels: 0
DB: Gaps: 0
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US-10-642-248-2 (1-972) x US-09-437-277-2 (1-2112)

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Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 1 ATGAATACATATTATCACAGCAATATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AATATTATTGAAAAGTCGGCGGAAATCTATGACGGAATAATTGTTGAATTTCAAAATACC 120
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 121 AATGCCAAGAAAAAATCTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTTCTGTAAT 180
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 181 AAAGAAGAAAAAGTCAATGTTTCGATAGTCGCTTAGATATTGCAACACAACTGTACTT 240
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100
Db 241 TCCACAGTAAAAAAATTAGTACTTTCTGACTCGAAAAAACAACACGTTAAAAAATAATGG 300
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 301 AATTTGCTCACTCAGAAAGAAATCTGAAAAATGCGAGGTAAGAGCGGTGCGCCCTGTACCA 360
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 361 AAAGATTTTCCCAAGATCTGGTTTTTAGCGCCTTTTACCTGATCATGTATATGATTTTACA 420
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 421 TGTATACAAAAGCGAAAGAAAGACATGGCATAAAACTGCAACATCAACATGTTGGTCTT 480
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 481 TCTATTATCGTTACAAACATTCATCGACCAACAAATTTTTCGATTACATTAGCGCTGTTTA 540
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAAACCAAAAAACACATTAACCGTTTGAAGTTTATCGTGACAGATGATGTTAGTCAGGAA 600
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 601 GATCTATCACCGATCAATTCGCCAATATGAANAATAAATTGGATATTGCTACGTCAGACAA 660
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 661 AAAGATAACGGTTTTTCAAGCCAGTCGCGCTCGGAATATGGGATTACGCTTAGCAAAATAT
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QY 241 AspPheileGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260
Db 721 GACTTTATGGCTTACTCGACTGTGATATGGCCCAATCCATATGGGTTCTTCTTAT 780
QY 261 ValAlaGluLeuLeuGluAspAspLeuThrileileGlyProArgLysTyrileAsp 280
Db 781 GTTCAGAGCTATTAGAAGATGATGATTTAAACATCATTTGGTCCAGAAAAATACATCGAT 840
QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 841 ACACAACATATTGACCCCAAGACTTCTTAATAAACGCGAGTTTGTGTAATCAATACCA 900
QY 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320
Db 901 GAAGTGAACCAATAATAGTTGTGGCCCAAAAGGGAGGACAGTTCCTCGATGG 960
QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 961 CGCTTAGACAAATTCGAAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTT 1020
QY 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPheAsp 360
Db 1021 TTTGCGCGGTAATTTGCTTTCGCTAAAAAATGGCTAAATAAATCCGGTTTCTTTGAT 1080
QY 361 GluGluPheAsnHisTrpGlyGlyLeuAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGTTAC 1140
QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1141 CGTAGTTTCTTTAAACTATTGATGGCATTATGGCTACCATCAAGACCCAGGTAAA 1200
QY 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGlyLys 420
Db 1201 GAAATGAACCGATCGTGAACGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAG 1260
QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAAGATTCGCATCATATAGATACCT 1320
QY 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1321 TTAGTTTCAATTTATATCCAGCTTATTAACCTGTGCAAACTATATTCAAGTTGCGTAGAT 1380
QY 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1381 AGTGCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTGTAACGATGGTTCAACA 1440
QY 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1441 GATAATACCTTAGAAGTGCATCAATAAGCTTTATGTGTAATAATCCCTAGGATCGCATCATG 1500
QY 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 1501 TCTAAACCAATGGCGGAATACCTTCAGCATCAATGCAGCCGTTCTTTGCTAAAGGT 1560
QY 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1561 TATTACATTTGGGCGAGTTAGATTAGATGATTTATCTTGAGCTGATGCAGTTGAACTGTGT 1620
QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1621 TTTAAAGAAATTTTAAAGATAAAGCGTAGCTGTGTGTTATATACCACATAATAGAACGTC 1680
QY 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGlyLys 580
Db 1681 AATCCGGATGGTAGCTTAATCGCTAATGTTACATATGGCCAGAAATTTTCACGAGAAAA 1740
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaThrHisLeu 600
Db 1741 CTCACACCGCTATGATGCTCACCACTTTAGAAATGTTTACGATATAGAGCTTGGCATTTA 1800
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QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1801 ACTGATGGATTCAATGAAAAAATTGAAATTCGCGTAGACTATGACATGTTCTCTCAAACTC 1860
QY 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT 1920
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660
Db 1921 GATAACACATCAATTAAGAAACTTGGCATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980
QY 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 1981 CAGTCATTAATAGACAGGCATAACTTATTATAATTTATGACGAATTTGATGATTTAGAT 2040
QY 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2041 GAAAGTAGAAGTATATTTTCAATTAACCCGCTGAATATCAAGNAGAGATTTGATATCTTA 2100
QY 701 LysAspIle 703
Db 2101 AAAGATATT 2109

RESULT 5
US-09-495-406-1
; Sequence 1, Application US/09495406
; Patent No. 6503744
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/495,406
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11474
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384
; OTHER INFORMATION: including LOS biosynthesis locus
US-09-495-406-1

Alignment Scores:
Pred. No.: 1,24e-30 Length: 11474
Score: 384.50 Matches: 243
Percent Similarity: 35.71% Conservative: 163
Best Local Similarity: 21.37% Mismatches: 337
Query Match: 7.53% Indels: 394
DB: 3 Gaps: 52

US-10-642-248-2 (1-972) x US-09-495-406-1 (1-11474)
QY 10 AlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu-----LysLeuPheGluLysSer 26
Db 1459 AGTTATGCAAAAAATGATTGGATTTTAAAGCATTCATGCTGATGAAGTCTTGAAAAATGAG 1518
QY 27 Ala-----GluIleTyrGlyArgLysIleValGluPheGlnIleThrLysCysValGlu 44
Db 1519 TGTATTAAAGAGCTTAAAAAATTTAAAACTTCAAGAAAGATAATATATCATCGCATTAGCCGT 1578
QY 45 LysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsnLysGluGluLys 64
Db 1579 AAA-----AATCTCTATAAAGCGCAATGG 1602
QY 65 ValAsnValCys-----AspSerProLeuAspIleAlaThrGln----- 77
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QY 719 rProAsnThrLeuAenGlyLeuValLysLeuAsnAenIleleGluTyrAsnLysAs 739
Db 3421 TAGAGATATTCTTTTGA-----TGGATCGAATGATGATTTAT----- 3463
QY 739 nIlePheValIleValLeuHisValAspLysAenHisLeuThrProAspIleLysLysGlu 759
Db 3464 -----TTTTAAAGCAAT 3477
QY 759 uIleLeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAenAspIleSer-- 778
Db 3478 TAAACTTAAATTT-----ATAAATTTTATTATCAATGAAGATATACACTT 3522
QY 779 -----TyrTyrThrSerAsnArgLysLeuLysThrGluAlaHisLeuSerAs 794
Db 3523 TGGGATAATTTTGTGTAGTCTTAATAAATTTATGTT-----TTATCACA 3570
QY 794 nIleAsnLysLeuSerGlnLeuAsnLeuAsnCysGluTyrIlelePheAspAsnHisAs 814
Db 3571 AAAGTTGATTGTGCTGTTTAAAGAGCAACAGT-----ATATCAAAATCATGA 3618
QY 814 pSerLeuPheValLysAsnAspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAs 834
Db 3619 T-----AAGAAG----- 3625
QY 834 nPheSerAlaLeuThrHisAspTyrIleGluLysIleAsnAlaHisProProPheLysLy 854
Db 3626 -----ATTACAAAGCAATGTGTCAGAGTATTTTAAAGA 3660
QY 854 sLeuIleLysThrTyrPheAsnAspAsnAspLysSerMetAsnValLysGlyAlaSe 874
Db 3661 TATATATGAACT---TTCCGGGAAACCGTAAAGGACAAATAATTTTAAAGCAGC 3717
QY 874 rGlnGlyMetPheMetThrTyrAlaLeu-----AlaHisGluLe 887
Db 3718 AAGCAGGTTATAACTGCTTTTAAATTTAGATAATTTTAAAGATCAAAAAACGAAA 3777
QY 887 uLeuThrIleleLysGluValIleThrSerCys----- 898
Db 3778 TGCACCTGCTATAAAGAAACATATTTTACCTTGCTATGCCAAAAAAGCTTTAATGATTAA 3837
QY 899 -----GlnSerIleAspSerValProGluTyr 907
Db 3838 AAAATTTAAAGAGATCTTTTAAATTTAAAGGAACAATTTAGTTTAAATTAACCTTTTAT 3897
QY 907 rAsnThrGlu-----AspIleTyr 913
Db 3898 TCAACAAACAACTCTCTTATGATATTGGAAATTTTGGCAAAAAATAAAAAATATTAAATA 3957
QY 913 ----- 913
Db 3958 ATAAAAATAAAAAATTAATTAATTTTGTAGTATAATCACTATTAATATAGGAGAAAT 4017
QY 914 -----PheGln-----PheAlaLeuLeuIleLeuGluLy 923
Db 4018 ATTTTATATGCTATTTCATCATACTTTGTGAAATAATTTGCTTTATTCATCCCTTTTAG 4077
QY 923 sLysThrGlyHisValPheAsnLysThrSerThrLeu----- 935
Db 4078 AAAAATTAGACATAAAATAAAAAAACAATTTTACTAAAAAACATACACGAGATAAAAT 4137
QY 936 -----ThrTyrMetProTyrGluArgLysLeuGln-----TrpThrAsnGluGlnI 951
Db 4138 CGATCTTATTTTACCAAAAAAACTCTGTGCAAAATAATAAATACACATGAAGATT 4197
QY 951 eGluSerAlaLysArgGlyGluAsnIleProValAsnLysPheIleIle 967
Db 4198 A-----ATTAACTTAATAAGCTATTATA 4222
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## RESULT 6

US-09-816-028A-1

; Sequence 1, Application US/09816028A

; Patent No. 6699705

## ; GENERAL INFORMATION:

```
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11474
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384
; OTHER INFORMATION: including LOS biosynthesis locus
US-09-816-028A-1
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## Alignment Scores:

Pred. No.:	1.24e-30	Length:	11474
Score:	384.50	Matches:	243
Percent Similarity:	35.71%	Conservative:	163
Best Local Similarity:	21.37%	Mismatches:	337
Query Match:	7.53%	Indels:	394
DB:	3	Gaps:	52

US-10-642-248-2 (1-972) x US-09-816-028A-1 (1-11474)

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QY 10 AlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu-----LysLeuPheGluLysSer 26
Db 1459 AGTTATGCAAAAATGATTGGATTTTAAAGCTTATGCTGTATGAAGTCTTGAAAAATGAG 1518
QY 27 Ala-----GluIleTyrGlyArgLysIleValGluPheGlnIleThrLysCysLysGlu 44
Db 1519 TGTATTAAGAGCTTAAAAATTTAAACTTCAAGAGATAATATCATCGCACTTAGCCGT 1578
QY 45 LysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsnLysGluGluLys 64
Db 1579 AAA-----AATCTCTATANAAGCGAATGG 1602
QY 65 ValAsnValCys-----AspSerProLeuAspIleAlaThrGln----- 77
Db 1603 ATAAAGGCATGTGGTGTGGCTGATATGTTTGGAAATTTTAAATAAAATTTCACT 1662
QY 78 -----LeuLeuLeuSerAsnValLysLysLeu 86
Db 1663 CGTTTATATGATAATTTAGTACATCAAGCCTTGTTTGGCAAGTAAATGCTAAAAAAATT 1722
QY 87 ValLeuSerAspSerGluLysAsnThrLeuLys----- 97
Db 1723 TATCTT-----AAAAATGGATTGAAGCATTTCTTTAAGGATATCTCTCAC 1770
QY 98 -----AsnLysTyr-----LysLeuLeuThrGluLysLys 107
Db 1771 TTAATTGCAAAAATGCACTACTACTCAAGCTCTTTGGGCAAAACAAAAATATACACAAAAA 1830
QY 108 SerGlu-----AsnAlaGluValArgAlaValAlaLeuValProLysAspPhe----- 123
Db 1831 AGTGTGTGTTTAAAGCAAAATTAAGACCTTTTGGACTTTTGGACTTTTGTAGAAATTTATTTTA 1890
QY 124 -----ProLysAspLeuValLeuAlaProLeuProAspHisVal 136
Db 1891 AAAAATGCTTTTATATGTTTATAAGGTTTATAAATTAGC---GTTTGTCTGCAATTG 1947
QY 137 AsnAspPheThrTyrTyrLysLysArgLysLysArgLeuGlyLysProGluHisGln 156
Db 1948 GGAACATTTTAAATATATGAAATTTATATGAACCTTCAAGACAAACAAAAACCAAAA----- 2001
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Qy 262 -----AlaGluLeuLeuGluAspAspAspLeuThrIleIle 273  
Db 2353 GTAATTTTAAATAAAGAAAGCAAGAAATTTTAAACAAAGATGATTCGCATAAAT 2412  
Qy 274 GlyProArgLysTyrIleAspThrGlnHisIleAspProLysAspPheLeuAsnAsnAla 293  
Db 2413 -----TTTAATAAATAAAGATTTTAAAGT- 2436  
Qy 294 SerLeuLeuGluSerLeuProGluValLysThrAsnAsnSerValAlaAlaLysGlyGlu 313  
Db 2437 -----TCTAAATAATCTCTTTTGTAGCTAAA- 2460  
Qy 314 GlyThrValSerLeuAspTrpArgLeuGlnPheGluLysThrGluAsnLeuArgLeu 333  
Db 2461 -----ATATTTTACAGTCTTTCAAAA-AAAAGATCAAAAAATCTTT-TTA 2502  
Qy 334 SerAspSerProPhe-ArgPhePheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLe 353  
Db 2503 AAAACCACTCTTATTAAGGTATTAGGGTGGCAATATAGTGTTTTTTAAACTGATTT 2562  
Qy 353 uAsnLysSerGlyPheAspGluGluPheAsnHisTrpGlyGlyGluAspValGluPh 373  
Db 2563 TGATGAACCTTGATGGTTTAAATGAATAATTTATTGGTTGGGTAGAGAAGATAGTGAAT 2622  
Qy 373 eGlyTyrArg--LeuPheArgTyrGlySerPhe-----PheLysThrIleAs 388  
Db 2623 TGTTCGTAGATTTTATTTAATAAAGGCATTTTATAGACGATTAATAATTTAAAGCTATT- 2680  
Qy 388 pGlyIleMetAlaTyrHisGlnGluProGlyLysGluAsnGluThrAspArgGluAl 408  
Db 2681 -GCTTATCATATTTATCACAAGAAATAAGCAAAATAATGCTTGAAGCAATCATCAA-- 2737  
Qy 408 aGlyLysAsnIleThrLeuAspIleMetArgGluLysValProTyrIleTyrArgLysLe 428  
Db 2738 -----ATTATTATAGATACCATCAAAATAA- 2764  
Qy 428 uLeuProIleGluAspSerHisIleAsnArgValProLeuValSerIleTyrIleProAl 448  
Db 2765 -----AAGATTTCTTGGAGATAAAACATGAAGAAATAATAGTGTAGTTATACCAAT 2814  
Qy 448 aTyrAsnCysAlaAsnTyrIleGlnArgCysValAspSerAlaLeuAsnGlnThrValVa 468  
Db 2815 CTATATGTAGAAAAATTTAAGAGATGTTTATAGATAGCGTTATCAATCAACTTATAC 2874  
Qy 468 lAspLeuGluValCysIleCysAsnAspGlySerThrAsp---AsnThrLeuGluValI 487  
Db 2875 TAACCTTAGAATCATACTTGTCAATGATGGTAGCACAGATGAACACTCACTCAATATTGC 2934  
Qy 487 eAsnLysLeuTyrGlyAsnAsnProArgValArgIleMetSerLysProAsnGlyGlyI 507  
Db 2935 AAAAGAATATACCTTAAAGATAAAGAAATAACTCTTTTGTATGAAGAAAAATGGGGTTT 2994  
Qy 507 eAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGlyTyrTyrIleGlyGlnLeuAs 527  
Db 2995 AAGTTCAGCTAGAATAATATAGTATAGAATATCTTTAGCGGGAATAT- 3040  
Qy 527 pSerAspAspTyrLeuGluProAspAlaValGluLeuCysLeuLysGluPheLeuLysAs 547  
Db 3041 -----AAATTAATAA- 3051  
Qy 547 pLysThrLeuAlaCysValTyrThrThrAsnArgAsnValAsnProAspGlySerLeuI 567  
Db 3052 CAAAACCTCAACATATAAAGAAAAATCTTTAATAAGAAATTTCAATTTGGTGAAT- 3106  
Qy 567 eAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLysLeuThrThrAlaMetIleAl 587  
Db 3107 -----AATCCTTATAAT- 3118  
Qy 587 aHisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPheAsnGluLy 607  
Db 3119 -----ATATATAAGCATATAAAGACTCTCAAGCTTTTATAATGA 3159

Qy 607 sIleGlu-----AsnAlaValAspTyrAspMetPheLeuLysLeuSe 621  
Db 3160 AAAAGATTTAAACCAATTTTACTTACCCTAGTATAGATATATATATATCTTAGATAGTGA 3219  
Qy 621 rGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGlyAs 641  
Db 3220 TAATTATTGGAACTA- 3235  
Qy 641 pAsnThrSerIleLysLeuGlyIleGlnLysLysAsnHisPheValValValAsnG 661  
Db 3236 -----AACTGCATAGAAGAAATGCGTTATAAGATGAAAAAT- 3271  
Qy 661 nSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAsp--GluPheAspAspLeuAs 680  
Db 3272 -----GTGGATGATTGGTGGTTTGACCATGATTGCACCTATGAAGAC- 3313  
Qy 680 pGluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIle---AspI 699  
Db 3314 -----AATATAAATAAATAGCACAAAAAACAGGATGGAATTTTGTATTT 3360  
Qy 699 eLeuLysAspIleLysIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTy 719  
Db 3361 TAAAAAAGAATGATATAATCACTCCAAAAGAATATGCAAAATCGAGCATTAAGTGTAGATC 3420  
Qy 719 rProAsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAs 739  
Db 3421 TAGAGATATTTCTTTTGG------TGAATGGAATGATTGATTTTAAT- 3463  
Qy 739 nIlePheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysG 759  
Db 3464 -----TTTTAAAGCAAT 3477  
Qy 759 uIleLeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSer-- 778  
Db 3478 TAAACTTAATTT------ATAAATTTTATTAATCAATGAAGATATACACTT 3522  
Qy 779 -----TyrTyrThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAs 794  
Db 3523 TGGGATAATTTGTTTGTAGTGTCTAATAAATTTATGTT------TTATCACA 3570  
Qy 794 nIleAsnLysLeuSerGlnLeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAs 814  
Db 3571 AAAGTTGTTATTTGTCGTCGTTTAAGACAAACACT------ATATCAATCATGA 3618  
Qy 814 pSerLeuPheValLysAsnAspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAs 834  
Db 3619 T-----AAGAAG- 3625  
Qy 834 nPheSerAlaLeuThrHisAspTrpIleGluLysIleAsnAlaHisProProPheLysLy 854  
Db 3626 -----ATTACAAAGCAAAATGTCAGAGTATTTTAAAGA 3660  
Qy 854 sLeuIleLysThrTyrPheAsnAspAsnLeuLysSerMetAsnValLysGlyAlaSe 874  
Db 3661 TATATATGAACCT---TTCGGGAAACCGCTAAGGAAGCAAAAAATTTTAAAGCAGC 3717  
Qy 874 rGlnGlyMetPheMetThrTyrAlaLeu-----AlaHisGluLe 887  
Db 3718 AAGCAGGCTTATAACTGCTTTAAATTTGATAGAATTTTAAAGATCAAAAAACGAAAA 3777  
Qy 887 uLeuThrIleLysGluValIleThrSerCys- 898  
Db 3778 TGCACCTGCTATAAAGAAACATTTTACCTTCTGCTATGCCAAAAAGCTTTAATGATTAA 3837  
Qy 899 -----GlnSerIleAspSerValProGluTy 907  
Db 3838 AAAATTTAAAAAGATCCITTAATTTAAAGGAACAATTAGTTTTAAATTAACCTTTTAT 3897  
Qy 907 rAsnThrGlu-----AspIleTrp 913  
Db 3898 TCAACCAAAACCTTCTTATGATATTTGGAAATTTTGGCAAAAAATAAAAAATATTTAATA 3957  
Qy 913 ----- 913



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Qy 373 eGlyTyrArg---LeuPheArgTyrGlySerPhe-----PheLysThrIleAs 388
Db 2623 TGTTGCTAGATTTTATTTAATAAAGGCATTTTGTAGACGATATAAAATTTAAAGCTATT-- 2680
Qy 388 pGlyIleMetAlaTyrHisGlnGluProProGlyLysGluAsnGluThrAspArgGluAl 408
Db 2681 -GCTTATCATATTATCACAAGAAATAATAGCAAAATAAGCTTGAAAGCAATCATCAA-- 2737
Qy 408 aGlyLysAsnIleThrLeuAspIleMetArgGluLysValProTyrIleTyrArgLysLe 428
Db 2738 -----ATTATTATTAGATACCATCAAAATAA-- 2764
Qy 428 uLeuProIleGluAspSerHisIleAsnArgValProLeuValSerIleTyrIleProAl 448
Db 2765 -----AAGATTCTTGGAGATAAAACGAAGAAATAAGTGTAGTTATACCAAT 2814
Qy 448 aTyrAsnCysAlaAsnTyrIleGlnArgCysValAspSerAlaLeuAsnGlnThrValVa 468
Db 2815 CTATAATGTAGAAAATAATTTAAGAGAATGTTTAGATAGCGTTATCAATCAAACTTATAC 2874
Qy 468 lAspLeuGluValCysIleCysAsnAspGlySerThrAsp---AsnThrLeuGluValIl 487
Db 2875 TAACTTAGAAATCATACTTGTCAATGATGTTAGTACACAGATGAACACTCACTCAATATTGC 2934
Qy 487 eAsnLysLeuTyrGlyAsnAsnProArgValArgIleMetSerLysProAsnGlyGlyIl 507
Db 2935 AAAAGAAATATACCTTAAAGAGATAAAGAATAAATCTTTTGTGATAAGAAAAATGGGGTTT 2994
Qy 507 eAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGlyTyrTyrIleGlyGlnLeuAs 527
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Qy 527 pSerAspAspTyrLeuGluProAspAlaValGluLeuCysLeuLysGluPheLeuLysAs 547
Db 3041 -----AAATTAAGAAAA 3051
Qy 547 pLysThrLeuAlaCysValTyrThrThrAsnArgAsnValAsnProAspGlySerLeuIl 567
Db 3052 CAAAACTCAACATATAAAGAAAAATCTTTAATAGAATTTCAATTTGGATGGTAAT-- 3106
Qy 567 eAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLysLeuThrThrAlaMetIleAl 587
Db 3107 -----AATCCTTATAAT 3118
Qy 587 aHisPhePheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPheAsnGluLy 607
Db 3119 -----ATATATAAGCATATAAAGACTCTCAAGCTTTTATAATAATGA 3159
Qy 607 sIleGlu-----AsnAlaValAspTyrAspMetPheLeuLysLeuSe 621
Db 3160 AAAAGATTTAAACCAATTTTACTTACCCTAGTATAGATTATATATATCTTTAGATAGTA 3219
Qy 621 rGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGlyAs 641
Db 3220 TAATTATTGGAACTA-- 3235
Qy 641 pAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsnGl 661
Db 3236 -----AACTGCATAGAGAATCGGTTATAAGAATGAAAAAT-- 3271
Qy 661 nSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAsp---GluPheAspAspLeuAs 680
Db 3272 -----GTGGATGTATTGTGGTTTGCACCATGATTGCACCTATGAAGAC-- 3313
Qy 680 pGluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIle---AspIl 699
Db 3314 -----AATATAAAAAATAACCAAAATAAAGAGATGGAATTTTGTATT 3360
Qy 699 eLeuLysAspIleLysIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTy 719
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Qy 719 rProAsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleLeuGluTyrAsnLysAs 739
Db 3421 TAGAGATATTCTTTTGG-----TGAATGGAATGATTGATTTTAAT-- 3463
Qy 739 nIlePheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGl 759
Db 3464 -----TTTTTAAAGCAAT 3477
Qy 759 uIleLeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSer-- 778
Db 3478 TAAACTTAATTTT-----ATAAATTTTATATCAATCAAGATATACACTT 3522
Qy 779 -----TyrTyrThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAs 794
Db 3523 TGGGATAATTTTGTCTAGTGTCTAATAAATTTATGTT-----TTATCACA 3570
Qy 794 nIleAsnLysLeuSerGlnLeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAs 814
Db 3571 AAAGTTGTATTGTGTGTCGTTTAAAGACAAACAGT-----ATATCAAAATCATGA 3618
Qy 814 pSerLeuPheValLysAsnAspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAs 834
Db 3619 T-----AAGAAG----- 3625
Qy 834 nPheSerAlaLeuThrHisAspTrpIleGluLysIleAsnAlaHisProProPheLysLy 854
Db 3626 -----ATTACAAAAGCAAAATGTGTACAGATATTTTAAAGA 3660
Qy 854 sLeuIleLysThrTyrPheAsnAspAspLeuLysSerMetAsnValLysGlyAlase 874
Db 3661 TATATATGAAACT---TTCGGGAAAAACGCTAAGGAAGCAAAAATATTTTAAAGCAGC 3717
Qy 874 rGlnGlyMetPheMetThrTyrAlaLeu-----AlaHisGluLe 887
Db 3718 AAGCAGGTTTATAACTGCTTTAAATTTGATAGAATTTTAAAGATCAAAAAAACGAAA 3777
Qy 887 uLeuThrIleLysGluValIleThrSerCys----- 898
Db 3778 TGCACCTTGCTATTAAGAAACATTTTACCTTCTGTCGCAAAAAAGCTTTAATGATTAA 3837
Qy 899 -----GlnSerIleAspSerValProGluTy 907
Db 3838 AAAATTTAAAAAAGATCCTTTAAATTTTAAAGGAACAATTAGTTTAAATTAACCTTTAT 3897
Qy 907 rAsnThrGlu-----AspIleTrp----- 913
Db 3898 TCAAACAAAACTTCTTATGATATTTGGAAATTTTGGCAAAAAATAAAAAATATTTAATA 3957
Qy 913 ----- 913
Db 3958 ATAAAAATATAAAAAATTAATTTTAGGTATATCACTATATTAATATAGGAGAAAAT 4017
Qy 914 -----PheGln-----PheAlaLeuLeuIleLeuGluTy 923
Db 4018 ATTTTATATGCTATTTCAATCATATTTGTGAAAAATAATTTGCTTATTCATCCTCTTAG 4077
Qy 923 sLysThrGlyHisValPheAsnLysThrSerThrLeu----- 935
Db 4078 AAAAAATTAGACATAAAAAATAAAAAACATTTTACTAAAAAACATACACAGAGATAAAAT 4137
Qy 936 -----ThrTyrMetProTrpGluArgLysLeuGln-----TyrThrAsnGluGlnIl 951
Db 4138 CGATTCTTATTACCAAAAAAACTCTGTGGCAAAATTAATAATACAAATGAAGATTT 4197
Qy 951 eGluSerAlaLysArgGlyGluAsnIleProValAsnLysPheIleIle 967
Db 4198 A-----ATTAAACTTAATAAGCTTATTATA 4222
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## RESULT 9

US-10-303-118-1

; Sequence 1, Application US/10303118

; Patent No. 6905867

; GENERAL INFORMATION:

; APPLICANT: Gilbert, Michel  
; APPLICANT: Wakarchuk, Warren W.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of  
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of  
; FILE REFERENCE: 019633-000111US  
; CURRENT APPLICATION NUMBER: US/10/303,118  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US/09/816,028  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/118,213  
; PRIOR FILING DATE: 1999-02-01  
; PRIOR APPLICATION NUMBER: US 09/495,406  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 11474  
; TYPE: DNA  
; ORGANISM: Campylobacter jejuni  
; FEATURE:  
; OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384  
; OTHER INFORMATION: including LOS biosynthesis locus  
US-10-303-118-1

Alignment Scores:  
Pred. No.: 1,246-30 Length: 11474  
Score: 384.50 Matches: 243  
Percent Similarity: 35.71% Conservative: 163  
Best Local Similarity: 21.37% Mismatches: 337  
Query Match: 7.53% Indels: 394  
DB: 3 Gaps: 52

US-10-642-248-2 (1-972) x US-10-303-118-1 (1-11474)

QY 10 AlaTyrAsnSerAspTyrGlnLeuAlaLeu-----LysLeuPheGluLysSer 26  
DB 1459 AGTTATGCAAAAATGATGGATTTTAAAGCATGCTGATGAAGTCTGGAATGAG 1518  
QY 27 Ala-----GluileTyrGlyArgLysIleValGluPheGlnIleThrLysCysLysGlu 44  
DB 1519 TGTATTAAAGAGCTTAAATAATTTAAACTTCAAGAAGATATATCATCGCACTTACCGGT 1578  
QY 45 LysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsnLysGluLys 64  
DB 1579 AAA-----AATCTCTATAAAGCGGAATGG 1602  
QY 65 ValAsnValCys-----AapSerProLeuAspIleAlaThrGln----- 77  
DB 1603 ATAAGGCATGGTGGTGGCTGATGATGTTTGAAGATTTTAAATAAAATTTCACT 1662  
QY 78 -----LeuLeuSerAsnValLysLysLeu 86  
DB 1663 CGTTTTTAATGATAATTTAGTACATGAAGCCCTGTTTGGCAAGTAATGCTAAAAAATT 1722  
QY 87 ValLeuSerAspSerGluLysAsnThrLeuLys----- 97  
DB 1723 TATCTT-----AAAAATGGATTGAAGCATATTATCTTATAAGGATATCTCTCAC 1770  
QY 98 -----AsnLysTyr-----LysLeuLeuThrGluLysLys 107  
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QY 108 SerGlu-----AsnAlaGluValArgAlaValAlaLeuValProLysAspPhe----- 123  
DB 1831 AGTGGTGTTTAAAGCAAAATTTAAGAGCTTTTGGACCTTTTGGACCTTTTATAGAAATTTTAA 1890  
QY 124 -----ProLysAspLeuValLeuAlaProLeuProAspHisVal 136  
DB 1891 AAAAAATGGCTTTTATATATGGTTATAGGGTTTATATAATAGC-----GTTTGTCTGCAATG 1947  
QY 137 AsnAspPheThrTrpTyrLysLysArgLysLysArgLysLeuGlyIleLysProGluHisGln 156  
DB 156  
1948 GGAACATTTTTTAAATATATGAATATATGAACCTTCAAAAGACAAAAACCAAAA----- 2001  
QY 157 HisValGlyLeuSerIleIleValThrPheAsnArgProAlaIleLeuSerIleThr 176  
DB 2002 -----ACTTGGCGCTTAAATAATAAATTAATTAATCAAAAGAACCGCTTAAACTAGTG 2055  
QY 177 LeuAlaCysLeuValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAsp 196  
DB 2056 CTTGATAGTGTAAAAAT---CTAGCCCTTTTACCCTAAAGTGTATTAATCGCAGATGAT 2112  
QY 197 GlySerGlnGluAspLeuSerProIleIleArgGlnTyrGluAsnLysLeu-----Aap 214  
DB 2113 GGTAGCAAGAAAGATACAGCAAGCTTATTGAGATATCAAAAGATTTTCCCTTGCTCT 2172  
QY 215 IleArgTyrValArgGlnLysAspAsnGlyPheGlnAlaSerAlaIleArgAsnMetGly 234  
DB 2173 TTAACAACATTTGGCAAGAGATGAAGGTTTAACTTAGTAAAGATCGCAACAAAACT 2232  
QY 235 LeuArgLeuAlaLysTyrAspPheIleGlyLeuLeuAspCysAspMetAlaProAsnPro 254  
DB 2233 ATAAAAAACGCTGATAGTGAATATATAATAGTTATTGATGCTGATATGATTTTGGAAAAA 2292  
QY 255 LeuTrpValHisSerTyrVal----- 261  
DB 2293 GATTTCAATAAAGAACATTTAGAAATTTGCACAAAGAAAGCTTTTTTACAAGTTCAAGA 2352  
QY 262 -----AlaGluLeuLeuGluAspAspAspLeuThrIleIle 273  
DB 2353 GTAATTTTAAATAAAGAAAGCGAAGAAATTTTAAACAAAGATGATTATCGCATATTT 2412  
QY 274 GlyProArgLysTyrIleAspThrGlnHisIleAspProLysAspPheLeuAsnAla 293  
DB 2413 -----TTTAATAAAGAAAGATTTTAAAGT----- 2436  
QY 294 SerLeuLeuGluSerLeuProGluValLysThrAsnAsnSerValAlaAlaLysGlyGlu 313  
DB 2437 -----TCTAAAAATCTCTTTTAAAGTAAA----- 2460  
QY 314 GlyThrValSerLeuAspTrpArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeu 333  
DB 2461 -----ATATTTTACAGTCTTTCAAAA---AAAAGATGAAAAATCTT---TTA 2502  
QY 334 SerAspSerProPhe-ArgPhePheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLe 353  
DB 2503 AAAAAACCATCTTATTAAAGCTTATAGGGTTGCAATATATGATTTTAAAACTGATTT 2562  
QY 353 uAsnLysSerGlyPheAspGluGluPheAsnHisTrpGlyGlyGluAspValGluPh 373  
DB 2563 TGATGAACCTGATGGTTTTTAATGAAAAATTTTATGCTGGGTGGGTAGAGAGATAGTGAAT 2622  
QY 373 eGlyTyrArg--LeuPheArgTyrGlySerPhe-----PheLysThrIleAs 388  
DB 2623 TGTTCTAGATTTTATTATTAAGGCATTTTATAGACGATTTAAATTTAAAGCTATT-- 2680  
QY 388 pGlyIleMetAlaTyrHisGlnGluProProGlyLysGluAsnGluThrAspArgGluAl 408  
DB 2681 -GCTTATCATATTTATCAAAAGAAATAGCAAAAAATGCTTGAAGAGCAATCATCA-- 2737  
QY 408 aGlyLysAsnIleThrLeuAspIleMetArgLysValProTyrIleTyrArgLysLe 428  
DB 2738 -----ATTATTTTAGATACCATCAAAATAAA----- 2764  
QY 428 uLeuProIleGluAspSerHisIleAsnArgValProLeuValSerIleTyrIleProAl 448  
DB 2765 -----AAGATTTCTGGAGATAAAAACATGAAGAAATAGGTGATGTTATACCAAT 2814  
QY 448 aTyrAsnCysAlaAsnTyrIleGlnArgCysValAspSerAlaLeuAsnGlnThrValVa 468  
DB 2815 CTATATGTAGAAAAATATTTAAGAGAATGTTTAGATAGCGTTTATCAATCAAACTTATAC 2874  
QY 468 lAspLeuGluValCysIleCysAsnAspCysSerThrAsp---AsnThrLeuGluValI 487  
DB 2875 TAACTTAGAAAAATCATACTTGTCAATGTTGGTAGCAGATGAACACTCACTCAATATGTC 2934

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Qy 487 eAsnLysLeuTyrGlyAsnAsnProArgValArgIleMetSerLysProAsnGlyGlyI1 507
Db 2935 AAAAGAAATACCTTAAAGAGATAAAGAAATCTTTTCGATAGAAAATGGGGTTT 2994
Qy 507 eAlaSerAlaSerAsnAlaValSerPheAlaLysGlyTyrTyrIleGlyGlnLeuAs 527
Db 2995 AAGTTCAGCTAGAAATATAGTATAGAACTCTTTAGCGGGGAATAT 3040
Qy 527 pSerAspTyrLeuGluProAspAlaValGluLeuCysLeuLysGluPheLeuLysAs 547
Db 3041 -----AAATTAAGAAA 3051
Qy 547 pLysThrLeuAlaCysValTyrThrThrAsnArgAsnValAsnProAspGlySerLeuI1 567
Db 3052 CAAACCTCAACATATAAAGAAAATCTTTTAATAGAATTTCAATGGATGGTAAT 3106
Qy 567 eAlaAsnGlyTyrAsnTrpProGluPheSerArgLysLeuThrAlaMetIleAl 587
Db 3107 -----AATCCTTATAAT 3118
Qy 587 aHisHisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPheAsnGluLy 607
Db 3119 -----ATATATAAGCATATAAAGCTCTCAAGCTTTTAATAATGA 3159
Qy 607 sIleGlu-----AsnAlaValAspTyrAspMetPheLeuLysLeuSe 621
Db 3160 AAAAGATTTAAACCAATTTTACTACCTCATAGTATATATATATATCTTTAGATAGTGA 3219
Qy 621 rGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGlyAs 641
Db 3220 TAATTATGGAACTA----- 3235
Qy 641 pAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsnGl 661
Db 3236 -----AACTGCATAGAAGATCGGTATAAGAAATGAAAAAT 3271
Qy 661 nSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAsp---GluPheAspAspLeuAs 680
Db 3272 -----GTGGATGTATTGTGGTTTGGACCATGATTCACCTATGAAGAC----- 3313
Qy 680 pGluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIle---AspI1 699
Db 3314 -----AATATAAATAATAGCACAAAAAACAAGGATGGAATTTTGATTT 3360
Qy 699 eLeuLysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTy 719
Db 3361 TAAAAAAGATGTATAATCACTCCAAAAGATATGCAAAATCGAGCATTAAGTGATGATC 3420
Qy 719 rProAsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAs 739
Db 3421 TAGAGATATTCTTTTGG-----TGAATGGAATGATGATTTAAT----- 3463
Qy 739 nIlePheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGl 759
Db 3464 -----TTTTTAAGCAAT 3477
Qy 759 uIleLeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSer-- 778
Db 3478 TAAACTTAAATTT-----ATAAATTTTATTATCAATGAAGATATACACTT 3522
Qy 779 -----TyrTyrThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAs 794
Db 3523 TGGGATAATTTGTGCTAGTGTGTAATAAATTTATGTT-----TTATCACA 3570
Qy 794 nIleAsnLysLeuSerGlnLeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAs 814
Db 3571 AAAGTTGATTGTGCTGTTTAAGAGCAACAGT-----ATATCAAAATCATGA 3618
Qy 814 pSerLeuPheValLysAsnAspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAs 834
Db 3619 T-----AAGAAG----- 3625
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Qy 834 nPheSerAlaLeuThrHisAspTrpIleGluLysIleAsnAlaHisProProPheLysLy 854
Db 3626 -----ATTACAAAAGCAATGTGTACAGATATTTTAAAGA 3660
Qy 854 sLeuIleLysThrTyrPheAsnAspAsnLeuLysSerMetAsnValLysGlyAlaSe 874
Db 3661 TATATATGAAACT---TTCGGGGAACCGCTAAGGAAGCAAAAAATATTTTAAAGCAGC 3717
Qy 874 rGlnGlyMetPheMetThrTyrAlaLeu-----AlaHisGluLe 887
Db 3718 AAGCAGGTGTATAACTGCTTTAAATTTGATAGAAATTTTAAAGATCAAAAAACGAAA 3777
Qy 887 uLeuThrIleLysGluValIleThrSerCys----- 898
Db 3778 TGCACCTTGCTATAAAGAACATTTTACCTGCTATGCCAAAAAGCTTTAATGATTAA 3837
Qy 899 -----GlnSerIleAspSerValProGluTy 907
Db 3838 AAAATTTAAAAAAGATCCTTTAAATTTAAAGGAACAATTAGTTTAAATTAACCTTTAT 3897
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Qy 913 ----- 913
Db 3958 ATAAAAATATAAAAAATTAATTAATTTTAGGTATATCACTATATATATAGGAGAAAT 4017
Qy 914 -----PheGln-----PheAlaLeuLeuIleLeuGluLy 923
Db 4018 ATTTTATATGCTATTTCAATCATCATCTTTGTGAAAAATAATTTGCTTATTCATCCTTTAG 4077
Qy 923 sLysThrGlyHisValPheAsnLysThrSerThrLeu----- 935
Db 4078 AAAAATTTAGACATAAAATAAAAAAACATTTTACTAAAAAACATACACAGAGATAAAAT 4137
Qy 936 -----ThrTyrMetProTrpGluArgLysLeuGln-----TyrThrAsnGluGlnI1 951
Db 4138 CGATTTCTATTACCAAAAAAAACTCTTGCGCAATTAATAATACACAAATGAAGATTT 4197
Qy 951 eGluSerAlaLysArgGlyGluAsnIleProValAsnLysPheIleIle 967
Db 4198 A-----ATTAACTTAATAAAGCTATTATA 4222

RESULT 10
US-10-303-128-1
; Sequence 1, Application US/10303128
; Patent No. 6911337
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,128
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11474
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384
; OTHER INFORMATION: including LOS biosynthesis locus
US-10-303-128-1
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QY 607 silleGlu-----AsnAlaValAspTyrAspMetPheLeuLysLeuSe 621
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D 3220 TAATTATTGGAACTA----- 3235
QY 641 pAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsnG1 661
D 3236 ----AACTGTCATAGAAGATGCGTTATAAGAATGAAATA----- 3271
QY 661 nSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAsp----GluPheAspAspLeuAs 680
D 3272 -----GTGGATGTATTGTGTTTGCACCATGATTGCGACCTATGAAGC----- 3313
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D 3314 -----AATATATAAAATAAGCACAAATAAAGGATGGAATTTTGTGATTT 3360
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D 3421 TAGAGATATTCTTTTTCGA-----TGGAAATGGAATGATGATTTTAA----- 3463
QY 739 nIlePheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysG1 759
D 3464 -----TTTTTAAGCAAT 3477
QY 759 uIleLeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSer-- 778
D 3478 TAAACTTTAAATTT-----ATAAATTTTATTATCAATCAAGATATACACTT 3522
QY 779 -----TyrTyrThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAs 794
D 3523 TGGGATAATTTTGTGCTAGTGTCTAATAAAATTTATGTT-----TTATCACA 3570
QY 794 nIleAsnLysLeuSerGlnLeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAs 814
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D 3619 T-----AAGAAG----- 3625
QY 834 nPheSerAlaLeuThrHisAspTrpIleGluLysIleAsnAlaHisProPropheLysLy 854
D 3626 -----ATTACAAAAGCAAAATGTGTACAGATATTTTAAAGA 3660
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D 3661 TATATATGAAGACT---TTCGGGGAACCGCTAAGAGCAAAATTTATTATAAGCAGC 3717
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D 3718 AAGCAGGTTATAACTGCTTTTAAATTTGATAGAATTTTAAAGATCAAAAACGAA 3777
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D 3778 TGCACCTTGCTATAAAGAAACATTTTACCTTGTCTATGCCAAAAGCTTTAAATGATTA 3837
QY 899 -----GlnSerIleAspSerValProGluTy 907
D 3838 AAAATTTTAAAGATCCTTTTAAATTTTAAAGCAACATTTAGTTTAAATAAACCTTTTAT 3897
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D 3898 TCAAAACAAACTTCTTTATGATATTGGAATTTTGGCAAAATATAAATAATATTTAATA 3957
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D 4018 ATTTTATATGCTATTTCATCAATCATCTTTGTGAAAAATAATTTTGCTTATTATCATCCCTTTAG 4077
QY 923 sLysThrGlyHisValPheAsnLysThrSerThrLeu----- 935
D 4078 AAAAATTAGACATATAAAATAAAAAACATTTTCTACTAAAAAACATACACAGATAAAAAT 4137
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D 4138 CGATTCCTTATTACCAAAAAAACTCTGTGCAAAATTAATAATACACAAATGAGATTT 4197
QY 951 eGluSerAlaLysArgGlyGluAsnIleProValAsnLysPheIleIle 967
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RESULT 11
US-09-634-238-29/c
; Sequence 29, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 13825
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-29

Alignment Scores:
Pred. No.: 4,88e-22 Length: 13825
Score: 308.00 Matches: 117
Percent Similarity: 43.65% Conservative: 72
Best Local Similarity: 27.02% Mismatches: 159
Query Match: 6.03% Indels: 86
DB: 3 Gaps: 18

US-10-642-248-2 (1-972) x US-09-634-238-29 (1-13825)
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D 11874 ATGCTTTAGTTTCTATATCGTTTCTATTATAATGTTGAAAAATACTTACACGATGC 11815
QY 459 ValAspSerAlaLeuAsnGlnThrValValAspLeuValCysIleCysAsnAspGly 478
D 11814 ATAGACAGTTTATTGTCGCAACATACGTCATATAGAGATGCTCTAGTTGACGCGGA 11755
QY 479 SerThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArg 498
D 11754 TCGCAGACCGCTTCTACCTGCTCAATCTGTAAAAAATGCTCAGCAGGATGAACGAGTCCA 11695
QY 499 IleMetSerLysProAsnGlyIleAlaSerAlaSerAsnAlaValSerPheAla 518
D 11694 GTCTTCTCAAAGCAAAATGTTGGGTTGCAGATACGCGTAATTTTGTGTATCGTTGCA 11635
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Qy 289 PheLeuAsnAenAlaSerLeuLeuGluSerLeuProGluValLysThrAsnAsnSerVal 308  
Dy 4402 TTTTAAACAAATAATCTTTTAAAGAAATTTTATCAGGTAAATAGAGTGGAAATATTTGTT 4461  
Qy 309 AlaAlaLysGlyGlu-----GlyThrValSerLeuAspTTPArgLeuGlu 323  
Dy 4462 TGTACAAAATTTATATAAAAAAGTATAATTGGTAACTTGAGGTTTGAT----- 4509  
Qy 324 GlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPheAlaAla 343  
Dy 4510 -----GAGAATTTTAAATAATTGGTGAG----- 4530  
Qy 344 GlyAsnValAlaPheAlaLysLysTrpLeu----- 353  
Dy 4531 ---GATTTACTTTTAAATTTGTAATAATTTTATGTCAGAGCACTGCATAGTCGTAGATACG 4587  
Qy 354 -----AsnLysSerGlyPhePheAspGluGluPheAsn 364  
Dy 4588 ACTTCTTCCTGTACACCTATCGCATCGTAAAGACTTCTGCAATGAATCAGGAGTTCAC 4647  
Qy 365 His----- 365  
Dy 4648 GAAATTCATTAGATTTTATAACAATTTTAAATGAAATAAGCAGTATTGTTCTCGCAAAA 4707  
Qy 366 -----TrpGlyGlyGluAspValGluPheGlyTyrArgLeu 377  
Dy 4708 TTAGCTAATTATGTGAAGCGCAAAATTTTAAAGAGAAAGGTAAAGTGCTCCGAAAAATG 4767  
Qy 378 PheArgTyrGlySer-----PhePheLys 385  
Dy 4768 TTTGAATTAGCTAGTAATATTGACAGTAAATCAAATTACACGAGAGATTTTTCAAA 4827  
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Dy 4828 GATGTTAAATTTATACCTCTTCTAT----- 4851  
Qy 406 ArgGluAlaGlyLysAsnIleThrLeuAsp-----IleMetArgGluLys 420  
Dy 4852 ---AAACGGTAAAGTACTTATCAATTAAGGGATTTAGTATTCTTAATGAAATGT 4908  
Qy 421 ValProTyrIleTyrArgLysLeuLeuPro-----IleGluAspSer 434  
Dy 4909 TCACCCATCTGTATATAAATTTATACACAGGTTTCAAAAACAGTAAGTAATCAAAAAT 4968  
Qy 435 HisIleAsnArgValProLeu-----ValSerIleTyrIle 446  
Dy 4969 TAAATTAACCTCAATTACCTTTTAAATTTATAGGAGTTGAAAAATGAATATAGTATCAT 5028  
Qy 446 eProAlaTyrAsn---CysAlaAsnTyrIleGlnArgCysValAspSerAlaLeuAsnG 465  
Dy 5029 GTCGGTATATAATGAGCCTTTAAATTTATGTGAGAGATTCAGTAGAATCTATATAATCA 5088  
Qy 465 nThrValValAspLeuValCysIleCysAsnAspGlySerThrAspAsnThrLeuG 485  
Dy 5089 AACGCTTACTGATTTTGATTCATAATTTGTCATTTGATATCAATCAAGTAGAGTGATTTAA 5148  
Qy 485 uValIleAsnLysLeuTyrGly---AsnAsnProArgValArgIle---MetSerLysPr 503  
Dy 5149 GCAATTCCTAACAGATATTTCAGTTGTAGATAATAAGATAAATAATCTTGTCTAATGAAGA 5208  
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Dy 5327 -TTTATGAGGAAAAATTCATTGGATTTCTCAGCAACTCTAATAGAAATTTGATAGACCAAAA 5385  
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Qy 583 r-----AlaMetIleAlaHisIlePheArgMetPheTh 594  
Dy 5437 TGATATACGGAAGATGTTATTGAATAGATCTATACTTGGCCCAACCGTGGCGGTAAA 5496  
Qy 594 rIleArgAlaTrpHisLeuThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyr 614  
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Qy 614 rAspMetPheLeuLeuSerGluValGlyLysPheLysHisLeuAsnLysIleCysTyr 634  
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Dy 5588 -----AAATCGGCTTACTCAATAAA-- 5608  
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Dy 5609 ---GTACTTTTACAGTATAGATTAAACGAGAATGGAAATATCAAAACCAATAAGTT 5661  
Qy 673 rAspGluPhe-----AspAspLeuAspGluSerArgLysTyrIle-- 686  
Dy 5662 TAAGCAATATATTACTCAGCTATTTTTACAAGATTTTATAAGAAAAAATCTTATATGA 5721  
Qy 687 -PheAsnLysThrAlaGluTyrGlnGluIleAspIle----- 699  
Dy 5722 TATCACAAAAATTTACTAATTTACTTTCAAGAGTAGTGTGATAAAGAAACGCTATACTCAGCA 5781  
Qy 700 -----LeuLysAspIleLysIleIleGlnAsnLysAspAlaLys 712  
Dy 5782 AGAGCTCTCTAAATATTTTGGAGCTAAATCTACCCCTAGTATTACTATTAGAAAACTATA 5841  
Qy 712 sIleAlaValSerIlePheTyrProAsnThrLeuAsnGlyLeuValLysLysLeu---- 730  
Dy 5842 TATTTGTTTATATTACTTTTAAGTCTCCC-----TTGGTTAGGAGGTATTAAAT 5892  
Qy 731 -AsnAsnIleIleGluTyrAsnLysAsnIlePheValIleValLeuHis-ValAspLysA 750  
Dy 5893 AAATGATATT-----AATATTTTAGTACTGAAATTTGTTGAGGAGAGAA 5937  
Qy 750 snHisLeuThrProAspIleLysLysGluIleLeuAlaPheTyrHisLysHisGlnVala 770  
Dy 5938 ACAAGTGACT-----AATAGAAAAATTTATGTATGCTCATCTCTTTTATCATTTAT 5988  
Qy 770 snIleLeuLeuAsnAsnAspIleSerTyrTyrThrSerAsnArgLeuIleLysThrGlu 790  
Dy 5989 TGATTTGTTTATATAAGAGAGATATAT-----TCAAATTTAGAAATTTATCTCTCTT 6042  
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Dy 6043 CTCTCTCTCTGATGTTGATAATTTAGAGAAAAAATAAATAAATAAATAAATAATATAC 6102  
Qy 806 luTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsnAspSerTyrAlaTyrM 826  
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Qy 826 etLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHisAspTrpIleGluLysI 846  
Dy 6151 TTAAA-----GATGCTGGTCTAAGTTATAGTAGTAAATTTGTTTATTTTATTTA 6204  
Qy 846 leAsnAlaHisProProPheLysLysLeuLys-----ThrTyrPheAsn-----A 862  
Dy 6205 ATGATGCAACGCCTATTGGGAGGACACTATAAAGCATGCTGTTATTATTATAATCTAATTG 6264  
Qy 862 spAsnAspIleLysSerMetAsnValLysGlyAlaSerGlnGlyMet----- 877  
Dy 6265 AAGATGGTTTAAATGTTTACTTACTCTATATTTAGTCAAAACCTTTGGAGGTATTATG 6324  
Qy 878 -----PheMetThrTyrAlaLeuAlaH 885

Db 6325 TAAAAAATATATTCTTCACAAAATTCAGCCACATGGATTTTCAGATATTGTTTACGGGA 6384  
Qy 885 isGluLeuThrIlelle----- 891  
Db 6385 TTGAAGTTAATCAATAGTTAATTTGGCAAGGATCCGCTTATAAAAAATTTATTGAAG 6444  
Qy 892 -----LysGluValIleThrSerCysGlnSerIleAspSerValProGluTyrAsnT 909  
Db 6445 TCCCTAGAAAGAACTT-----TTTGACAATGTAAACAGATATCAAA 6486  
Qy 909 hrGluAspIleTrpPheGlnPheAlaLeuLeuLeuGluLysLysThrClyHisValP 929  
Db 6487 AAGAAATGGCAATAAATCTTTTGGAGCAGTAAGAGTTAGTATTAAATCACTTCAGTAC 6546  
Qy 929 heAsnLysThrSerThrLeuThr-----TyrMetProTIPGluArgLysLeuG 945  
Db 6547 TAGTATTAAACGACGCTCTATCTATAGATAAAGAGTTTATGAGTTATAACAAATAGATAG 6606  
Qy 945 InTIPThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIleProValAsnLys 964  
Db 6607 AACGTCGGAAGAACATTTAATTTTATATAAATCAATAGTCAATGAATATATAATAAA 6665

RESULT 13  
US-09-107-532A-3235  
; Sequence 3235, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD/ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arinello, Pamela Deneka  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 3235:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2166 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...2166  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3235:

## US-09-107-532A-3235

Alignment Scores:  
Pred. No.: 1.19e-22 Length: 2166  
Score: 301.50 Matches: 153  
Percent Similarity: 38.06% Conservative: 121  
Best Local Similarity: 21.25% Mismatches: 259  
Query Match: 5.90% Indels: 187  
DB: 3 Gaps: 28

## US-10-642-248-2 (1-972) x US-09-107-532A-3235 (1-2166)

Qy 269 AspLeuThrIlelleGly-----ProArgLysTyrIleAspThrGlnHis 283  
Db 88 GATTTCGTTATTGTCGGCTCGGCAATTTGTAAGATGACCAAGAAATCCCTACGATAAAG 147  
Qy 284 IleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro----- 300  
Db 148 GTAGAAAAGAAATGATGTTGCTGAAGCAACACATGCTGTAGATTGGATATCAATCAT 207  
Qy 301 -----GluValLysThrAsnAsnSer-----ValAlaLysGly 312  
Db 208 TTATATAATCTTGATGTTAAGACCCAAAGCGGTTTTAAGGTACGTTTATCAGGAAATATG 267  
Qy 313 GluGlyThrValSerLeuAspTrpArgLeuGluGlnPheGluLysThrGluAsnLeuArg 332  
Db 268 AGAGGAAAAGCAATCTTTAGACTTCCAAACACAGCAACATCAAAATGGCATAGCTGTGAAA 327  
Qy 333 LeuSerAspSer---ProPheArgPhePheAlaAlaGlyAsnValAlaPheAlaLysLys 351  
Db 328 TTAACCGTAAATATCTCTTAT-----GATGACGGCATTTGAATCTTCA 369  
Qy 352 TrpLeuAsnLysSerGlyPhePheAspGluGluPheAsnHisTrpGlyGlyGluAspVal 371  
Db 370 TGGGAAAAGAAAAGAAAGATTACTGAAAAAGGGATAAATTTATGCAAGGACTCATGCGCTA 429  
Qy 372 GluPheGlyTyrArgLeuPheArgTyrGlySerPhePheLysThrIleAspGlyIle--- 390  
Db 430 AAAAAAGCAATCCCGCGGTCAAACTCGAATTTGAACCCAGGATCGATCGATGACAGAG 489  
Qy 391 ---MetAlaTyrHisGlnGluProGlyLysGluAsnGluThrAspArgGluAlaGly 409  
Db 490 TGGATCAGTCGTCATGAGAAACCTGATCTGAAAGAGCAAGG----- 531  
Qy 410 LysAsnIleThrLeuAspIleMetArgGluLysValProTyrIleTyrArgLysLeuLeu 429  
Db 532 -----AAAGAAGTACAAAGGATTTGCCTACCGC----- 558  
Qy 430 ProIleGluAspSerHisIleAsnArgValProLeuValSerIleTyrIleProAlaTyr 449  
Db 559 -----CCATTGATTTCCATCTTATGCTGCTCTAT 588  
Qy 450 AsnCys---AlaAsnTyrIleGlnArgCysValAspSerAlaLeuAsnGlnThrValVal 468  
Db 589 AACGTTGAAATCAAAATGGCTCGAAAATGCAATTCGTTGATCTTGATCAACAGTATGAT 648  
Qy 469 AspLeuGluValCysIleCysAsnAspGlySerThrAspAsnThrLeu---GluValIle 487  
Db 649 CACTGGGAACATGATGATCAGTGATGCTTCTACTGATCCAGCTATCCGAAAGTGCTTA 708  
Qy 488 AsnLysLeuTyrGlyAsnAsnProArgValArgIleMet---SerLysProAsnGlyGly 506  
Db 709 GAATCCTATCAAGCAAAAGATGATAGATAAAGTCGTTTTCCGACAAAGAAATGGACAC 768  
Qy 507 IleAlaSerAlaSerAsnAlaValSerPheAlaLysGlyTyrIleGlyGlnLeu 526  
Db 769 ATCAGTCTGGCAACTAATTTCTGCATTGGAATGCGAAGGAGAGATTTATACGCTCTTA 828  
Qy 527 AspSerAspAspTyrLeuGluProAspAlaValGluLeuCysLeuLysGluPheLeuLys 546  
Db 829 GATAATGATGACGAATTAACCTCCATTTGCCTTTATGAAAGTGGCAAAAGTGTAAACGCTA 888  
Qy 547 AspLysThrLeuAlaCysValTyrThrThrAsnArgAsnValAsnProAspGlySerLeu 566

Db	889	CATCCGAACTGGATTGATCTACAGTGCAGAAATAAAATCGATGCAGATGGGAATCGC	948
Qy	567	IlealaasnGlyTyrAsnTyrProGluPheSerArgGluLysLeuThrThrAlaMetIle	586
Db	949	TTTGACCCGACATCTCAAAA---GCAGATCTGGTCTCCCATCATTTGATGGGAAATAATATAT	1005
Qy	587	AlaHisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPheAsnGlu	606
Db	1006	ATCTCTCACTTAGCGGTATATCGCAAGCATTTGTTAAGGNACTTGGCGGTTCCGTAAA	1065
Qy	607	LysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeuSerGluValGlyLysPhe	626
Db	1066	GGATATGAAGGCTCTCAAGATTATGATTTGGTCTTCGTGTGACAGAACAAATTCCTGCA	1125
Qy	627	LysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGlyAspAsnThrSerIleLys	646
Db	1126	GAACACATTTACCACATT---GACCGTGTCTTGTTAT---	1158
Qy	647	LysLeuGlyIleGlnLysLysAsnHisPheValValValAsnGlnSerLeuAsnArgGln	666
Db	1159	---CATTGGCGGACGATCCCGGATCAACTGCAGCAAT	1194
Qy	667	GlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAspGluSerTyrIle	686
Db	1195	GGG---GAAGCTAAAGCTACATC	1215
Qy	687	PheAsnLysThrAlaGluTyrGlnGluLysLeuAspIleLysIleLysIle	706
Db	1216	---TATGATCTCGAGTGAACGATTTGACAGATCTCTATCTPAGA	1257
Qy	707	GlnAsnLysAspAlaLysIle---AlaValSerIlePheTyrProAsnThrLeu	723
Db	1258	AGAANTATCAAGGACGCTACATCTCTGGCAGAAATTTCTGGTTTATGAATCACTTAT	1317
Qy	724	AsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIlePhe---	741
Db	1318	GATGTTTTGCAAGAAGACTTGGTCAGTGTGATCATCTCAACTAAGAATGGCTATGAAGAT	1377
Qy	742	---ValIle---ValLeu	745
Db	1378	CTAAAAACTGTGTGGATTCGATCTCGAAAAAAGCTCTTATCCAAATTATGAATCATTT	1437
Qy	746	HisValAspLysAsnHisLeuThrProAspIleLysLysGluIleLeuAlaPheTyrHis	765
Db	1438	ATTGCAGATATGGAAGTACAGATCTCTAAATG---CAAGATTTATTTGAGAAATAC---	1491
Qy	766	LysHisGlnValAsn---IleLeuLeuAsnAsnAspIleSerTyrTyrThrSer	782
Db	1492	AAGCATCAGCTGAAAGACCGATTATCGTC---	1521
Qy	783	AsnArgIleuLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGlnLeuAsn	802
Db	1522	---GAATTAATTTGACATTCCTCAATTTATTCAGTATCAACAATCTGGCAGCAGAAAA	1578
Qy	803	LeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsnAsp---	821
Db	1579	GCAACCGGCAATACTTTTATTTCTTGATTAACGATACAGAGTGATTTGAACCTGCTGG	1638
Qy	822	---SerTyrAlaTyr---SerTyrAlaTyr---	825
Db	1639	ATGACAGCGATGGTTCTTATGACAGTTTGCATCGAATCGGCTGTGTAGGAGCAAAATTA	1698
Qy	825	---	825
Db	1699	TTTTATCCGGATGATACAACGACGATGCAGGTGTATTTATGAGGATCGGTGGCGTTGCA	1758
Qy	826	---MetLysLysTyrAsp---	831
Db	1759	GGACATGCATTAATACTATGATCGAACACATTTGTGGTTACTTTGGCCGATTTGGTCAAT	1818
Qy	832	GlyMetAsnPheSerAlaLeuThrHisAspTrpIle-----GluLysIleAsn	847

QY 313 GluGlyThrValSerLeuAsp-----TyrArgLeu-----GluGlnPheGluLeuThrGlu 329  
Db 394 GAAGNAGGTTGAGCGAGATATATTATGGCAATATCCGATAAATCAATCAATTTGATT 453  
QY 330 AsnLeuArgLeuSerAspSerProPheArgPheAlaAlaGlyAsnValAlaPheAla 349  
Db 454 GACTTAAACCGCGGATTAAATTGATCAAGTTTAT---CCATGGAATGCCATTATATAA 510  
QY 350 LysLysTrpLeuAsnLysSerGlyPhe---PheAspGluGluPheAsnHisTyrGlyGly 368  
Db 511 AAAAGTAGTAGTGAAGAAACGTAACCTAGGATGAGGAATAATAAGTTATGGGAC 570  
QY 369 GluAspValGluPheGlyTyrArgLeuPheArgTyrGlySerPhePheLys----- 385  
Db 571 ACT-----GGTCTATTGTGAAATAATCAATTCA 597  
QY 386 -----ThrLeAspGlyLeuMetAlaTyrHisGlnGluProPro 398  
Db 598 GCATCTCAGAATGTTATTTTATTAAAGATTGTTGTATTTTATAGACAAGCAACCCA 657  
QY 399 GlyLysGluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArg 418  
Db 658 -----AATTCGACAGTAATAATGTTGCA 681  
QY 419 GluLysValProTyrIleTyrArg----- 426  
Db 682 ACAAGGTTCCCTTCTGTTTCAACAATTTAACTAAATTCGTTCAAATTTAAATGAACAA 741  
QY 426 ----- 426  
Db 742 AATAAATTTGAACGCTACAAAGTTATTTTATATAACAAATGTTTCAAAAAATACTTTTGG 801  
QY 427 -----LysLeuLeuProIleGluAsp----- 433  
Db 802 GCGATTGAAATAATTAACCCATTACGTGTGATGAGTCGGTTTATGAAGTAGTCAAAAGGTG 861  
QY 433 ----- 433  
Db 862 CGAGTAGATTTTAGACAAGCTTTAGACAAGCAGCAGCTGAATGATATCGATTTTGAATAC 921  
QY 434 -----SerHisIleAsn 437  
Db 922 ATCAACAATTTTATCAAAATGCAATGATCCAGCAGCTTATTATGAGGACTACTTTGAAA 981  
QY 438 ArgValProLeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArg 457  
Db 982 AATCTGTATAAAGTTAGTGTGTCATGCGGATTCAAAATGCTTCAAAATATTATTAAGACAA 1041  
QY 458 CysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAsp 477  
Db 1042 ACATTAGAAACTGTTTGTGAGCAGCTTTTACGTGAGATTGAATCATTTTAGTAGAAT 1101  
QY 478 GlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgVal 497  
Db 1102 GCGCTACAGATAATACCATGATGATATTATTAACGAATTTGCGAGTAAAGATCCGAGAATT 1161  
QY 498 ArgIleMetSerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaValSerPhe 517  
Db 1162 ACGGGATTCTTATTGGCAAAAGTAATCTCGACACGCAAGAAATGTGGGCATTTTCGATG 1221  
QY 518 AlaLysGlyTyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGlu----- 533  
Db 1222 GCACGAGGACGGTATTTGCAATTTCTGGATGAGATGATCATTTTGGACGAATTTATTA 1281  
QY 534 -----ProAspAlaValGluLeuCysLeuLys 542  
Db 1282 CAAGACGCTTATATCGTCATATGATAGTACACAGATATCTGTATTATTTGGCATGAAA 1341  
QY 543 GluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnValAsnPro 562  
Db 1342 GAAAGTTACCAAAATGGAGAGTGCACGTTGTTTCAC-----AATCCA 1383  
QY 563 AspGlySerLeuIleAlaAsnGly-----TyrAsnTrpProGluPheSerArgGluLys 580

Db 1384 -----TTACTAACTAATGCGGACGATGCTCGTGAAGAAATTTATTGGATGAA 1434  
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1435 GTAACCCCTTATTATATGATAAATATTATTTATTAGATACATCAAGAAATAACTTG 1494  
QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeu----- 618  
Db 1495 GTAAAC-----TTAGAACAAATTTGTTGCGGAGGATGCTTATTTTCCACTTAT 1539  
QY 619 ---LysLeuSerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgVal 637  
Db 1540 ACAGCATTTATAGTACGAAATAATTTGTCACATAACAAATATTGCTGCACAGCAATC 1599  
QY 638 LeuHisGlyAspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheVal 657  
Db 1600 GTTAGACAAGATGCTTGTG---ATGCTACGTATGGAATGAATTCGTGATGAGTTCAAT 1656  
QY 658 ValValAsnGlnSerLeu-----AsnArg----- 665  
Db 1657 TTACATGACAAATGTTGGAGTACTTAAACCAACATGCTCCAAATCGAAATTTGAAGCATPAT 1716  
QY 666 ---GlnGlyIleThrTyrTyrAsnTyrAspGluPheAsp-----AspLeuAspGlu 681  
Db 1717 CGGTAAATAATTTATTAATACATTAACACTGGTTTATTTTGTATGATGAATCGTGTGATCNA 1776  
QY 682 SerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeuLys 701  
Db 1777 GCATTTAAAGNACGTTTC-----TATCAAGAA-----TTAAAA 1809  
QY 702 AspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrProAsn 721  
Db 1810 GAG---AAATACATCCAACTATTAGGGCTAGACTTAGTGAAGAAAGAAATAATTTCTAAT 1866  
QY 722 ThrLeuAsnGlyLeu-----ValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsn 739  
Db 1867 GATCAGAACAAAGTAGAGCGTATCACAGCAATCCAAATAATTTTACAATACAACTAGAA 1926  
QY 740 IlePheValIleVal-----LeuHisValAspLysAsnHisLeuThrProAspIle 756  
Db 1927 ATATATCAAAATATTTATTAAGATTTTGGGATGAAGAAADACCTTTATTTCCGATGTT 1986  
QY 757 Lys-----LysGluIleLeuAlaPheTyrHisLysHisGlnValAsn--- 770  
Db 1987 CATATTCAGAGCGTGGAGGTAAAGTAATTTTGGACAAGAGAGACCCAGGGAATGGG 2046  
QY 771 -----IleLeuLeuAsnAsnAspIleSerTyrTyrThrSer 782  
Db 2047 ACGCAATTTGAAATGTTTTCAATTTATTTATTCAGATAACGAT-----ACAAGC 2094  
QY 783 AsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGlnLeuAsn 802  
Db 2095 AAT-----GCCAGCGGAGTATGATTTTCGTTTATATGGGT 2130  
QY 803 LeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsnAspSer 822  
Db 2131 GACATACAAAAATAAT-----CATGATAGTTTATTAGTATCT----- 2169  
QY 823 TyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHisAspTrp 842  
Db 2170 ---TTATTAATTTAAAGAAAGAGGTACTACTTTTAAATCGATTTGTTTACACCCGAGTGG 2226  
QY 843 IleGluLysIleAsnAlaHis---ProProPheLysLysLeuIleLysThrTyrPheAsnAs 862  
Db 2227 ---GAAAAA-----GGCTATACCTACTACTACAGAAATAATGATATATA----- 2266  
QY 862 pAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThrTyrAl 882  
Db 2267 -----CTTTGCTAGACAATGTTTTTACAAATTTGG 2295  
QY 882 aleuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSerIleAs 902

Db 2296 GCGGCT-----ATACTCAAAATATGCACATTTGATTACA----- 2332  
Qy 902 pSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuLeuG1 922  
Db 2333 -----ATGTTGCAATTTTGGACTTCTC----- 2353  
Qy 922 uLysLysThrGlyHisVal-----PheAsnLysThrSerThrLeuThr 936  
Db 2354 -GAGAGGGGAAACACATCTTTAGTGTCTGACAAAACCAAGGCTATATCC 2404  
RESULT 15  
US-08-961-527-71  
; Sequence 71, Application US/08961527  
; Patent No. 6420135  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 391  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,527  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32768 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-961-527-71  
Alignment Scores:  
Pred. No.: 1,74e-18 Length: 32768  
Score: 281.50 Matches: 113  
Percent Similarity: 38.31% Conservative: 87  
Best Local Similarity: 21.65% Mismatches: 173  
Query Match: 5.51% Indels: 149  
DB: 3 Gaps: 19  
US-10-642-248-2 (1-972) x US-08-961-527-71 (1-32768)  
Qy 426 ArgLysLeuLeuProIleGluAspSerHisIleAsnArgValProLeuValSerIleTyr 445  
Db 6166 AGAAATTTGCTA---GTGGATGATAA-----ATAACAGTCATT 6201  
Qy 446 IleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAspSerAlaLeuAsnGln 465  
Db 6202 GTACCAGTATACAAATGTGGAAACATCTCTGAGGAAGTCCTAGATAGTATTATTACTCAA 6261  
Qy 466 ThrValValAspLeuGluValCysIleCysAsnAspGlySerThrAspAsnThrLeuGlu 485  
Db 6262 ACATATAAAATATAGATTGTGTCTTAATGATGGTCTACGGATGCTTCAGGTGAA 6321

Qy 486 ValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMetSerLysProAsnGly 505  
Db 6322 ATTTGTAAGAATTTTCAGAAATGGATCACCGAATTTCTTATATAGAACAAAGAAATGCT 6381  
Qy 506 GlyIleAlaSerAsnAlaAlaValSerPheAlaLysGlyTyrTyrIleGlyGln 525  
Db 6382 GGTCTTTTCGCCACGAAACACCGGTCTGAAATATATGTCGGAATATATGTGACCTTT 6441  
Qy 526 LeuAspSerAspTyrLeuGluProAspAlaValGluLeuCysLeuLys----- 542  
Db 6442 GTGGACTCGGATGATTGGATTGAGCAAGATTATGTAGAACTCTATATAAAAAATAGTA 6501  
Qy 543 GluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsn----- 559  
Db 6502 GAGTATCAGCTGATATTGCGTTGTAATATTATTCTTCAACGAAGTGAAGGAATG 6561  
Qy 560 -----ValAsnProAspGlySerLeu 566  
Db 6562 TTCTACTTTTCATATATTGGAGACTCCTATTATGAGAAAGTATATGATATGTTCTATC 6621  
Qy 567 IleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLysLeuThrAlaMetIle 586  
Db 6622 TTTGAGAACTTGATGAA-----ACTCAAGAAATGAAGAGTTTGTCTTGATA 6669  
Qy 587 AlaHisPheArgMetPheThrIleArgAlaTrpHisLeu----- 600  
Db 6670 TCTGCTTGGGTAAACTCTATAGGCAAGATTGTTGAGCAGTTGCGCTTTTGACATAGGT 6729  
Qy 601 -----ThrAspGlyPhe---AsnGluLysIleGluAsnAlaValAspTyrAspMet 616  
Db 6730 AATTAGGAGAGATGTTACTCTCAATCAAAAGGTA----- 6765  
Qy 617 PheLeuLysLeuSerGluValGlyLysPheLysHisLeuAsnLysIleCysTyr---Asn 635  
Db 6766 ---TATTATTATCAGAA-----AAGGTAATTTATTAAATAAAGTCTTTATGCTTAT 6816  
Qy 636 ArgValLeuHisGlyAsp----- 641  
Db 6817 CGGATTAGAAAAGGTAGTTTATCAAGAGTTTGGACAGAAAGTGGATGCACGCTTAGTT 6876  
Qy 642 -----AsnThrSerIleLysLeuGlyIleGlnLysLysAsnHis 655  
Db 6877 GATGCTATGCTGAACGTATTACGTACTAGCTAATATGGTTATCTCTAGAGAAACAC 6936  
Qy 656 PheValValValAsnGlnSerLeu-----AsnArgGlnGly----- 667  
Db 6937 TTGGCAGTTTATCGTCAGATGTTTGGAAAGTCAGTCTGCCAACCGTCAAGCTAGTGGTTA 6996  
Qy 668 -----IleThrTyrTyrAsnTyrAsp-----GluPheAsp 677  
Db 6997 TCTGACACAGCAACGTATAAGAGTTTGAATGAAACAAAGCGCTTTAAATCAGCTATCG 7056  
Qy 678 AspLeuAspGluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIle 697  
Db 7057 AGACAGAGGAAAGTGAAGAAAGCCATTGCTCTCGCAACAACTATGGCTATGTAGAC 7116  
Qy 698 AspIleLeuLysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIle 717  
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Db 7177 ATTATAGCGATTTTCCAAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 7230  
Qy 738 LysAsnIlePheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLys 757  
Db 7231 -----AGTTTGATCTCAGAAATTAATTAATTCGCGGTAAC 7266  
Qy 758 LysGluIleLeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAspIle 777  
Db 7267 TCTGAGCAAAATTTTCATGTTAT-----AAATCGGATATT 7299

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QY 778 SerTyrTyrThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLys 797
|||
Db 7300 AGTTACACAGCTTTTACGCTATTTCATAGCTGATTTC-----GTGCAAGAA 7347
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QY 798 LeuSerGlnLeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPhe 817
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Db 7348 GACAAGGCCCTCTACTTGGACTGTGATCTAGTTGTACGAAAAAATCTGGATGACTTGT 7407
|||
QY 817 ----- 817
|||
Db 7408 GCTACAGACTTACAAGATTATCCTTTGGCTGCTGTAGAGATTTTGGGGCAGACCTTAT 7467
|||
QY 818 -----ValLysAsnAspSerTyrAlaTyr 825
|||
Db 7468 TTGTGTCAGAAATCTTTAATGCCGGTGTCTCTTGGTAAACAAT-----GCTTTT 7518
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QY 826 MetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHisAspTrpIleGluLys 845
|||
Db 7519 TGGAAAAAAGAGATATGACCCAAAAATTAATTGATGTAAACCAATGAATGGCATGATAAG 7578
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QY 846 IleAsn 847
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Db 7579 GTGGAT 7584
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Search completed: January 8, 2006, 23:09:22  
Job time : 560 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:05:28 ; Search time 30 Seconds  
(without alignments)

274.974 Million cell updates/sec

Title: US-10-642-248-2

Perfect score: 5108

Sequence: 1 MNTLSQAIKAYNSNDYQLAL.....SAGRGENIPWKNFIINSITL 972

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 61072 seqs, 8486849 residues

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5108	100.0	972	7	US-11-172-145-2
2	5104	99.9	972	7	US-11-124-215-1
3	5104	99.9	972	7	US-11-120-422-10
4	4733	92.7	972	7	US-11-124-215-7
5	4511	88.3	972	7	US-11-124-215-3
6	4502.5	88.1	965	7	US-11-172-145-4
7	3697	72.4	703	7	US-11-124-215-17
8	3697	72.4	703	7	US-11-172-145-12
9	3687	72.2	703	7	US-11-172-145-21
10	3687	72.2	703	7	US-11-172-145-22
11	3151.5	61.7	704	7	US-11-172-145-25
12	529	10.4	101	7	US-11-124-215-8
13	223	4.4	101	7	US-11-124-215-9
14	212	4.2	99	7	US-11-124-215-10
15	210	4.1	651	7	US-11-172-145-10
16	209	4.1	37	7	US-11-124-215-14
17	209	4.1	337	7	US-11-102-497-5
18	209	4.1	337	7	US-11-102-497-12
19	208.5	4.1	348	7	US-11-102-497-3
20	208.5	4.1	348	7	US-11-102-497-11
21	202	4.0	252	6	US-10-510-386-104
22	193.5	3.8	617	7	US-11-172-145-8
23	192.5	3.8	101	7	US-11-124-215-11
24	184	3.6	2710	7	US-11-051-453-41
25	180.5	3.5	615	7	US-11-172-145-6

Sequence 1318, Ap  
Sequence 145, App  
Sequence 144, App  
Sequence 154, App  
Sequence 196, App  
Sequence 2408, Ap  
Sequence 285, App  
Sequence 285, App  
Sequence 214, App  
Sequence 121, App  
Sequence 215, App  
Sequence 339, Appl  
Sequence 5, Appl  
Sequence 2864, Ap  
Sequence 1432, Ap  
Sequence 3, Appl  
Sequence 62, Appl  
Sequence 42, Appl  
Sequence 87, Appl  
Sequence 110, App  
Sequence 43, Appl

26 161.5 3.2 306 6 US-10-467-657-1318  
27 153 3.0 1613 6 US-10-055-877-145  
28 153 3.0 1637 6 US-10-055-877-144  
29 150.5 2.9 1006 6 US-10-793-626-154  
30 149 2.9 552 6 US-10-131-826A-196  
31 148.5 2.9 347 6 US-10-467-657-2408  
32 145.5 2.8 412 6 US-10-485-517-285  
33 142.5 2.8 2665 7 US-11-124-368A-214  
34 142 2.8 1167 7 US-11-052-554A-215  
35 141 2.8 2668 7 US-11-124-368A-215  
36 140.5 2.8 588 7 US-11-052-554A-339  
37 134.5 2.6 1147 6 US-10-815-668-5  
38 132 2.6 5024 6 US-10-793-626-2964  
39 132 2.6 1145 6 US-10-793-626-1432  
40 131.5 2.6 1067 7 US-11/062  
41 131.5 2.6 1092 7 US-11/062  
42 131 2.5 2367 7 US-11-051-453-42  
43 130 2.5 179 6 US-10-873-528-87  
44 125 2.4 1420 7 US-11-077-550-110  
45 124 2.4 603 7 US-11-134-241-43

## ALIGNMENTS

RESULT 1  
US-11-172-145-2  
; Sequence 2, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172.145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 2  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-11-172-145-2

Query Match 100.0%; Score 5108; DB 7; Length 972;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MNTLSQAIKAYNSNDYQLALFKSAIYGRKIVEFOITCKEKLSAHPSVNSAHL5VN 60

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Qy 121 KDFPKDLVLAPLDPHVNDFWYKKRKRKLGKPEHQHVGLSIIVTFNRPAILSIITLACL 180
Db 121 KDFPKDLVLAPLDPHVNDFWYKKRKRKLGKPEHQHVGLSIIVTFNRPAILSIITLACL 180
Qy 181 VNOKTHYPFVIVTDGSGQEDLSPIIROYENKLDIRYVQKONGFOASARNMGLRLAKY 240
Db 181 VNOKTHYPFVIVTDGSGQEDLSPIIROYENKLDIRYVQKONGFOASARNMGLRLAKY 240
Qy 241 DFIGLDDCMAPNPLVHVSVAELLEDDDLTIIGPRKYIDTQHDIDPKDFLNNASLLESPL 300
Db 241 DFIGLDDCMAPNPLVHVSVAELLEDDDLTIIGPRKYIDTQHDIDPKDFLNNASLLESPL 300
Qy 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSDSPFFFAAGNVAFAKKWLNKSGFFD 360
Db 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSDSPFFFAAGNVAFAKKWLNKSGFFD 360
Qy 361 EEFNHHGGEDVEFGYRLFYSGSPFKTIIDGIMAYHQEPGKENETDREAGKNIITLDMREK 420
Db 361 EEFNHHGGEDVEFGYRLFYSGSPFKTIIDGIMAYHQEPGKENETDREAGKNIITLDMREK 420
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Db 481 DNTLEVINKLYGNPNRVRIMSKPENGASNAVAASFAGYIIGQDSDDDYLPDVELC 540
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Db 541 LKEFLKDKTLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIENAVDDYDMFLKLVSEVGFKEHLNKI CYNRVLHGDNTSIKKLGIOKKNHFVVVN 660
Db 601 TDGFNEKIENAVDDYDMFLKLVSEVGFKEHLNKI CYNRVLHGDNTSIKKLGIOKKNHFVVVN 660
Qy 661 QSLNRQGITYYNYDEFDLDESRYIFNKTAEQEEDILKDIKIQNKDAKIAVSI FYP 720
Db 661 QSLNRQGITYYNYDEFDLDESRYIFNKTAEQEEDILKDIKIQNKDAKIAVSI FYP 720
Qy 721 NTNLGLVKKLNNIIEYNKNI FVILVHVDKNHLPDIKKEILAFYKHQVNNILNNDISYY 780
Db 721 NTNLGLVKKLNNIIEYNKNI FVILVHVDKNHLPDIKKEILAFYKHQVNNILNNDISYY 780
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Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIPDNHDSLFVKNDSYAYMKKYDVGNFSA LTH 840
Qy 841 DWTEKINAHPPPKKLIKTYFENDNLDKSMNVKGSQGMFTYALAHELLTTI KEVITSCQS 900
Db 841 DWTEKINAHPPPKKLIKTYFENDNLDKSMNVKGSQGMFTYALAHELLTTI KEVITSCQS 900
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLQWNTNEQIESAKR GENI 960
Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLQWNTNEQIESAKR GENI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
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## RESULT 2

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US-11-124-215-1
; Sequence 1, Application US/11124215
; Publication No. US20050266460A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTEURELLA MULTOCIDA AND
; TITLE OF INVENTION: USBS THEREOF
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; FILE REFERENCE: 35541.101
; CURRENT APPLICATION NUMBER: US/11/124,215
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: 10/217,613
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/178,951
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-124-215-1
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 KEEKVNVCDSPDLATQALLSNVKKLVLSDEKNTLKNKWLKTEKSENAEVAVALVP 120
Db 61 KEEKVNVCDSPDLATQALLSNVKKLVLSDEKNTLKNKWLKTEKSENAEVAVALVP 120
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Db 121 KDFPKDLVLAPLDPHVNDFWYKKRKRKLGKPEHQHVGLSIIVTFNRPAILSIITLACL 180
Qy 181 VNOKTHYPFVIVTDGSGQEDLSPIIROYENKLDIRYVQKONGFOASARNMGLRLAKY 240
Db 181 VNOKTHYPFVIVTDGSGQEDLSPIIROYENKLDIRYVQKONGFOASARNMGLRLAKY 240
Qy 241 DFIGLDDCMAPNPLVHVSVAELLEDDDLTIIGPRKYIDTQHDIDPKDFLNNASLLESPL 300
Db 241 DFIGLDDCMAPNPLVHVSVAELLEDDDLTIIGPRKYIDTQHDIDPKDFLNNASLLESPL 300
Qy 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSDSPFFFAAGNVAFAKKWLNKSGFFD 360
Db 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSDSPFFFAAGNVAFAKKWLNKSGFFD 360
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Db 361 EEFNHHGGEDVEFGYRLFYSGSPFKTIIDGIMAYHQEPGKENETDREAGKNIITLDMREK 420
Qy 421 VPYIYRKLLPIEDSHINRVLPSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
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Db 481 DNTLEVINKLYGNPNRVRIMSKPENGASNAVAASFAGYIIGQDSDDDYLPDVELC 540
Qy 541 LKEFLKDKTLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIENAVDDYDMFLKLVSEVGFKEHLNKI CYNRVLHGDNTSIKKLGIOKKNHFVVVN 660
Db 601 TDGFNEKIENAVDDYDMFLKLVSEVGFKEHLNKI CYNRVLHGDNTSIKKLGIOKKNHFVVVN 660
Qy 661 QSLNRQGITYYNYDEFDLDESRYIFNKTAEQEEDILKDIKIQNKDAKIAVSI FYP 720
Db 661 QSLNRQGITYYNYDEFDLDESRYIFNKTAEQEEDILKDIKIQNKDAKIAVSI FYP 720
Qy 721 NTNLGLVKKLNNIIEYNKNI FVILVHVDKNHLPDIKKEILAFYKHQVNNILNNDISYY 780
Db 721 NTNLGLVKKLNNIIEYNKNI FVILVHVDKNHLPDIKKEILAFYKHQVNNILNNDISYY 780
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Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIPDNHDSLFVKQDSYAYMKKYDVGWNFSAALTH 840
Qy 841 DWIEKINAHPPFKKLKITYFENDNDLSMNKVGASQGMFMTYALAHELLTTIIKEVITSQCS 900
Db 841 DWIEKINAHPPFKKLKITYFENDNDLSMNKVGASQGMFMTYALAHELLTTIIKEVITSQCS 900
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Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972

RESULT 3
US-11-120-422-10
; Sequence 10, Application US/11120422
; Publication No. US20050287646A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H
; APPLICANT: Kumari, Kshana
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION
; FILE REFERENCE: 3554.049
; CURRENT APPLICATION NUMBER: US/11/120,422
; CURRENT FILING DATE: 2005-05-02
; PRIOR APPLICATION NUMBER: US/09/879,959
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/469,200
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 972
; TYPE: PRT
; ORGANISM: pasteurella multocida
US-11-120-422-10

Query Match 99.9%; Score 5104; DB 7; Length 972;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 KEEKVNVCDSPDIATQALLSNVKKVLSDSEKNTLKNKWLTTTEKSENAEVRVALVLP 120
Db 61 KEEKVNVCDSPDIATQALLSNVKKVLSDSEKNTLKNKWLTTTEKSENAEVRVALVLP 120
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Db 121 KDFPKDLVLPDHPNDFTWYKKRKLGLIKPEHQHVGSLSIIVTFNRPAILSLITLACL 180
Qy 181 VNQKTHYPFVITVDGSOEDLSPIIROYENKLDIRYVRQKNDGQASAAARMGLRLAKY 240
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Qy 421 VPIYIRKLLPIEDSHINRVLPLSIYIPAYCANYIQCVDLSALNOTVVDLEVCICNDGST 480
Db 421 VPIYIRKLLPIEDSHINRVLPLSIYIPAYCANYIQCVDLSALNOTVVDLEVCICNDGST 480
Qy 481 DNTLEVINKLYGNPNVRIMSKPNKGISASNAVAFKAGYIQCQLSDDDYDLEPDAVELC 540
Db 481 DNTLEVINKLYGNPNVRIMSKPNKGISASNAVAFKAGYIQCQLSDDDYDLEPDAVELC 540
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Qy 601 TDGFNEKIENAVDYDMPLKLSVKGFKHLNKKIYNRVLHGDNTSIKKLGIOKKNHFVVVN 660
Db 601 TDGFNEKIENAVDYDMPLKLSVKGFKHLNKKIYNRVLHGDNTSIKKLGIOKKNHFVVVN 660
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Db 721 NTNLGLVKKLNNIIIEYNKNIFVIVLVHVDKXHLTPDIKCEILAFVYKHQVNNILLNNDISYY 780
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIPDNHDSLFVKQDSYAYMKKYDVGWNFSAALTH 840
Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIPDNHDSLFVKQDSYAYMKKYDVGWNFSAALTH 840
Qy 841 DWIEKINAHPPFKKLKITYFENDNDLSMNKVGASQGMFMTYALAHELLTTIIKEVITSQCS 900
Db 841 DWIEKINAHPPFKKLKITYFENDNDLSMNKVGASQGMFMTYALAHELLTTIIKEVITSQCS 900
Qy 901 IDSVPEYNTEDIMFQFALLILEKKTGHVFNKSTLTLYMPWERKLQWNTNEQIESAKRGNI 960
Db 901 IDSVPEYNTEDIMFQFALLILEKKTGHVFNKSTLTLYMPWERKLQWNTNEQIESAKRGNI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
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RESULT 4
US-11-124-215-7
; Sequence 7, Application US/11124215
; Publication No. US20050266460A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTEURELLA MULTOCIDA AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 35541.101
; CURRENT APPLICATION NUMBER: US/11/124,215
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: 10/217,613
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 7
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus of alignment of SEQ ID NOS:1 and 3
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/ LOCATION: (17)..(17)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/
/ NAME/KEY: MISC FEATURE
/ LOCATION: (62)..(62)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
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/ NAME/KEY: MISC FEATURE
/ LOCATION: (90)..(90)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
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/ LOCATION: (113)..(113)
/ OTHER INFORMATION: Ile or Val
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/ LOCATION: (243)..(243)
/ OTHER INFORMATION: Ile or Val
/
/ NAME/KEY: MISC FEATURE
/ LOCATION: (253)..(253)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/
/ NAME/KEY: MISC FEATURE
/ LOCATION: (279)..(279)
/ OTHER INFORMATION: Ile or Val
/
/ NAME/KEY: MISC FEATURE
/ LOCATION: (288)..(288)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/
/ NAME/KEY: MISC FEATURE
/ LOCATION: (292)..(292)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/
/ NAME/KEY: MISC FEATURE
/ LOCATION: (316)..(316)
/ OTHER INFORMATION: Ile or Val
/
/
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/ NAME/KEY: MISC FEATURE
/ LOCATION: (329)..(329)
/ OTHER INFORMATION: Phe or Tyr
/
/ NAME/KEY: MISC FEATURE
/ LOCATION: (340)..(340)
/ OTHER INFORMATION: Phe or Tyr
/
/ NAME/KEY: MISC FEATURE
/ LOCATION: (405)..(405)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/
/ NAME/KEY: MISC FEATURE
/ LOCATION: (439)..(439)
/ OTHER INFORMATION: Ile or Val
/
/ NAME/KEY: MISC FEATURE
/ LOCATION: (744)..(744)
/ OTHER INFORMATION: Ile or Val
/
/ NAME/KEY: MISC FEATURE
/ LOCATION: (952)..(952)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/
/ US-11-124-215-7
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Query Match 92.7%; Score 4733; DB 7; Length 972;
Best Local Similarity 92.7%; Pred. No. 1.4e-299;
Matches 901; Conservative 22; Mismatches 49; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQALAKLFEKSAEYGRKIVFQITKCKEKLSAHPSVNSAHLVSN 60
Db 1 MNTLSQAIKAYNCNDYXLLAKLFEKSAEYGRKIVFQITKCKEKLSAHPSVNSAHLVSN 60

Qy 61 KEKVNVCDSPLDIATQLLSNVKLVLSDSSEKNTLKNWKLLTEKKSNAEYRAVALVP 120
Db 61 EXEKNVVCDSPLDIATQLLSNVKLVLSDSSEKNTLKNWKLLTEKKSNAEYRAVALVP 120

Qy 121 KOPPKDLVLAPLDHVNDFWYKKRKRKLGIRKPEHGHVGLSIIVTFNRPAILSITLACL 180
Db 121 KOPPKDLVLAPLDHVNDFWYKKRKRKLGIRKPEHGHVGLSIIVTFNRPAILDITLACL 180

Qy 181 VNOKTHYFPEVIVTDGSOEDLSPIRQYENKLDIRYVRQKONGFOASAARNMGLRLAKY 240
Db 181 VNOKTHYFPEVIVTDGSOEDLSPIRQYENKLDIRYVRQKONGFOASAARNMGLRLAKY 240

Qy 241 DFIGLLDCDMPNPLWHSYVAELLEDDLTITIGPRKYIDTOHIDPKOFLNNASLESPL 300
Db 241 DFIGLLDCDMPNPLWHSYVAELLEDDLTITIGPRKYIDTOHIDPKOFLNNASLESPL 300

Qy 301 EVKTNNSVAAKGGTYSLDWRLEOPEKTENLRSDSPFRFAAGNVAFKAKWLKSGFFD 360
Db 301 EVKTNNSVAAKGGTYSLDWRLEOPEKTENLRSDSPFRFAAGNVAFKAKWLKSGFFD 360

Qy 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQBPBGKENETDREAGNITLDMREK 420
Db 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQBPBGKENETDREAGNITLDMREK 420

Qy 421 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Db 421 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480

Qy 481 DNTLEVINKLYGNPRVRIMSKPBGGLIASNAASVFAKGYIIGQDSDDDYLPDPAVELC 540
Db 481 DNTLEVINKLYGNPRVRIMSKPBGGLIASNAASVFAKGYIIGQDSDDDYLPDPAVELC 540

Qy 541 LKEFLKDKTLCVYITNRNVPDGLIANGYNWPEFSREKLTAMIAHFRMETIRAWHL 600
Db 541 LKEFLKDKTLCVYITNRNVPDGLIANGYNWPEFSREKLTAMIAHFRMETIRAWHL 600

Qy 601 TDGFNEKIENAVDYMFLKLSVEGKPKHLNKI CYNRVLHGDNTSIIKGLGIQKQNHFFVFN 660
Db 601 TDGFNEKIENAVDYMFLKLSVEGKPKHLNKI CYNRVLHGDNTSIIKGLGIQKQNHFFVFN 660
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Qy 661 QSLNRQGITVYNDYDFDLDSESRKYIFNKTAEBYQEEIDILKDIKIQNDKAKIAVSIFYP 720
Db 661 QSLNRQGITVYNDYDFDLDSESRKYIFNKTAEBYQEEIDILKDIKIQNDKAKIAVSIFYP 720
Qy 721 NTNLGLVKLNIIIEYNKNIIFVILVHVDKXHLTPDIKKEILAFYHKKHQVNILLNNDISYY 780
Db 721 NTNLGLVKLNIIIEYNKNIIFVILVHVDKXHLTPDIKKEILAFYHKKHQVNILLNNDISYY 780
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAETH 840
Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAETH 840
Qy 841 DWIEKINAHPPFKKLIKITYFNDNDLKSNNVKGASQGMFMTYALAHELLTIIKEVITSQS 900
Db 841 DWIEKINAHPPFKKLIKITYFNDNDLKSNNVKGASQGMFMTYALAHELLTIIKEVITSQS 900
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGNI 960
Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGNI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
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## RESULT 5

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US-11-124-215-3
; Sequence 3, Application US/11124215
; Publication No. US20050266460A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTEURRELLA MULTOCIDA AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 35541.101
; CURRENT APPLICATION NUMBER: US/11/124,215
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: 10/217,613
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 3
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-124-215-3
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Query Match 88.3%; Score 4511; DB 7; Length 972;
Best Local Similarity 86.7%; Pred. No. 3.4e-285;
Matches 843; Conservative 64; Mismatches 65; Indels 0; Gaps 0;
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Qy 1 MNTLSQAIKAYNSNDYQALALFEKSAETIGRKIVFEQITCKEKLKSAHPSVNSAHLVN 60
Db 1 MNTLSQAIKAYNCNDYELALALFEKSAETIGRKIVFEQITCKEKLKSTNSYVSEDNSYVS 60
Qy 61 KEEKVNCDSPLDIATQILLNKKLVLSDESKNTLKNKKLLTEKKSNAEVRVALVP 120
Db 61 EDKKNSVCDSSLDIATQILLNKKLVLSDESKNTLKNKKLLTEKKSNAEVRVALVP 120
Qy 121 KDFPKDLVLAUPDPVNDFTWYKKKQKLGIKPEHQHVGSLIIVTFNRPAILSLITLACL 180
Db 121 KDFPKDLVLAUPDPVNDFTWYKKKQKLGIKPEHQHVGSLIIVTFNRSRILDTLACL 180
Qy 181 VNQKTHYPPEVITVDGSGOEDLSPRIQYENKLDIRYVRQKXNGFQASARNMGLRLAKY 240
Db 181 VNQKTHYPPEVVVADGSGENLLTIVQKYEQLDKIVRQKDYGYQLCAVRNLGLRTAKY 240
Qy 241 DFIGLLDCDMPNPLVWHSYVAELLEDLDTIIGRPKIDTQHDIDPKOFLNNALESILP 300
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## RESULT 6

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US-11-172-145-4
; Sequence 4, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; FILE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
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Db 241 DFVSIILDCDMPQOLVHVSYLELLEDNDIVLIGPRKYVDTHNITABQFNDPVLIESLP 300
Qy 301 EVKTNNSVAAKGGTVSLDWRLSQFTEKTNRLSDSPFRFFAAGNVAFAKWLNKSGFFD 360
Db 301 ETATNNPSTISGNISLSDWRLEHFKTDLNRLCDSFFRYFCGNVAFSKWLNKVGWFD 360
Qy 361 EEFNHMGGEDEVFGRYLFYRGSFFKTIDIGIMAYHQBPBGKENETDRAGKNITLIDIREK 420
Db 361 EEFNHMGGEDEVFGRYLFAGKCFRVIDGGMAYHQBPBGKENETDRAGKSIITLKIYKEK 420
Qy 421 VPYIYRKLLPIEDSHINRPVLVSIYYPAYNCANYIQRCVDSALNOTVVDLEVCICNDGST 480
Db 421 VPYIYRKLLPIEDSHIHRIPLVSIYYPAYNCANYIQRCVDSALNOTVVDLEVCICNDGST 480
Qy 481 DNTLEVINKLYGNNPRVRIMSKPBGGIASASNAVSPAKGYIYQGLSDDDYLEPDAVELC 540
Db 481 DNTLEVINKLYGNNPRVRIMSKPBGGIASASNAVSPAKGYIYQGLSDDDYLEPDAVELC 540
Qy 541 LKEFLKDKTILACVYTTNRYNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL 600
Db 541 LKEFLKDKTILACVYTTNRYNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL 600
Qy 601 TDGFNEKIENAVDYDMPLKLSEVCKFKHLNKKIYCNRVLHGDNTSIKKGIOKKHFFVVVN 660
Db 601 TDGFNEKIENAVDYDMPLKLSEVCKFKHLNKKIYCNRVLHGDNTSIKKGIOKKHFFVVVN 660
Qy 661 QSLNRQGITVYNDYDFDLDSESRKYIFNKTAEBYQEEIDILKDIKIQNDKAKIAVSIFYP 720
Db 661 QSLNRQGITVYNDYDFDLDSESRKYIFNKTAEBYQEEIDILKDIKIQNDKAKIAVSIFYP 720
Qy 721 NTNLGLVKLNIIIEYNKNIIFVILVHVDKXHLTPDIKKEILAFYHKKHQVNILLNNDISYY 780
Db 721 NTNLGLVKLNIIIEYNKNIIFVILVHVDKXHLTPDIKKEILAFYHKKHQVNILLNNDISYY 780
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAETH 840
Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAETH 840
Qy 841 DWIEKINAHPPFKKLIKITYFNDNDLKSNNVKGASQGMFMTYALAHELLTIIKEVITSQS 900
Db 841 DWIEKINAHPPFKKLIKITYFNDNDLKSNNVKGASQGMFMTYALAHELLTIIKEVITSQS 900
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGNI 960
Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGNI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
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; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-172-145-4

Query Match      88.1%; Score 4502.5; DB 7; Length 965;
Best Local Similarity 86.3%; Pred. No. 1.2e-284;
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

QY 1 MNTLSQAIKAYNSNDYQLALKLFKESAEIYGRKIVFQITKCKEKLKSAHPSVNSAHLNVN 60
DB 1 MNTLSQAIKAYNSNDYELALKLFKESAEIYGRKIVFQITKCKEKLKSAHPSVNSAHLNVN 53
QY 61 KEEKVNVCDSPDIATQALLSNVKKLVLSSEKNTLKNKKWKLTEKKSENAEVRVALVP 120
DB 54 EDKNSVCSSLDIATQALLSNVKKLVLSSEKNTLKNKKWKLTEKKSENAEVRVALVP 113
QY 121 KOPPKDLVLAFLPDHVNDFWYKRRKLGIKPEHQHVGLSIIIVTFNRPAILSLTACL 180
DB 114 KOPPKDLVLAFLPDHVNDFWYKRRKLGIKPEHQHVGLSIIIVTFNRPAILSLTACL 173
QY 181 VNOKTHYPEVITDDGSOEDLSPIIROYENKLDIRYVROKNGFOASARNMGLSLAKY 240
DB 174 VNOKTHYPEVITDDGSOEDLSPIIROYENKLDIRYVROKNGFOASARNMGLSLAKY 233
QY 241 DFTGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTQHIDPKDFLNNASLESPL 300
DB 234 DFTGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTQHIDPKDFLNNASLESPL 293
QY 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTEKNTENLRSLSDSPFRFAAGNVAFACKWLNKSGFFD 360
DB 294 EVKTNNSVAAKGEGTVSLDWRLEQFEKTEKNTENLRSLSDSPFRFAAGNVAFACKWLNKSGFFD 353
QY 361 EBFNHWGGEDVEFGYRLFRYGSFFKIDGIMAYHQBPFGKENETDREAGNITFLDMREK 420
DB 354 EBFNHWGGEDVEFGYRLFRYGSFFKIDGIMAYHQBPFGKENETDREAGNITFLDMREK 413
QY 421 VPIYIRKLLPIEDSHINRVLPSIYIIPAYNCANYIQCVDSDALNQTVDLVLCINDGST 480
DB 414 VPIYIRKLLPIEDSHINRVLPSIYIIPAYNCANYIQCVDSDALNQTVDLVLCINDGST 473
QY 481 DNTLEVINKLYGNPNVRIMSKNGGIGTASASNAVAFKAGYIIGOLDSDYLPDPAVELC 540
DB 474 DNTLEVINKLYGNPNVRIMSKNGGIGTASASNAVAFKAGYIIGOLDSDYLPDPAVELC 533
QY 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMTAHAFHFMFTIRAWHL 600
DB 534 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMTAHAFHFMFTIRAWHL 593
QY 601 TDGFNEKINADVDMFLKSEVGKPKHLNKICYNRVLHGDNTSIKKLGIGQKKNHFWVNV 660
DB 594 TDGFNEKINADVDMFLKSEVGKPKHLNKICYNRVLHGDNTSIKKLGIGQKKNHFWVNV 653
QY 661 QSLNRQGIITYNVDDEDDDESRYIFNKTAEQEEDILDKITONKDAKTAVSIFYP 720
DB 654 QSLNRQGIITYNVDDEDDDESRYIFNKTAEQEEDILDKITONKDAKTAVSIFYP 713
QY 721 NTLNGLVKKLNNIIEYNKNI FVILHVDKNHLPDIIKKEILAFYKHQVNNILNNDISYY 780
DB 714 NTLNGLVKKLNNIIEYNKNI FVILHVDKNHLPDIIKKEILAFYKHQVNNILNNDISYY 773
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DB 714 NTLNGLVKKLNNIIEYNKNI FVILHVDKNHLPDIIKKEILAFYKHQVNNILNNDISYY 773
QY 781 TSNRLIKTEAHLNSNINKLSQMLNCEYIIIFDNHDSLFVKXNDSYAYNKKYDVGWNFSAALTH 840
DB 774 TSNRLIKTEAHLNSNINKLSQMLNCEYIIIFDNHDSLFVKXNDSYAYNKKYDVGWNFSAALTH 833
QY 841 DMIEKINAHPPPKKIKTYFNDNDLKSMMVKGASQGMFTYALAHELLTTIKKEVITSCQS 900
DB 834 DMIEKINAHPPPKKIKTYFNDNDLKSMMVKGASQGMFTYALAHELLTTIKKEVITSCQS 893
QY 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPWERKLOMTNEQIESAKRGENI 960
DB 894 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPWERKLOMTNEQIESAKRGENI 953
QY 961 PVNKFIIINSITL 972
DB 954 PVNKFIIINSITL 965
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## RESULT 7

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US-11-124-215-17
; Sequence 17, Application US/11124215
; Publication No. US20050266460A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTEURELLA MULTOCIDA AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 35541.101
; CURRENT APPLICATION NUMBER: US/11/124,215
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: 10/217,613
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-124-215-17
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Query Match      72.4%; Score 3697; DB 7; Length 703;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 703; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MNTLSQAIKAYNSNDYQLALKLFKESAEIYGRKIVFQITKCKEKLKSAHPSVNSAHLNVN 60
DB 1 MNTLSQAIKAYNSNDYQLALKLFKESAEIYGRKIVFQITKCKEKLKSAHPSVNSAHLNVN 60
QY 61 KEEKVNVCDSPDIATQALLSNVKKLVLSSEKNTLKNKKWKLTEKKSENAEVRVALVP 120
DB 61 KEEKVNVCDSPDIATQALLSNVKKLVLSSEKNTLKNKKWKLTEKKSENAEVRVALVP 120
QY 121 KOPPKDLVLAFLPDHVNDFWYKRRKLGIKPEHQHVGLSIIIVTFNRPAILSLTACL 180
DB 121 KOPPKDLVLAFLPDHVNDFWYKRRKLGIKPEHQHVGLSIIIVTFNRPAILSLTACL 180
QY 181 VNOKTHYPEVITDDGSOEDLSPIIROYENKLDIRYVROKNGFOASARNMGLSLAKY 240
DB 181 VNOKTHYPEVITDDGSOEDLSPIIROYENKLDIRYVROKNGFOASARNMGLSLAKY 240
QY 241 DFTGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTQHIDPKDFLNNASLESPL 300
DB 241 DFTGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTQHIDPKDFLNNASLESPL 300
QY 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTEKNTENLRSLSDSPFRFAAGNVAFACKWLNKSGFFD 360
DB 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTEKNTENLRSLSDSPFRFAAGNVAFACKWLNKSGFFD 360
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QY 361 EEFNHGGEDVEGYRLFRYGSFFKTIIDGIMAYHQBPCKENETDREAGKNIITLDMREK 420
DB 361 EEFNHGGEDVEGYRLFRYGSFFKTIIDGIMAYHQBPCKENETDREAGKNIITLDMREK 420
QY 421 VPYIYRKLPIEDSHINRVLVSIYIPAYNCANYIQCVDLSALNQTVVDLEVCICNDGST 480
DB 421 VPYIYRKLPIEDSHINRVLVSIYIPAYNCANYIQCVDLSALNQTVVDLEVCICNDGST 480
QY 481 DNTLEVINKLYGNPNRVRIMSKPENGASASNAVSPAKGYIIGOLDSDDDYLEPDAVELC 540
DB 481 DNTLEVINKLYGNPNRVRIMSKPENGASASNAVSPAKGYIIGOLDSDDDYLEPDAVELC 540
QY 541 LKBEFKDKTKLACVYTTNRNVPDGSLLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
DB 541 LKBEFKDKTKLACVYTTNRNVPDGSLLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
QY 601 TDGFNEKIEANVDYDMFLKLSSEVGKFKHLNKICYNRVLHGDNTSIKKLGIOKKNHFVVVN 660
DB 601 TDGFNEKIEANVDYDMFLKLSSEVGKFKHLNKICYNRVLHGDNTSIKKLGIOKKNHFVVVN 660
QY 661 QSLNRQGITVYNYDEFDLDESRYIIFNKTAEOEEIDILKDI 703
DB 661 QSLNRQGITVYNYDEFDLDESRYIIFNKTAEOEEIDILKDI 703

RESULT 8
US-11-172-145-12
; Sequence 12, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-172-145-12

Query Match 72.4%; Score 3697; DB 7: Length 703;
Best Local Similarity 100.0%; Pred. No. 1.4e-232; Indels 0; Gaps 0;
Matches 703; Conservative 0; Mismatches 0;

QY 1 MNTLSQAIKAYNSNDYQLALKLFKESAEIYGRKIVEFOITKCKELSAHPSVNSAHLNVN 60
DB 1 MNTLSQAIKAYNSNDYQLALKLFKESAEIYGRKIVEFOITKCKELSAHPSVNSAHLNVN 60
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; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 21
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-172-145-21

Query Match      72.2%; Score 3687; DB 7; Length 703;
Best Local Similarity 99.7%; Pred. No. 6e-232;
Matches 701; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQALALFEKSAEYIGRKIVFEQITKCKEKLSAHPSVNSAHLNVN 60
Db 1 MNTLSQAIKAYNSNDYQALALFEKSAEYIGRKIVFEQITKCKEKLSAHPSVNSAHLNVN 60
Qy 61 KEEKVNVCDSPDIATQALLSNVKKLVLSDEKNTLKNWKLLTEKKSENAEVRVALVP 120
Db 61 KEEKVNVCDSPDIATQALLSNVKKLVLSDEKNTLKNWKLLTEKKSENAEVRVALVP 120
Qy 121 KOPPKDLVLAPLDPHVNDFTWYKKRKLGIKPEHQHVGLSIIIVTTFNRPAILSLITLACL 180
Db 121 KOPPKDLVLAPLDPHVNDFTWYKKRKLGIKPEHQHVGLSIIIVTTFNRPAILSLITLACL 180
Qy 181 VNOKTHYPPEVIVTDDGSQEDLSPIIQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240
Db 181 VNOKTHYPPEVIVTDDGSQEDLSPIIQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240
Qy 241 DFTGLLDCMAPNPLVHVSVAELLEDLTIIGPKYIDTQHIDPKDFLNNASLLESPL 300
Db 241 DFTGLLDCMAPNPLVHVSVAELLEDLTIIGPKYIDTQHIDPKDFLNNASLLESPL 300
Qy 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFPAKWLKNGSGFFD 360
Db 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFPAKWLKNGSGFFD 360
Qy 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQBPCKENETDREAGKNITLDMREK 420
Db 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQBPCKENETDREAGKNITLDMREK 420
Qy 421 VPYIYRKLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
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Qy 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNPFESREKLTMTAMIAHPRMETIRAWHL 600
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Db 661 QSLNRQGITVYNYDEFDLDESRYIFNKTAEQEIEIDILKDI 703
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RESULT 10

US-11-172-145-22

; Sequence 22, Application US/11172145

; Publication No. US20050272696A1

; GENERAL INFORMATION:

; APPLICANT: DeAngelis, Paul

; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC

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; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 22
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-172-145-22
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Query Match      72.2%; Score 3687; DB 7; Length 703;
Best Local Similarity 99.7%; Pred. No. 6e-232;
Matches 701; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQALALFEKSAEYIGRKIVFEQITKCKEKLSAHPSVNSAHLNVN 60
Db 1 MNTLSQAIKAYNSNDYQALALFEKSAEYIGRKIVFEQITKCKEKLSAHPSVNSAHLNVN 60
Qy 61 KEEKVNVCDSPDIATQALLSNVKKLVLSDEKNTLKNWKLLTEKKSENAEVRVALVP 120
Db 61 KEEKVNVCDSPDIATQALLSNVKKLVLSDEKNTLKNWKLLTEKKSENAEVRVALVP 120
Qy 121 KOPPKDLVLAPLDPHVNDFTWYKKRKLGIKPEHQHVGLSIIIVTTFNRPAILSLITLACL 180
Db 121 KOPPKDLVLAPLDPHVNDFTWYKKRKLGIKPEHQHVGLSIIIVTTFNRPAILSLITLACL 180
Qy 181 VNOKTHYPPEVIVTDDGSQEDLSPIIQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240
Db 181 VNOKTHYPPEVIVTDDGSQEDLSPIIQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240
Qy 241 DFTGLLDCMAPNPLVHVSVAELLEDLTIIGPKYIDTQHIDPKDFLNNASLLESPL 300
Db 241 DFTGLLDCMAPNPLVHVSVAELLEDLTIIGPKYIDTQHIDPKDFLNNASLLESPL 300
Qy 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFPAKWLKNGSGFFD 360
Db 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFPAKWLKNGSGFFD 360
Qy 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQBPCKENETDREAGKNITLDMREK 420
Db 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQBPCKENETDREAGKNITLDMREK 420
Qy 421 VPYIYRKLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Db 421 VPYIYRKLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Qy 481 DNTLEVINIKLYGNPRVRIMSKPNGGIASASNAAVSFAKGYIIGQLDSDDDYLEPDAVELC 540
Db 481 DNTLEVINIKLYGNPRVRIMSKPNGGIASASNAAVSFAKGYIIGQLDSDDDYLEPDAVELC 540
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541 LKEFLKDKTTLACVTTNNRNVNPDGSLIANGYNNWPEFSREKLTAMIAHHFMTTIRAWHL 600  
Db  
541 LKEFLKDKTTLACVTTNNRNVNPDGSLIANGYNNWPEFSREKLTAMIAHHFMTTIRAWHL 600  
Qy 601 TDGFNEKIENAVDYDMFLKJSEVGKFKHLNKKICYNRVLHGDNTSIKKLGIOKQNHFFVVVN 660  
Db 601 TDGFNEKIENAVDYDMFLKJSEVGKFKHLNKKICYNRVLHGDNTSIKKLGIOKQNHFFVVVN 660  
Qy 661 QSLNRQGITYYNDEFDLDESRYKIFNKTAEOEIDILKDI 703  
Db 661 QSLNRQGITYYNDEFDLDESRYKIFNKTAEOEIDILKDI 703

RESULT 11  
US-11-172-145-25  
; Sequence 25, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172.145  
; PRIOR FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 25  
; LENGTH: 704  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-11-172-145-25

Query Match 61.7%; Score 3151.5; DB 7; Length 704;  
Best Local Similarity 83.0%; Pred. No. 3.3e-197;  
Matches 590; Conservative 57; Mismatches 57; Indels 7; Gaps 2;

Qy 1 MNTLSQAIKAYNSNDYQALALFKESAETIYGRKIVEPQITCKEKLKLSAHPNSVNSAHLVN 60  
Db 1 MNTLSQAIKAYNSNDYQALALFKESAETIYGRKIVEPQITCKEKLKLSAHPNSVNSAHLVN 53  
Qy 61 KEKKNVCDSPDIATOLLNKKVLLSDSEKNTLKNKKWLLTEKKSSENAEVRVALVP 120  
Db 54 EDKKNVCDSSDDIATOLLNKKVLLSDSEKNTLKNKKWLLTEKKSSENAEVRVALVP 113  
Qy 121 KDPKDLVLAPLDPHVDFTWYKKGKRLGKPEHGVGLSIIVTTFNRPAILISITLACL 180  
Db 114 KDPKDLVLAPLDPHVDFTWYKKGKRLGKPEHGVGLSIIVTTFNRSRILDTLACL 173  
Qy 181 VNQKTHYPEFVITDDGQEDLSPIROYENKLDIYRVQKNGFQASARNGLRLAKY 240  
Db 174 VNQKTHYPEFVIVADDGSKENLLTIYQKYEQKLDIKYVRQKDYQYQLCVARNGLRLAKY 233

Qy 241 DFTGLDCDMPNPLVHVSIVAELEDDDLTIIGPRKYIDTOHIDPKDFLNNASLLSPLP 300  
Db 234 DFVSLDCDMPNPLVHVSIVAELEDDDLTIIGPRKYIDTOHIDPKDFLNNASLLSPLP 293  
Qy 301 EVKTNNSVAAKGEGTUSLDMRLSQFECTENLRSLSDSPRFPFAAGNVAFAPAKWLNKSGPFD 360  
Db 294 ETATNNPSTTSKGNISLDMRLSHEFKTKTDNURLCDSFRYFSCGNVAFSKEWLNKVGWFD 353  
Qy 361 EEFNHWGGEDEVFGYRLFRYSGPFTTIDGIMAYHQBPPEKNETDREAGKNITLDMREK 420  
Db 354 EEFNHWGGEDEVFGYRLFAKGCFFRVIDGGMAYHQBPPEKNETDREAGKSITLKIVKEK 413  
Qy 421 VPIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGST 480  
Db 414 VPIYRKLLPIEDSHIHRIPLVSIYIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGST 473  
Qy 481 DNTLEVINKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYIIGQLSDDDVLEPDAVELC 540  
Db 474 DNTLEVINKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYIIGQLSDDDVLEPDAVELC 533  
Qy 541 LKEFLKDKTTLACVTTNNRNVNPDGSLIANGYNNWPEFSREKLTAMIAHHFMTTIRAWHL 600  
Db 534 LKEFLKDKTTLACVTTNNRNVNPDGSLIANGYNNWPEFSREKLTAMIAHHFMTTIRAWHL 593  
Qy 601 TDGFNEKIENAVDYDMFLKJSEVGKFKHLNKKICYNRVLHGDNTSIKKLGIOKQNHFFVVVN 660  
Db 594 TDGFNEKIENAVDYDMFLKJSEVGKFKHLNKKICYNRVLHGDNTSIKKLGIOKQNHFFVVVN 653  
Qy 661 QSLNRQGITYYNDEFDLDESRYKIFNKTAEOEIDILKDIQNKDA 711  
Db 654 QSLNRQGITYYNDEFDLDESRYKIFNKTAEOEIDILKDIQNKDA 704

RESULT 12  
US-11-124-215-8  
; Sequence 8, Application US/11124215  
; Publication No. US20050266460A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL  
; TITLE OF INVENTION: DNA ENCODING HVALURONAN SYNTHASE FROM PASTEURELLA MULTOCIDA AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 35541.101  
; CURRENT APPLICATION NUMBER: US/11/124.215  
; PRIOR FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: 10/217,613  
; PRIOR FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-11-124-215-8

Query Match 10.4%; Score 529; DB 7; Length 101;  
Best Local Similarity 100.0%; Pred. No. 2.8e-28;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 496 RVRIMSKPNGGIASASNAAVSFAKGYIIGQLSDDDVLEPDA 536  
Db 61 RVRIMSKPNGGIASASNAAVSFAKGYIIGQLSDDDVLEPDA 101



Db 409 RIIGILKNQCDHPHIIYLDGYEIPDFIKNLGNKATVVHCKDKONSIRDNGKFILLBELIE 468  
Qy 716 -----SIFYPNT-LNGLVKKLNNIIENKNI FVIVLH--VDKNHLPDIKKE- 759  
Db 469 KNQDGYIITCDDDIYPSDYINTMIKLN---EYDDKA-VIGLHGILFPSRMTKYFSADR 524  
Qy 760 -ILAFYHKHQ-----VNIILANDISYTS--NRLIK---TEAHLNSI-----NKLSQL 801  
Db 525 LVYSFYKPLEKDKAVNVLGTGTVSFRVSLFNQFSLSDFTHSGMADIYFSLCKKNILQI 584  
Qy 802 NLN--CEYIIIFDNHDS-----LFVKND SYAYMKKYDVGMMNFSALTHDWI 843  
Db 585 CISRPANWLTEDNEDSETLYHQYEDNDEQQTQLIMENGPWGYSSIIYPLVKN----- 635  
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Db 636 -----HPKFTDLI 643

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Job time : 32 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 05:19:53 ; Search time 14204 Seconds  
(without alignments)

11685.643 Million cell updates/sec

Title: US-10-642-248-1

Perfect score: 2920

Sequence: 1 atgaatacattatcacagc.....taatagataactctataaa 2920

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.hcg.\*  
15: gb.pl.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2919	100.0	2937	6	AR616925
3	2917.4	99.9	2919	1	AF237926
4	2917.4	99.9	2937	6	BD087261
5	2917.4	99.9	2937	6	BD205371
6	2913.6	99.8	16727	1	AF067175
7	2271.2	77.8	2979	6	BD228712
8	2271.2	77.8	2979	6	AR225814
9	2266.4	77.6	2979	1	AF195517
10	2108.8	72.2	2112	6	BD228711
11	2108.8	72.2	2112	6	AR225813
12	2066.4	70.8	11885	1	AE006116
13	2064.8	70.7	3156	1	AY604234
14	2063.2	70.7	8838	1	AF302467
15	765.8	26.2	14483	1	AB079602
16	765.8	26.2	14483	1	AX698178
17	760.6	26.0	2058	6	AX698176
18	747	25.6	998	1	AY225345

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20	652.4	22.3	864	1	AY225346
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22	110.8	3.8	110000	14	CT009752_4
23	110.8	3.8	110000	14	CT009752_5
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28	105.4	3.6	226847	14	AX664721
29	105.2	3.6	154561	5	CR391989
30	102.2	3.5	168212	5	CR352223
31	101.6	3.5	79882	14	AX908758_5
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c 38	96.6	3.3	144375	14	CR354586
39	96.6	3.3	250029	2	AE014820
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## ALIGNMENTS

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LOCUS	AF036004	Pasteurella multocida				
DEFINITION	AF036004.2	GI:44986831				
ACCESSION	AF036004					
VERSION	AF036004.2					
KEYWORDS	Pasteurella multocida					
SOURCE	Pasteurella multocida					
ORGANISM	Pasteurella multocida					
REFERENCE	1 (bases 1 to 2920)					
AUTHORS	DeAngelis, P.L., Jing, W., Drake, R.R. and Achuthan, A.M.					
TITLE	Identification and molecular cloning of a unique hyaluronan synthase from Pasteurella multocida					
JOURNAL	J. Biol. Chem. 273 (14), 8454-8458 (1998)					
PUBMED	9525958					
REFERENCE	2 (bases 1 to 2920)					
AUTHORS	DeAngelis, P.L., Jing, W. and Achuthan, A.M.					
TITLE	Direct Submission					
JOURNAL	Submitted (26-NOV-1997) Biochem. & Molec. Biol., Univ. of Oklahoma Health Sciences Center, 940 Stanton L. Young Blvd., Oklahoma City, OK 73104, USA					
REFERENCE	3 (bases 1 to 2920)					
AUTHORS	DeAngelis, P.L., Jing, W. and Achuthan, A.M.					
TITLE	Direct Submission					
JOURNAL	Submitted (04-MAR-2004) Biochem. & Molec. Biol., Univ. of Oklahoma Health Sciences Center, 940 Stanton L. Young Blvd., Oklahoma City, OK 73104, USA					
REMARK	Sequence update by submitter					
COMMENT	On Mar 4, 2004 this sequence version replaced gi:3043922.					
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	/organism="Pasteurella multocida"					
	/mol_type="genomic DNA"					
	/strain="P-1059: ATCC 15742"					
	/db_xref="ATCC:15742"					
	/db_xref="taxon:747"					
	/note="Carter Type A strain"					
	1..2919					
	gene					



1561 Db TATTACATTGGCGAGTTAGATTAGATTGATTAATCTTTGAGCCGTGAGTCAGTTGAACGTGTGT 1620  
1621 Qy TTTAAAGAAATTTTAAAGATTAATAACCGCTAGCTGTGTTTATACACATAATAGAAACGTC 1680  
1621 Db TTTAAAGAAATTTTAAAGATTAATAACCGCTAGCTGTGTTTATACACATAATAGAAACGTC 1680  
1681 Qy AATCCGGATGGTAGCTTAATCGCTAATGGTTTACAAATGGCCAGAAATTTTCACGAGAAAAA 1740  
1681 Db AATCCGGATGGTAGCTTAATCGCTAATGGTTTACAAATGGCCAGAAATTTTCACGAGAAAAA 1740  
1741 Qy CTCACACGGCTATGATTTGCTCACACATTTAGAAATGTTTACAGATTTAGAGCTTGGCATTTA 1800  
1741 Db CTCACACGGCTATGATTTGCTCACACATTTAGAAATGTTTACAGATTTAGAGCTTGGCATTTA 1800  
1801 Qy ACTGATGGATTCAAATGAAATAATTCGAAATGCGTAGACTATGACATGTTCTCTCAACGTC 1860  
1801 Db ACTGATGGATTCAAATGAAATAATTCGAAATGCGTAGACTATGACATGTTCTCTCAACGTC 1860  
1861 Qy AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATATAACCGTGTATTACATGGT 1920  
1861 Db AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATATAACCGTGTATTACATGGT 1920  
1921 Qy GATAACACATCAATTAAGAACTTGGCAATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
1921 Db GATAACACATCAATTAAGAACTTGGCAATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
1981 Qy CAGTCATTAATAGACAGGCACTTAATTAATTAATTAATGACGAATTTGATGATTTAGAT 2040  
1981 Db CAGTCATTAATAGACAGGCACTTAATTAATTAATTAATGACGAATTTGATGATTTAGAT 2040  
2041 Qy GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAAATATCAAGAAAGAGATTCATATCTTA 2100  
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2101 Qy AAAGATATTTAAATCATCCAGAAATAAGATGCGAAATGCGAGTCAGTATTTTATCC 2160  
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2701 Qy ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTTCCAATTTTGCATTTTAAATC 2760  
2701 Db ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTTCCAATTTTGCATTTTAAATC 2760  
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2761 Db TTAGAAAAGAAAACCGGCCATGTATTTAATAAAACATCGACCTGACTTATATGCTTGG 2820  
2821 Qy GAACGAAAATTTACAAATGGACAAAATGAACAAATTTGAAAGTGCAAAAGAGGAGAAAATATA 2880  
2821 Db GAACGAAAATTTACAAATGGACAAAATGAACAAATTTGAAAGTGCAAAAGAGGAGAAAATATA 2880  
2881 Qy CCTGTTAAACAAGTTCATTTAATAAGTATATACTCTATAAA 2920  
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RESULT 2  
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ACCESSION AR616925  
VERSION AR616925.1 GI:59720260  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2937)  
AUTHORS Weigel,P.H., Kumari,K. and DeAngelis,P.  
TITLE Hyaluronan synthase gene and uses thereof  
JOURNAL Patent: US 6833264-A 8 21-DEC-2004;  
The Board of Regents of the University of Oklahoma; Norman, OK  
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RESULT 3  
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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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Pasteurella multocida  
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
Pasteurellaceae; Pasteurella.  
1 (bases 1 to 2919)  
Fuller,T.E., Kennedy,M.J. and Lowery,D.E.  
Identification of Pasteurella multocida virulence genes in a  
septicemic mouse model using signature-tagged mutagenesis  
unpublished  
2 (bases 1 to 2919)  
Fuller,T.E., Kennedy,M.J. and Lowery,D.E.  
Direct Submission  
Submitted (24-FEB-2000) Discovery Research, Pharmacia & Upjohn  
Animal Health, 7923-25-434, 7000 Portage Road, Kalamazoo, MI  
49001-0199, USA

## FEATURES

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RESULT 4  
BD087261  
LOCUS BD087261  
DEFINITION Hyaluronan synthase gene and utilization thereof.  
ACCESSION BD087261  
VERSION BD087261.1 GI:22632871  
KEYWORDS JP 2001521741-A/13.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2937)  
AUTHORS Weigel,P.H., Kumari,K. and Deangelis,P.  
TITLE Hyaluronan synthase gene and utilization thereof

JOURNAL	Patent: JP 2001521741-A 13 13-NOV-2001; THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
COMMENT	OS Pasturella multocida PN JP 2001521741-A/13 PD 13-NOV-2001 PF 30-OCT-1998 JP 2000519083 PR 31-OCT-1997 US 60/064435,26-OCT-1998 US 09/178851 PI PAUL H WEIGEL, KSHAMA KUMARI, PAUL DEANGELIS PC C12N15/09,A61K31/728,A61P43/00,C12N1/21,C12N9/10,C12P19/04, PC C12Q1/68// PC (C12N15/09,C12R1:46),C12N15/00,(C12N15/00,C12R1:46) CC Hyaluronan synthase gene and utilization thereof FH Key Location/Qualifiers FT source 1..2899 /organism='Pasturella multocida'. FT Location/Qualifiers 1..2937 /organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'
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LOCUS 2937 bp DNA linear PAT 17-JUL-2003
DEFINITION Nucleic acid encoding hyaluronan synthase and method of using the
same.
ACCESSION BD205371
VERSION BD205371.1 GI:33015141
KEYWORDS JP 2002510648-A/1.
SOURCE Pasteurella multocida
ORGANISM Pasteurella multocida
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
REFERENCE 1 (bases 1 to 2937)
AUTHORS Deangelis,P.
TITLE Nucleic acid encoding hyaluronan synthase and method of using the
JOURNAL Patent: JP 2002510648-A 1 09-APR-2002;
BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
COMMENT OS Pasteurella multocida
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PD 09-APR-2002
PF 01-APR-1999 JP 2000542035
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CC Nucleic acid encoding hyaluronan synthase and method of using
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DEFINITION Pasteurella multocida capsule biosynthesis gene cluster, complete sequence.  
ACCESSION AF067175  
VERSION AF067175.2 GI:7710189  
KEYWORDS  
SOURCE Pasteurella multocida  
ORGANISM Pasteurella multocida  
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella.  
REFERENCE 1 (bases 1 to 16727)  
Chung,J.Y., Zhang,Y. and Adler,B.  
The capsule biosynthetic locus of Pasteurella multocida A:1  
FEMS Microbiol. Lett. 166 (2), 289-296 (1998)  
9770287  
REFERENCE 2 (bases 1 to 16727)  
Chung,J.Y., Zhang,Y. and Adler,B.  
Direct Submission  
Submitted (19-MAY-1998) Microbiology, Monash University, Wellington Road, Clayton, VIC 3168, Australia  
3 (bases 1 to 16727)  
Chung,J.Y., Zhang,Y. and Adler,B.  
Direct Submission  
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LOCUS  
DEFINITION Polymer grafting by polysaccharide syntheses.  
ACCESSION BD228712  
VERSION BD228712.1 GI:33038482  
KEYWORDS JP 2002529064-A/2.

SOURCE  
ORGANISM  
Pasteurella multocida  
Bacteria: Proteobacteria; Gammaproteobacteria; Pasteurellales;  
Pasteurellaceae; Pasteurella.

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AUTHORS  
TITLE  
JOURNAL  
COMMENT

Deangelis, P.L.  
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Patent: JP 2002529064-A 2 10-SEP-2002;  
THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA  
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VERSION AR225814.1 GI:27263929  
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ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2979)  
AUTHORS DeAngelis,P.L.  
TITLE Polymer grafting by polysaccharide syntheses  
JOURNAL Patent: US 644447-A 4 03-SEP-2002;  
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LOCUS  
DEFINITION  
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VERSION

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BD228711  
BD228711.1 GI:33038481

KEYWORDS JP 2002529064-A/1.  
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ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
Pasteurellaceae; Pasteurella.  
REFERENCE 1 (bases 1 to 2112)  
AUTHORS Deangelis, P.L.  
TITLE Polymer grafting by polysaccharide syntheses  
JOURNAL Patent: JP 2002529064-A 1 10-SEP-2002;  
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PR 11-NOV-1998 US 60/107929, 01-APR-1999 US 09/283402 PI  
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REFERENCE 1 (bases 1 to 11885)  
AUTHORS May,B.J., Zhang,Q., Li,L.L., Paustian,M.L., Whittam,T.S. and Kapur,V.  
TITLE Complete genomic sequence of Pasteurella multocida, Pm70  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)  
PUBMED 11248100

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

FEATURES  
source

2 (bases 1 to 11885)  
Zhang,Q. and Kapur,V.  
Direct Submission  
Submitted (24-Oct-2000) Department of Veterinary Pathobiology,  
University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN  
55108, USA  
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Db 3149 GAAGAAATTTAATCATTTGGGGGGGGAAGATGTAGAAATTTGGTTACAGATTATTTGCCAAA 3208  
Qy 1141 GGTAGTTTCTTTAAAACATATTGATGGCATTTATGCGCTTACCATCAAGGCCACCAAGGTAAA 1200  
Db 3209 GGCTGTGTTTTTCAGAGTAATTTGACGGGGGAATGGCATCCATCAAGAACCAACCTGGTAAA 3268  
Qy 1201 GAAATGAACCGGATCGTGAACGGGGAATAATATTAGCTCGATATTATGAGAGAAAAG 1260  
Db 3269 GAAATGNAACAGACCGGAAGCTGGTAAAAGTATTAGCTTAAATTTGTGAAGAAAAG 3328  
Qy 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAGATTCGCGATATCAATPAGAGTACCT 1320  
Db 3329 GTACCTTACATCTATAGAAGCTTTTACCAATAGAAGATTCACATATTTATPAGAATACCT 3388  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATAAATGTCGCAACTATATTCAACGTTGCGTAGAT 1380  
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Qy 1381 AGTCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTAAGATGTTTCAACA 1440  
Db 3449 AGTGTCTTATACAACTGTTGTGCACTCGAGGTTTGTATTGTAACGATGGTTCAACA 3508  
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Db 3569 TCTAAACCAATGGGGAATAGCCTCAGCATCAATGCGAGCGTTTCTTTTGTCTAAAGGT 3628  
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Qy 1621 TTTAAAGAAATTTTAAAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATPAGAAAACGTC 1680  
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Qy 1861 AGTGAAGTTGGAATAATTTAAACAATCTTAATAAAATCTGCTATAACCGTGTATTACATGGT 1920  
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Qy 2041 GAAAGTAGAAAGTATATTTTCAATAAAAACCGCTGAATATCAAGAAAGAGATTGATATCTTA 2100  
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Db 2282 AATAGATTAGTGGTTAGTTAAAAAATTAACCAATATTTATCGAATATAACAAAAATGTA 2341

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## RESULT 14

AF302467  
LOCUS Pasteurella multocida p4218 region 2 capsule biosynthesis gene  
DEFINITION cluster, partial sequence.

ACCESSION AF302467

VERSION AF302467.1

KEYWORDS GI:13274373

SOURCE

ORGANISM

Pasteurella multocida  
Pasteurella multocida  
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

Pasteurellaceae; Pasteurella.

REFERENCE 1 (bases 1 to 8838)

AUTHORS Townsend,K.M., Boyce,J.D., Chung,J.Y., Frost,A.J. and Adler,B.

TITLE Genetic organization of Pasteurella multocida cap loci and

development of a multiplex capsular PCR typing system

J. Clin. Microbiol. 39 (3), 924-929 (2001)

PUBMED 11230405

AUTHORS 2 (bases 1 to 8838)

Townsend,K.M., Boyce,J.D., Chung,J.Y., Frost,A.J. and Adler,B.

TITLE Direct Submission

JOURNAL Submitted (03-SEP-2000) Veterinary Pathology and Anatomy, The

University of Queensland, School of Veterinary Science, Brisbane,



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5083 GATTGGATAATAATAATTAATGCACACTCACCATTTTAAABATCTGATAAAAAATATTTT 5142
QY 2581 AATGCAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTATGACG 2640
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5203 TACACTTTAGCAGATGATATTCCTACGATTATGAAGAAGTCAATACATTTATGCCAATCT 5262
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RESULT 15  
AB079602/cLOCUS  
DEFINITION

14483 bp DNA linear BCT 11-JUN-2002  
Escherichia coli kpsS, kfoG, kfoF, kfoE, kfoD, kfoIs, kfoC, kfoB,  
kfoA, kpsT genes for kpsS hypothetical protein, predicted  
glycosyltransferase, UDP-glucose dehydrogenase, kfoB hypothetical  
protein, kfoD hypothetical protein, is hypothetical protein,  
chondroitin polymerase, kfoB hypothetical protein, UDP-glucose  
4-epimerase, ABC transporter, partial and complete cds.

AB079602  
AB079602.1 GI:21326777VERSION  
KEYWORDSSOURCE  
ORGANISM

Escherichia coli  
Escherichia coli  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Escherichia.

REFERENCE  
AUTHORS

1  
Ninomiya, T., Sugiura, N., Tawada, A., Sugimoto, K., Watanabe, H. and  
Kimata, K.

TITLE  
JOURNAL

Molecular Cloning and Characterization of Chondroitin Polymerase  
from Escherichia coli Strain K4

PUBMED  
REFERENCES

J. Biol. Chem. 277 (24), 21567-21575 (2002)  
11943778

AUTHORS  
TITLE

2 (bases 1 to 14483)  
Sugiura, N., Kimata, K., Ninomiya, T. and Watanabe, H.

JOURNAL  
FEATURES

Submitted (07-FEB-2002) Nobuo Sugiura, Aichi Medical University,  
Aichi 480-1195, Japan (E-mail: nsugiura@aichi-med-u.ac.jp,  
URL: http://www2.aichi-med-u.ac.jp/ims/index-e.html,  
Tel: 81-52-264-4811 (ex. 2087), Fax: 81-561-63-3532)

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Location/Qualifiers

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2914.4	99.8	2916	9	Abt44090 Pasteurel
6	2271.2	77.8	2979	6	Aaa27449 P. multoc
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13	2110.4	72.3	2112	14	Aea04964 Hyaluron
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AC AAX58857;  
XX  
DT 16-AUG-1999 (first entry)  
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XX  
KW Hyaluronate synthase; pmHAS; hyaluronic acid; hyaluronan; ss.  
XX  
OS Pasteurella multocida.  
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FH Key Location/Qualifiers  
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PA (OKLA ) UNIV OKLAHOMA STATE.  
XX  
PI Weigel PH, Kumari K, Deangelis P;  
XX  
DR WPI: 1999-137486/28.  
XX  
DR P-PSDB; AAY06212.  
XX  
CC Nucleic acid encoding hyaluronate synthase for production of hyaluronic acid with controlled molecular weight and targeting specificity.  
XX  
CC Disclosure; Page 123-125; 125pp; English.  
XX  
CC This DNA sequence codes for the hyaluronate synthase (pmHAS, see AAY06212) of Pasteurella multocida Carter type A. The pmHAS enzyme has different kinetic optima with respect to pH and metal ion dependence, and

CC different Km values compared with the HAS enzymes of Streptococcus  
CC equisimilis (see AY06206) and Streptococcus pyogenes. Km values are  
CC about 2- to 3-fold lower for UDP sugars, and Vmax values are about 2- to  
CC 3-fold higher. The invention provides recombinant vectors containing  
CC hyaluronate synthase DNA, especially S. equisimilis hyaluronate synthase  
CC DNA (see AX58841), and prokaryotic or eukaryotic host cells which  
CC produce the enzyme and its hyaluronic acid product, particularly a  
CC product with modified structure or molecular size. The hyaluronic acid  
CC produced this way is purer than that produced by conventional methods  
XX  
SQ Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

Query Match 99.9%; Score 2917.4; DB 2; Length 2937;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGAATACATATCACAGCAATATAAGCAATATACAGCAATGACTATCAATTAGCACTC	60
Db	19	ATGAATACATATCACAGCAATATAAGCAATATACAGCAATGACTATCAATTAGCACTC	78
Qy	61	AAATTTATTTGAAAGTCGGCGGAATCTATGACGCGGAAATTTGTTGAATTTCAAATTACC	120
Db	79	AAATTTATTTGAAAGTCGGCGGAATCTATGACGCGGAAATTTGTTGAATTTCAAATTACC	138
Qy	121	AAATGCAAGAAATCTCTGACACATCTTCTGTTAAATTCAGCACATCTTCTGTTAAAT	180
Db	139	AAATGCAAGAAATCTCTGACACATCTTCTGTTAAATTCAGCACATCTTCTGTTAAAT	198
Qy	181	AAAGAAGAAAGTCAATGTTTGGATGATGCGTTAGATATTGCAACACACTGTTACTT	240
Db	199	AAAGAAGAAAGTCAATGTTTGGATGATGCGTTAGATATTGCAACACACTGTTACTT	258
Qy	241	TCCAACTGAAAAAATAGTACTTCTGACTCGGAAAAAACAAGCTTTAAAAAATAAATGG	300
Db	259	TCCAACTGAAAAAATAGTACTTCTGACTCGGAAAAAACAAGCTTTAAAAAATAAATGG	318
Qy	301	AAATTGCTCACTGAGAGAAATCTGAAATTCGGAGGTAAAGCGGTCGCCCTTGTACCA	360
Db	319	AAATTGCTCACTGAGAGAAATCTGAAATTCGGAGGTAAAGCGGTCGCCCTTGTACCA	378
Qy	361	AAAGATTTTCCCAAGATCTGTTTATAGCGCTTTACTGATCATGTTTAATGATTTTACA	420
Db	379	AAAGATTTTCCCAAGATCTGTTTATAGCGCTTTACTGATCATGTTTAATGATTTTACA	438
Qy	421	TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAACTCAACATGTTGGCTT	480
Db	439	TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAACTCAACATGTTGGCTT	498
Qy	481	TCTATTATCGTTTACAACTCAATCGACCGCAATTTTATCGATTACATTTAGCCCTGTTTA	540
Db	499	TCTATTATCGTTTACAACTCAATCGACCGCAATTTTATCGATTACATTTAGCCCTGTTTA	558
Qy	541	GTAACCAAAAAACACATTTACCCGTTTGAAGTATCGTGACAGATGATGGTAGTCAGGAA	600
Db	559	GTAACCAAAAAACACATTTACCCGTTTGAAGTATCGTGACAGATGATGGTAGTCAGGAA	618
Qy	601	GATCTATCACCAGATCATTCGCGCAATATGAAATATAAATTTGGATATTCGCTACGTCAGACAA	660
Db	619	GATCTATCACCAGATCATTCGCGCAATATGAAATATAAATTTGGATATTCGCTACGTCAGACAA	678
Qy	661	AAAGATAACCGTTTTCAGGCGAGTCGCCCTCGGAATATGGGATTAACGTTTAGGCAAAATAT	720
Db	679	AAAGATAACCGTTTTCAGGCGAGTCGCCCTCGGAATATGGGATTAACGTTTAGGCAAAATAT	738
Qy	721	GACTTTATTTGCTTACTCGATGATGATGGCCCAATCCATTATGGTTTCATTCTTAT	780
Db	739	GACTTTATTTGCTTACTCGATGATGATGGCCCAATCCATTATGGTTTCATTCTTAT	798
Qy	781	GTTGCAGAGCTATTAGAGATGATGATTTAAACAATCATTTGGTCCAAAGAAAAATACATCGAT	840
Db	799	GTTGCAGAGCTATTAGAGATGATGATTTAAACAATCATTTGGTCCAAAGAAAAATACATCGAT	858
Qy	841	ACACAACATATTGACCCCAAGAGACTTCTTAATAATACCGGAGTTTGTGTAGTCAAT	900

Db	859	ACACAACATANTGACCCAAAGACTTCTTAATAATACCGAGTTTGTGTGATCATTTACCA	918
Qy	901	GAAGTGAAAAACCAATATAGTGTTCGCCGCAAAAGGGGAAAGAAACAGTTCTCTGGATTGG	960
Db	919	GAAGTGAAAAACCAATATAGTGTTCGCCGCAAAAGGGGAAAGAAACAGTTCTCTGGATTGG	978
Qy	961	CGTTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCCTTTCCGTTTT	1020
Db	979	CGTTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCCTTTCCGTTTT	1038
Qy	1021	TTTGGCGCGGTAATGTTGCTTTTAAATAATGCTAAATAATGCTAAATAATGCTAAATAATGCT	1080
Db	1039	TTTGGCGCGGTAATGTTGCTTTTAAATAATGCTAAATAATGCTAAATAATGCTAAATAATGCT	1098
Qy	1081	GAGGAATTTTAAATCACTGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGCTTAC	1140
Db	1099	GAGGAATTTTAAATCACTGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGCTTAC	1158
Qy	1141	GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCCACCAGGTAAA	1200
Db	1159	GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCCACCAGGTAAA	1218
Qy	1201	GAAAAAGAAACCGATCGTGAAGCGGAAAAAATAATTACGCTCGATATTATGAGAGAAAAAG	1260
Db	1219	GAAAAAGAAACCGATCGTGAAGCGGAAAAAATAATTACGCTCGATATTATGAGAGAAAAAG	1278
Qy	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT	1320
Db	1279	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT	1338
Qy	1321	TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTTCAACGTTGCGGTAGAT	1380
Db	1339	TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTTCAACGTTGCGGTAGAT	1398
Qy	1381	AGTGCACTGAATCAGACTGTTTGTGATCTCGAGGTTTGTATTTGTAACTAGTGTCAACA	1440
Db	1399	AGTGCACTGAATCAGACTGTTTGTGATCTCGAGGTTTGTATTTGTAACTAGTGTCAACA	1458
Qy	1441	GATAATACTTTAGAAAGTGATCAATAAGCTTTTATGGTAATAATCTTAGGGTACGCATCATG	1500
Db	1459	GATAATACTTTAGAAAGTGATCAATAAGCTTTTATGGTAATAATCTTAGGGTACGCATCATG	1518
Qy	1501	TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCGAGCGGTTCTTTTGTCTAAAGGT	1560
Db	1519	TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCGAGCGGTTCTTTTGTCTAAAGGT	1578
Qy	1561	TATTACATTTGGGAGTTAGATTTCAGATGATTCTTGAGGCTGTATGCACTGTGAACTGTGT	1620
Db	1579	TATTACATTTGGGAGTTAGATTTCAGATGATTCTTGAGGCTGTATGCACTGTGAACTGTGT	1638
Qy	1621	TTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAAATAGAAACGTC	1680
Db	1639	TTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAAATAGAAACGTC	1698
Qy	1681	AATCCGGAATGGTAGTTTAAATCGCTAATGGTTTCAATTTGGGCGAGAAATTTTACGAGAAAAA	1740
Db	1699	AATCCGGAATGGTAGTTTAAATCGCTAATGGTTTCAATTTGGGCGAGAAATTTTACGAGAAAAA	1758
Qy	1741	CTCAACACGCTATGATTGCTCACCCTTTAGAAATGTTTACGATTAGAGCTTTGGCATTTTA	1800
Db	1759	CTCAACACGCTATGATTGCTCACCCTTTAGAAATGTTTACGATTAGAGCTTTGGCATTTTA	1818
Qy	1801	ACTGATGGATTCAATGAAAAAATTTGAAAAATGCGGTAGACTATGACATGTTTCTCTCAAACTC	1860
Db	1819	ACTGATGGATTCAATGAAAAAATTTGAAAAATGCGGTAGACTATGACATGTTTCTCTCAAACTC	1878
Qy	1861	AGTGAAGTTGGAAAAATTTAAACATCTTTAAATAAATCTGCTTATAACCGTGTATTTACATGGT	1920
Db	1879	AGTGAAGTTGGAAAAATTTAAACATCTTTAAATAAATCTGCTTATAACCGTGTATTTACATGGT	1938
Qy	1921	GATAACACATCAATTAAGAAACCTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT	1980

Db 1939 GATAACACATCAATTAAGAAACCTTGGCATTCAAAAGAAAAACCACTTTTGTGTAGTCAAT 1998  
Qy 1981 CAGTCATTAAATAGACAGGCATTAACCTTATTATATATATGACGAATTTGATGATTAGAT 2040  
Db 1999 CAGTCATTAAATAGACAGGCATTAACCTTATTATATATATGACGAATTTGATGATTAGAT 2058  
Qy 2041 GAAAGTGAAGATATATTTTCAATAAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
Db 2059 GAAAGTGAAGATATATTTTCAATAAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2118  
Qy 2101 AAAGATATTAATAATCATCCAGATTAAGATGCGCAAAATCGCAGTCAGTATTTTATATCCC 2160  
Db 2119 AAAGATATTAATAATCATCCAGATTAAGATGCGCAAAATCGCAGTCAGTATTTTATATCCC 2178  
Qy 2161 AATACATTAACCGCTTGTAGTGAAGAACTTAACCAATATTTTGAATATAAATAAATAATA 2220  
Db 2179 AATACATTAACCGCTTGTAGTGAAGAACTTAACCAATATTTTGAATATAAATAAATAATA 2238  
Qy 2221 TTGCTTATTTGTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db 2239 TTGCTTATTTGTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2298  
Qy 2281 CTAGCCTTCTATCATATAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
Db 2299 CTAGCCTTCTATCATATAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2358  
Qy 2341 ACGAGTATAGATTAATAAATACTGAGGGCACTTTAAGTAAATTAATAAATAAAGTCAG 2400  
Db 2359 ACGAGTATAGATTAATAAATACTGAGGGCACTTTAAGTAAATTAATAAATAAAGTCAG 2418  
Qy 2401 TTAATATCAAAATTTGTAATACATCATCTTTTGAATATCATGACAGCCTATTCGTTAAAAAT 2460  
Db 2419 TTAATATCAAAATTTGTAATACATCATCTTTTGAATATCATGACAGCCTATTCGTTAAAAAT 2478  
Qy 2461 GACAGCTATGCTTATATGAAAAATATGATGCGGCATGAATTTCTCAGCATTAACAT 2520  
Db 2479 GACAGCTATGCTTATATGAAAAATATGATGCGGCATGAATTTCTCAGCATTAACAT 2538  
Qy 2521 GATTGATCGAGAAATCAATCGCATCCACCATTTAAAGCTCATTAATAACTTATTTT 2580  
Db 2539 GATTGATCGAGAAATCAATCGCATCCACCATTTAAAGCTCATTAATAACTTATTTT 2598  
Qy 2581 AATGCAATGACTTAAAGATGATGAATGTAAGGGGCATCAAGGATGTTTATGAGC 2640  
Db 2599 AATGCAATGACTTAAAGATGATGAATGTAAGGGGCATCAAGGATGTTTATGAGC 2658  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTAAGAAAGTCATCAATCTTGCAGTCA 2700  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTTAAGAAAGTCATCAATCTTGCAGTCA 2718  
Qy 2701 ATTGATAGTGTGCGAATATTAACACTGAGGATATTTGTTTCCAATTTGCACTTTTAATC 2760  
Db 2719 ATTGATAGTGTGCGAATATTAACACTGAGGATATTTGTTTCCAATTTGCACTTTTAATC 2778  
Qy 2761 TTAGAAAGAAACCGGCCATGTTATTTAATAAATCATCCACTGACTTATATGCTTGG 2820  
Db 2779 TTAGAAAGAAACCGGCCATGTTATTTAATAAATCATCCACTGACTTATATGCTTGG 2838  
Qy 2821 GAACGAAATTAACAATGGAACAAATGAACAAATTTGAAGTGAAGAGAGAGAGAAATATA 2880  
Db 2839 GAACGAAATTAACAATGGAACAAATGAACAAATTTGAAGTGAAGAGAGAGAGAGAAATATA 2898  
Qy 2881 CCGTTTAAACAGTTCTATTATTAATAGTATTAACCTCTATAA 2919  
Db 2899 CCGTTTAAACAGTTCTATTATTAATAGTATTAACCTCTATAA 2937

RESULT 2

AAZ35589

ID AAZ35589 standard; DNA; 2937 BP.

XX

AC AAZ35589;

XX

DT 06-AUG-2003 (revised)  
DT 01-FEB-2000 (first entry)  
XX  
DE P. multocida hyaluronate synthase (PmHAS) nucleotide sequence.  
XX  
KW Hyaluronate synthase; PmHAS; hyaluronan; hyaluronic acid; HA; cosmetic;  
KW drug delivery; angiogenesis; wound healing; capsule synthesis;  
KW fowl cholera; shipping fever; ss.  
XX  
OS Pasteurella multocida.  
XX  
FH Key Location/Qualifiers  
FH CDS 19. .2937  
FT /\*tag= a  
FT /product= "PmHAS"  
FT /note= "Hyaluronate synthase"  
XX  
PW WO9951265-A1.  
XX  
XX 14-OCT-1999.  
XX PF 01-APR-1999; 99WO-US007289.  
XX  
PR 02-APR-1998; 98US-0080414P.  
PR 26-OCT-1998; 98US-00178851.  
XX  
XX (OKLA ) UNIV OKLAHOMA.  
XX  
XX Deangelis P;  
XX  
XX WPI; 2000-013032/01.  
DR P-PSDB; AAY43099.  
XX  
PT New isolated hyaluronate synthase nucleic acids, used for the production  
PT of hyaluronic acid, for developing antibiotics and vaccines and for  
PT diagnostic applications.  
XX  
PS Claim 3; Page 113-114; 121pp; English.  
XX  
CC This is the Pasteurella multocida hyaluronate synthase (PmHAS) nucleic  
CC acid sequence. Hyaluronic acid (HA) or hyaluronan, is a polysaccharide  
CC that serves both structural and recognition roles in higher animals.  
CC Bacteria produce extracellular capsules of HA which mimic their host HA  
CC and aid escape from a host immune response. The invention includes a  
CC vector containing the PmHAS nucleotide sequence which can be used to  
CC express PmHAS in a foreign host. The HS nucleic acids can be used for the  
CC production of HA. Also, specific changes to the HS coding sequence can  
CC result in the production of HA having a modified size distribution or  
CC structural configuration and functional properties. The HA products can  
CC be used in e.g. drug delivery, angiogenesis and wound healing.  
CC stabilization of recombinant proteins and in cosmetics. The HS nucleic  
CC acids can also be used to develop agents to block capsule synthesis by  
CC pathogens and act as antibiotics. The avirulent P. multocida strains can  
CC be used as vaccines for fowl cholera or shipping fever. (Updated on 06-  
CC AUG-2003 to correct OS field.)  
XX  
SQ Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

Query Match 99.9%; Score 2917.4; DB 3; Length 2937;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAATACATTTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
Db 19 ATGAATACATTTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 78  
Qy 61 AAATTTATTTGAAAGTCGGCGAAATCTATGAGCGGAAATTTGTTGAATTTCAATATACC 120  
Db 79 AAATTTATTTGAAAGTCGGCGAAATCTATGAGCGGAAATTTGTTGAATTTCAATATACC 138  
Qy 121 AAATGCAAGAAAGAACTCTCAGCACATCTCTTCTGTTAAATTTTCAGCACATCTTTCTGTAAT 180  
Db 139 AAATGCAAGAAAGAACTCTCAGCACATCTCTTCTGTTAAATTTTCAGCACATCTTTCTGTAAT 198

Qy	181	AAAGAGAAAAAGTCAATGTTTGGGATAGTCCGTTAGATATTGCAACACAACTGTTACTT	240
Db	199	AAAGAGAAAAAGTCAATGTTTGGGATAGTCCGTTAGATATTGCAACACAACTGTTACTT	258
Qy	241	TCCAAAGTAAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAAGTGTAAAAAATAAATGG	300
Db	259	TCCAAAGTAAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAAGTGTAAAAAATAAATGG	318
Qy	301	AAATTTGCTCACTGAGAGAGAAATCTGAAAAATCGGAGGTAAGAGCGGTGCGCCCTTGTACCA	360
Db	319	AAATTTGCTCACTGAGAGAGAAATCTGAAAAATCGGAGGTAAGAGCGGTGCGCCCTTGTACCA	378
Qy	361	AAAGATTTTCCAAAGATCTGTTTTAGCGCTTTTACCTGATCATGTTAATGATTTTACCA	420
Db	379	AAAGATTTTCCAAAGATCTGTTTTAGCGCTTTTACCTGATCATGTTAATGATTTTACCA	438
Qy	421	TGGTACAAAAGCGAAGAAAGACTTGGCATAAACCTGAAACATCAACATGTTGGTCTT	480
Db	439	TGGTACAAAAGCGAAGAAAGACTTGGCATAAACCTGAAACATCAACATGTTGGTCTT	498
Qy	481	TCTATTATCGTTACAAACATTCATCGACCCAGCAATTTTATCGATTACATTAGCCCTGTTA	540
Db	499	TCTATTATCGTTACAAACATTCATCGACCCAGCAATTTTATCGATTACATTAGCCCTGTTA	558
Qy	541	GTAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	600
Db	559	GTAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	618
Qy	601	GATCTATCACCGATCATTCCGCAATATCAAAATAAATTTGGATATTCGCTAGTCAGACAA	660
Db	619	GATCTATCACCGATCATTCCGCAATATCAAAATAAATTTGGATATTCGCTAGTCAGACAA	678
Qy	661	AAAGATAACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATTACGCTTAGCAAAAATAT	720
Db	679	AAAGATAACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATTACGCTTAGCAAAAATAT	738
Qy	721	GACTTTATGCGCTTACTCGACTGTGATATGCGGCCAAATCCATTTAGGGTTCACTCTTAT	780
Db	739	GACTTTATGCGCTTACTCGACTGTGATATGCGGCCAAATCCATTTAGGGTTCACTCTTAT	798
Qy	781	GTTCCAGAGCTATTAGAGATGATGATTTTACAACTATGCTGCCAAGAAATACATCGAT	840
Db	799	GTTCCAGAGCTATTAGAGATGATGATTTTACAACTATGCTGCCAAGAAATACATCGAT	858
Qy	841	ACACAACATATTGACCCAAAGACTTCTTAATAAACCGAGTTTGTCTGAAATCATTACCA	900
Db	859	ACACAACATATTGACCCAAAGACTTCTTAATAAACCGAGTTTGTCTGAAATCATTACCA	918
Qy	901	GAAGTGAAAAACCAATAATAGTGTGCGCCAAAGGGAAGGAAACAGTTTCTCTGGATTGG	960
Db	919	GAAGTGAAAAACCAATAATAGTGTGCGCCAAAGGGAAGGAAACAGTTTCTCTGGATTGG	978
Qy	961	CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCCGCTTTCCGTTTT	1020
Db	979	CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCCGCTTTCCGTTTT	1038
Qy	1021	TTTCCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTTAAATAAATCCGGTTTCTTGGAT	1080
Db	1039	TTTCCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTTAAATAAATCCGGTTTCTTGGAT	1098
Qy	1081	GAGAAATTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC	1140
Db	1099	GAGAAATTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC	1158
Qy	1141	GGTAGTTCTTTTAAACCTATTGATGGCATATGCGCTTACCATCAAGACCCACAGGTAAA	1200
Db	1159	GGTAGTTCTTTTAAACCTATTGATGGCATATGCGCTTACCATCAAGACCCACAGGTAAA	1218
Qy	1201	GAATAAGAAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAAG	1260
Db	1219	GAATAAGAAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAAG	1278

Qy	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCCGATATCAATAGAGTACCT	1320
Db	1279	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCCGATATCAATAGAGTACCT	1338
Qy	1321	TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACGTTCCGTAGAT	1380
Db	1339	TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACGTTCCGTAGAT	1398
Qy	1381	AGTGCACTGAACTCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGCTTCAACA	1440
Db	1399	AGTGCACTGAACTCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGCTTCAACA	1458
Qy	1441	GATAATACCTTTAGAACTGATCAATAAGCTTTTATGGTAAATCTTAGGGTACCCATCATG	1500
Db	1459	GATAATACCTTTAGAACTGATCAATAAGCTTTTATGGTAAATCTTAGGGTACCCATCATG	1518
Qy	1501	TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATCGAGCCGTTTCTTTTGTAAAGGT	1560
Db	1519	TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATCGAGCCGTTTCTTTTGTAAAGGT	1578
Qy	1561	TATTACATTTGGGCGAGTTAGATTCCAGATGATTATCTTTAGGCTGATGCGAGTTGAACTGTGT	1620
Db	1579	TATTACATTTGGGCGAGTTAGATTCCAGATGATTATCTTTAGGCTGATGCGAGTTGAACTGTGT	1638
Qy	1621	TTAAAGAAATTTTAAAGATAAAACGCTAGCTTTGTGTTTATACCACTAATAGAAACGTC	1680
Db	1639	TTAAAGAAATTTTAAAGATAAAACGCTAGCTTTGTGTTTATACCACTAATAGAAACGTC	1698
Qy	1681	AATCCGGATGGTAGCTTAATCGCTAATGTTTACAATTTGGCCAGAAATTTTCCAGAGAAAAA	1740
Db	1699	AATCCGGATGGTAGCTTAATCGCTAATGTTTACAATTTGGCCAGAAATTTTCCAGAGAAAAA	1758
Qy	1741	CTCACAACCGCTATGATTTGCTCACCCTTTAGAAATGTTTACAGATTTAGAGCTTTGGCATTTA	1800
Db	1759	CTCACAACCGCTATGATTTGCTCACCCTTTAGAAATGTTTACAGATTTAGAGCTTTGGCATTTA	1818
Qy	1801	ACTGATGGATTCATGAAAAATTTGAAAAATGCGGTAGACTATGACATGTTTCTCTCAAACTC	1860
Db	1819	ACTGATGGATTCATGAAAAATTTGAAAAATGCGGTAGACTATGACATGTTTCTCTCAAACTC	1878
Qy	1861	AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTTATAACCGTGTATTACATGGT	1920
Db	1879	AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTTATAACCGTGTATTACATGGT	1938
Qy	1921	GATAACACATCAATTTAAGAAACTTTGGCATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT	1980
Db	1939	GATAACACATCAATTTAAGAAACTTTGGCATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT	1998
Qy	1981	CAGTCATTAATAAGAACGCATAACTTATTATAATTTATGACGAAATTTGATGATTAGAT	2040
Db	1999	CAGTCATTAATAAGAACGCATAACTTATTATAATTTATGACGAAATTTGATGATTAGAT	2058
Qy	2041	GAAGTAGAAGATATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTTGATATCTTA	2100
Db	2059	GAAGTAGAAGATATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTTGATATCTTA	2118
Qy	2101	AAAGATATTAATAATCATCCAGAAATAAGATGCCAAAATCCGAGTCAGTATTTTTTATCCC	2160
Db	2119	AAAGATATTAATAATCATCCAGAAATAAGATGCCAAAATCCGAGTCAGTATTTTTTATCCC	2178
Qy	2161	AATACATTTAAACCGCTTAGTGAAAAAACTAAAATAATTTTGAATAATAATAAAAAATA	2220
Db	2179	AATACATTTAAACCGCTTAGTGAAAAAACTAAAATAATTTTGAATAATAATAAAAAATA	2238
Qy	2221	TTCCGTTATTTCTACATGTTTGAAGAATCATCTTACACCAGATATCAAAAAAGAAATA	2280
Db	2239	TTCCGTTATTTCTACATGTTTGAAGAATCATCTTACACCAGATATCAAAAAAGAAATA	2298
Qy	2281	CTAGCCCTTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC	2340
Db	2299	CTAGCCCTTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC	2358
Qy	2341	ACGAGTAAATAGATTAAATAAAAACTGAGGCGCATTTTAAGTAATAATTAATAAATAAGTCAG	2400



Db 499 TCTATTATCGTTACAAACATTCATCGACCGACGACCAATTTTTATCGATTACATTAGCCTGTTTA 558  
Qy 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Db 559 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTGACAGATGATGGTAGTCAGGAA 618  
Qy 601 GATCTATACCGATCATTCGCCATATAGAAATAAAATGGATATTCGCTACGTCAGACAA 660  
Db 619 GATCTATACCGATCATTCGCAATATAGAAATAAAATGGATATTCGCTACGTCAGACAA 678  
Qy 661 AAAGATAACGGTTTTCAAGCCAGTCGCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 720  
Db 679 AAAGATAACGGTTTTCAAGCCAGTCGCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 738  
Qy 721 GACTTTATGGCTTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGGTTCACTTTAT 780  
Db 739 GACTTTATGGCTTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGGTTCACTTTAT 798  
Qy 781 GTTCGACAGCTATTAGAGATGATTTAAACATCATTCGTCCAGAAATACATCGAT 840  
Db 799 GTTCGACAGCTATTAGAGATGATTTAAACATCATTCGTCCAGAAATACATCGAT 858  
Qy 841 ACACAAATATGTACCCAAAGACTTCTTAAATAACCGAGTTTGTCTTGAATCAATTACCA 900  
Db 859 ACACAAATATGTACCCAAAGACTTCTTAAATAACCGAGTTTGTCTTGAATCAATTACCA 918  
Qy 901 GAAGTGAACCAATATATAGTGTGGCGCAAAAGGGGAAGGAAACAGTTTCTCGGATGG 960  
Db 919 GAAGTGAACCAATATATAGTGTGGCGCAAAAGGGGAAGGAAACAGTTTCTCTGGATGG 978  
Qy 961 CGCTTAGAACCAATTCGAAARAAACAGAAATCTCGCTTATCCGATTCGCTTTCCGTTTT 1020  
Db 979 CGCTTAGAACCAATTCGAAARAAACAGAAATCTCGCTTATCCGATTCGCTTTCCGTTTT 1038  
Qy 1021 TTTCCGGCGGTAATGTGCTTTTCGCTAAATAATGGCTAAATAATCCGTTTCTTTGAT 1080  
Db 1039 TTTCCGGCGGTAATGTGCTTTTCGCTAAATAATGGCTAAATAATCCGTTTCTTTGAT 1098  
Qy 1081 GAGAAATTTAATCATCGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTAC 1140  
Db 1099 GAGAAATTTAATCATCGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTAC 1158  
Qy 1141 GGTAGTTCTTTAAACTATTTGATGGCATTTATGCGCTTACCATCAAGGCCACCAAGTAA 1200  
Db 1159 GGTAGTTCTTTAAACTATTTGATGGCATTTATGCGCTTACCATCAAGGCCACCAAGTAA 1218  
Qy 1201 GAAATGAACCGATCGTGAAGCGGAAAAATATTACGCTCGATATTATCAGAGAAAAAG 1260  
Db 1219 GAAATGAACCGATCGTGAAGCGGAAAAATATTACGCTCGATATTATCAGAGAAAAAG 1278  
Qy 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCAATCAATAGAGTACCT 1320  
Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCAATCAATAGAGTACCT 1338  
Qy 1321 TTAGTTTCAATTTATATCCGAGCTTATACTGTGCAACTATATTCAACGTTGCGTAGAT 1380  
Db 1339 TTAGTTTCAATTTATATCCGAGCTTATACTGTGCAACTATATTCAACGTTGCGTAGAT 1398  
Qy 1381 AGTGACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTAAGCATGGTTCAACA 1440  
Db 1399 AGTGACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTAAGCATGGTTCAACA 1458  
Qy 1441 GATAATACCTTTAGAGTGATCAATAAGCTTTATGGTAATAATTCCTAGGGTACGATCATG 1500  
Db 1459 GATAATACCTTTAGAGTGATCAATAAGCTTTTATGGTAATAATTCCTAGGGTACGATCATG 1518  
Qy 1501 TCTAAACCAATGGCGAATAGCCTCAGCATCAATGCAAGCGGTTCTTTTGGCTTAAAGGT 1560  
Db 1519 TCTAAACCAATGGCGAATAGCCTCAGCATCAATGCAAGCGGTTCTTTTGGCTTAAAGGT 1578  
Qy 1561 TATTACATTTGGCGAGTTAGATTAGATTATCTTTGAGCCTGATGCAAGTTGAACTGTG 1620  
Db 1579 TATTACATTTGGCGAGTTAGATTAGATTATCTTTGAGCCTGATGCAAGTTGAACTGTG 1638

Qy 1621 TTTAAAGAAATTTTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680  
Db 1639 TTTAAAGAAATTTTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1698  
Qy 1681 AATCCGGATGGTAGCTTAATCGCTAATGTTTACAATTTGGCCAGAAATTTTTCACGAGAAAA 1740  
Db 1699 AATCCGGATGGTAGCTTAATCGCTAATGTTTACAATTTGGCCAGAAATTTTTCACGAGAAAA 1758  
Qy 1741 CTCAAAACGGCTATGATTTGCTCACCACTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1800  
Db 1759 CTCAAAACGGCTATGATTTGCTCACCACTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1818  
Qy 1801 ACTGATGGATTCATCAAGAAAAATTTGAAAAATGCGGTAGACTATCAGCATGTTCTTCAAACTC 1860  
Db 1819 ACTGATGGATTCATCAAGAAAAATTTGAAAAATGCGGTAGACTATGAGCATGTTCTTCAAACTC 1878  
Qy 1861 AGTGAAGTTGAAAAATTTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT 1920  
Db 1879 AGTGAAGTTGAAAAATTTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT 1938  
Qy 1921 GATAACACATCAATTTAAGAAAATTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 1980  
Db 1939 GATAACACATCAATTTAAGAAAATTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 1998  
Qy 1981 CAGTCATTAATAAGACAGGCATAAATTTATTAATAATTTATGACGAAATTTGATGATTTAGAT 2040  
Db 1999 CAGTCATTAATAAGACAGGCATAAATTTATTAATAATTTATGACGAAATTTGATGATTTAGAT 2058  
Qy 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTTGATATCTTA 2100  
Db 2059 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTTGATATCTTA 2118  
Qy 2101 AAAGATATTAAATCATCCAGAAATAAGATGCCAAAATCGCAGTCAGTATTTTTTATCCC 2160  
Db 2119 AAAGATATTAAATCATCCAGAAATAAGATGCCAAAATCGCAGTCAGTATTTTTTATCCC 2178  
Qy 2161 AATACATATAAACCGCTTAGTGAAGAACTAAACAAATATTATTGAATATAATAAATAATA 2220  
Db 2179 AATACATATAAACCGCTTAGTGAAGAACTAAACAAATATTATTGAATATAATAAATAATA 2238  
Qy 2221 TTGGTTATTCTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db 2239 TTGGTTATTCTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2298  
Qy 2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTTACTAAATTAATGATATCTCATATTAC 2340  
Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTTACTAAATTAATGATATCTCATATTAC 2358  
Qy 2341 ACCAGTAATAGATTTAATAAACTGAGGCGCATTTAAGTAATATTATAAATTAAGTCAG 2400  
Db 2359 ACCAGTAATAGATTTAATAAACTGAGGCGCATTTAAGTAATATTATAAATTAAGTCAG 2418  
Qy 2401 TTTAAATCTAAATTTGTAATACATCATTTTTTGAATAATCATGACAGCTTATCGTTAAAAAT 2460  
Db 2419 TTTAAATCTAAATTTGTAATACATCATTTTTTGAATAATCATGACAGCTTATCGTTAAAAAT 2478  
Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGTGGCATGAATTTCTCAGCATTTAACACAT 2520  
Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTGGCATGAATTTCTCAGCATTTAACACAT 2538  
Qy 2521 GATTGGATCCAGAAAAATCAATGCGCATCCACCATTTTAAAAAGCTCATTTAAACCTTATTTT 2580  
Db 2539 GATTGGATCCAGAAAAATCAATGCGCATCCACCATTTTAAAAAGCTCATTTAAACCTTATTTT 2598  
Qy 2581 AATGACAAATGACTTTAAAAAGTATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGACG 2640  
Db 2599 AATGACAAATGACTTTAAAAAGTATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGACG 2658  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAGTCATCAGATCTTTCGCGAGTCA 2700  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAGTCATCAGATCTTTCGCGAGTCA 2718

Qy 2701 ATTGATAGTGTGCGAGAAATATAACACACGAGGATATTTGGTTCCAAATTTGCACTTTTAATC 2760  
Db |||||||  
Qy 2719 ATTGATAGTGTGCGAGAAATATAACACGAGGATATTTGGTTCCAAATTTGCACTTTTAATC 2778  
Db |||||||  
Qy 2761 TTAGAAAGAAAACCGGCATGTATTTAATAAACAATCGACCCCTGACTTATATGCTTGG 2820  
Db |||||||  
Qy 2779 TTAGAAAGAAAACCGGCATGTATTTAATAAACAATCGACCCCTGACTTATATGCTTGG 2838  
Db |||||||  
Qy 2821 GAACGAAATTTACAAATGACAAATGAACAAATTCGAAAGTGCAGAAAGAGGAGAAATATA 2880  
Db |||||||  
Qy 2839 GAACGAAATTTACAAATGACAAATGAACAAATTCGAAAGTGCAGAAAGAGGAGAAATATA 2898  
Db |||||||  
Qy 2881 CCTGTTAAACAGTTCAATTAATTAATAGTATATACTCTATAA 2919  
Db |||||||  
Qy 2899 CCTGTTAAACAGTTCAATTAATTAATAGTATATACTCTATAA 2937  
Db |||||||  
RESULT 4  
ADD93925  
ID ADD93925 standard; DNA; 2937 BP.  
XX  
AC ADD93925;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Pasteurella multocida hyaluronan synthase gene.  
XX  
KW hyaluronan synthase; HAS; Streptococcal infection;  
KW Streptococcal bacterium; phagocytic cell; macrophage;  
KW polymorphonuclear cell; PMN; polysaccharide capsule; hyaluronic acid;  
KW HA capsule; vaccine; gene; ds.  
XX  
OS Pasteurella multocida.  
XX  
PN WO2003048330-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 03-DEC-2002; 2002WO-US038596.  
XX  
PR 03-DEC-2001; 2001US-0336105P.  
PR 11-DEC-2001; 2001US-00011771.  
XX  
PA (WEIG/) WEIGEL P H.  
PA (KUMARI) KUMARI K.  
XX  
PI Weigel PH, Kumari K;  
XX  
DR WPI: 2003-482708/45.  
DR P-PSDB; ADD93926.  
XX  
XX Novel functionally active hyaluronan synthase having at least one  
PT modified amino acid residue in it as compared to a corresponding  
PT functionally active native hyaluronan synthase, useful for producing  
PT hyaluronic acid.  
XX  
PS Disclosure; SEQ ID NO 7; 362pp; English.  
XX  
CC This invention relates to a novel functionally active hyaluronan synthase  
CC (HAS) having at least one modified amino acid residue in it or having  
CC altered enzymatic activity as compared to a corresponding functionally  
CC active native hyaluronan synthase. Streptococcal infection is a major  
CC health and economic problem worldwide, particularly in developing  
CC countries. Streptococcal bacteria can grow undetected by the body's  
CC phagocytic cells (macrophages and polymorphonuclear cells; PMNs). The  
CC bacteria can evade detection by coating itself with polysaccharide  
CC capsules, such as a hyaluronic acid (HA) capsule. The invention is useful  
CC for producing hyaluronic acid and may aid the production of therapeutics  
CC and vaccines against Streptococcal infection. The present sequence is the  
CC HAS gene of Pasteurella multocida which is related to the invention.  
XX  
SQ Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

Query Match 99.9%; Score 2917.4; DB 10; Length 2937;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGATATCATTATACAAAGCAATAAAGACATATAACAGCAATGACTACTCAATTAAGCACTC 60  
Db |||||||  
Qy 19 ATGATATCATTATACAAAGCAATAAAGACATATAACAGCAATGACTACTCAATTAAGCACTC 78  
Db |||||||  
Qy 61 AAATTTATTTGAAAGTGGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAATTAACC 120  
Db |||||||  
Qy 79 AAATTTATTTGAAAGTGGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAATTAACC 138  
Db |||||||  
Qy 121 AAATGCAAGAAACATCTCAGCAATCTCTGTTAAATTCAGCAATCTCTCTGTTAAAT 180  
Db |||||||  
Qy 139 AAATGCAAGAAACATCTCAGCAATCTCTGTTAAATTCAGCAATCTCTCTGTTAAAT 198  
Db |||||||  
Qy 181 AAAGAAGAAAGTCAATGTTGGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 240  
Db |||||||  
Qy 199 AAAGAAGAAAGTCAATGTTGGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 258  
Db |||||||  
Qy 241 TCCAAACGTAAATAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300  
Db |||||||  
Qy 259 TCCAAACGTAAATAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 318  
Db |||||||  
Qy 301 AAATGCTCACTGAGAAAGAAATCTGAAAAATCGCGAGGTAGAGCGGTGCGCCCTGTACCA 360  
Db |||||||  
Qy 319 AAATGCTCACTGAGAAAGAAATCTGAAAAATCGCGAGGTAGAGCGGTGCGCCCTGTACCA 378  
Db |||||||  
Qy 361 AAAGATTTCCCAAGATCTGTTTGTAGCGCTTTTACCTGATCATGTTAAATGATTTTACA 420  
Db |||||||  
Qy 379 AAAGATTTCCCAAGATCTGTTTGTAGCGCTTTTACCTGATCATGTTAAATGATTTTACA 438  
Db |||||||  
Qy 421 TGGTACAAAAAGCGAAAAAGAAAGACTTTGGCATATAAAACCTGAAACATCAATGTTGGTCTT 480  
Db |||||||  
Qy 439 TGGTACAAAAAGCGAAAAAGAAAGACTTTGGCATATAAAACCTGAAACATCAATGTTGGTCTT 498  
Db |||||||  
Qy 481 TCTATATTCGTTACAAATTCATTCAGACCAAGCAATTTTATCGATACATTAAGCTGTTTAA 540  
Db |||||||  
Qy 499 TCTATATTCGTTACAAATTCATTCAGACCAAGCAATTTTATCGATACATTAAGCTGTTTAA 558  
Db |||||||  
Qy 541 GTAAACCAAAAAACACATTAACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Db |||||||  
Qy 559 GTAAACCAAAAAACACATTAACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618  
Db |||||||  
Qy 601 GATCTATCACCGATCATTCGCAATATGAAATTAATTTGGATATTCGCTACGTACAGCAA 660  
Db |||||||  
Qy 619 GATCTATCACCGATCATTCGCAATATGAAATTAATTTGGATATTCGCTACGTACAGCAA 678  
Db |||||||  
Qy 661 AAAGATAACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATTAAGCTTACGCTTACGCAAAATAT 720  
Db |||||||  
Qy 679 AAAGATAACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATTAAGCTTACGCTTACGCAAAATAT 738  
Db |||||||  
Qy 721 GACTTTATGCTTACTCGACTGTGATATGCGCCAAATCCATTAATGCTTCAATTCCTTAT 780  
Db |||||||  
Qy 739 GACTTTATGCTTACTCGACTGTGATATGCGCCAAATCCATTAATGCTTCAATTCCTTAT 798  
Db |||||||  
Qy 781 GTTGACAGAGCTATTAGAAAGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT 840  
Db |||||||  
Qy 799 GTTGACAGAGCTATTAGAAAGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT 858  
Db |||||||  
Qy 841 ACACAACATATGACCCCAAAAGACTTCTTAATAAATACGGAGTTTGGCTTGAATCATTAACA 900  
Db |||||||  
Qy 859 ACACAACATATGACCCCAAAAGACTTCTTAATAAATACGGAGTTTGGCTTGAATCATTAACA 918  
Db |||||||  
Qy 901 GAAGTGAACCAATTAATAGTGTTCGCCCAAAAGGGAGGAAACAGTTTCTCTGATTTGG 960  
Db |||||||  
Qy 919 GAAGTGAACCAATTAATAGTGTTCGCCCAAAAGGGAGGAAACAGTTTCTCTGATTTGG 978  
Db |||||||  
Qy 961 CGCTTTAGAACAAATTCGAAAAAACAAAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1020  
Db |||||||  
Qy 979 CGCTTTAGAACAAATTCGAAAAAACAAAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1038  
Db |||||||  
Qy 1021 TTTGCGGGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAATAATTCGGTTCTTTGAT 1080  
Db |||||||

Db 1039 TTTGCGGGGTAATGTTGCTTCCTGCTTAAATAATGGCTTAAATAATCGGTTTCCTTGAT 1098  
Qy 1081 GAGGAATTTAATCACTCGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTAC 1140  
Db 1099 GAGGAATTTAATCACTCGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTAC 1158  
Qy 1141 GGTAGTTTCTTTAAACTATTTGATGGCATTTATGCGCTACCATCAAGAGCCACAGGTAAA 1200  
Db 1159 GGTAGTTTCTTTAAACTATTTGATGGCATTTATGCGCTACCATCAAGAGCCACAGGTAAA 1218  
Qy 1201 GAAATGAACCCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAAG 1260  
Db 1219 GAAATGAACCCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAAG 1278  
Qy 1261 GTCCTTTATATCTATAGAAAATCTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320  
Db 1279 GTCCTTTATATCTATAGAAAATCTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1338  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTTATAA CTGTGCAAACTATATTTCAACGTTGGGTAGAT 1380  
Db 1339 TTAGTTTCAATTTATATCCAGCTTTATAA CTGTGCAAACTATATTTCAACGTTGGGTAGAT 1398  
Qy 1381 AGTCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGATTTCTGTAACGATGGTTCAACA 1440  
Db 1399 AGTCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGATTTCTGTAACGATGGTTCAACA 1458  
Qy 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATCTCCTAGGTCAGCATATG 1500  
Db 1459 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATCTCCTAGGTCAGCATATG 1518  
Qy 1501 TCTAAACCAAATGGGGAATAGCCTCAGCATCAAAATGCGAGCGTTTCTTTTGTCTAAAGGT 1560  
Db 1519 TCTAAACCAAATGGGGAATAGCCTCAGCATCAAAATGCGAGCGTTTCTTTTGTCTAAAGGT 1578  
Qy 1561 TATTACATTTGGGCACTTAGATTTAGATGATTTATCTTGAGCCTGATGCAAGTTGAAGTGT 1620  
Db 1579 TATTACATTTGGGCACTTAGATTTAGATGATTTATCTTGAGCCTGATGCAAGTTGAAGTGT 1638  
Qy 1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTGTTATATACCACTTAATAGAAACGTC 1680  
Db 1639 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTGTTATATACCACTTAATAGAAACGTC 1698  
Qy 1681 AATCCGATGTAGCTTTAATCGCTTAATGGTTACAAATTTGGCCAGAAATTTTTCACGAGAAAAA 1740  
Db 1699 AATCCGATGTAGCTTTAATCGCTTAATGGTTTACAAATTTGGCCAGAAATTTTTCACGAGAAAAA 1758  
Qy 1741 CTCAACGCGCTATGATTTGCTCACCACCTTTTAGAATGTTTACGATTTAGAGCTTTGGCATTTA 1800  
Db 1759 CTCAACGCGCTATGATTTGCTCACCACCTTTTAGAATGTTTACGATTTAGAGCTTTGGCATTTA 1818  
Qy 1801 ACTGATGGATTTCAATGAAAAAATTTGAAATGCCGTAGACATATGACATGTTTCTCTCAAACTC 1860  
Db 1819 ACTGATGGATTTCAATGAAAAAATTTGAAATGCCGTAGACATATGACATGTTTCTCTCAAACTC 1878  
Qy 1861 AGTGAAGTTGAAAAATTTTAAACATCTTAAATTTAAATCTGCTATAACCCGTGATTTACATGGT 1920  
Db 1879 AGTGAAGTTGAAAAATTTTAAACATCTTAAATTTAAATCTGCTATAACCCGTGATTTACATGGT 1938  
Qy 1921 GATAACACATCAATTTAGAACTTTGGCATTTCAAAGAAAAACCATTTTGTGTAGTCAAT 1980  
Db 1939 GATAACACATCAATTTAGAACTTTGGCATTTCAAAGAAAAACCATTTTGTGTAGTCAAT 1998  
Qy 1981 CAGTCATTAAATAGACAGGCATACTTATTATATTAATTTATGACGAATTTTGATGATTTAGAT 2040  
Db 1999 CAGTCATTAAATAGACAGGCATACTTATTATTAATTTATGACGAATTTTGATGATTTAGAT 2058  
Qy 2041 GAAAGTGAAGATATATTTTCAATAAAAACCGCTGAATATCAAGAGAGATTTGATCTTTA 2100  
Db 2059 GAAAGTGAAGATATATTTTCAATAAAAACCGCTGAATATCAAGAGAGATTTGATCTTTA 2118  
Qy 2101 AAAGATATTAATATCCTCAGAAATAAGATGCCAAAATCGCAGTCAGTATTTTTTATCC 2160

Db 2119 AAAGATATTAATATCCTCAGAAATAAGATGCCAAAATCGCAGTCAGTATTTTTTATCC 2178  
Qy 2161 AATACATTTAAACCGCTTAGTGAATAAACTTAAACAAATATTATTGAATATAATAAAATATA 2220  
Db 2179 AATACATTTAAACCGCTTAGTGAATAAACTTAAACAAATATTATTGAATATAATAAAATATA 2238  
Qy 2221 TTCGTTATTGTTCTACATGTTGATAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2280  
Db 2239 TTCGTTATTGTTCTACATGTTGATAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2298  
Qy 2281 CTAGCCTTCTATCATAAACATCAAGTGAATTTTACTTAAATATGATATCTCATATTC 2340  
Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATTTTACTTAAATATGATATCTCATATTC 2358  
Qy 2341 ACAGTAATAGATTAATAAAAACTGAGGCGCATTTAAGTAATATTAAATTAAGTCAG 2400  
Db 2359 ACAGTAATAGATTAATAAAAACTGAGGCGCATTTAAGTAATATTAAATTAAGTCAG 2418  
Qy 2401 TTAATCTAAATTTGTAATACATCATTTTGTAAATCATGCAGCCCTATTTCGTTAAAAAT 2460  
Db 2419 TTAATCTAAATTTGTAATACATCATTTTGTAAATCATGCAGCCCTATTTCGTTAAAAAT 2478  
Qy 2461 GACAGCTATCTTATATGAAAAATATGATGTCGCGATGAATTTCTCAGCATTAACACAT 2520  
Db 2479 GACAGCTATGCTTATGAAAAATATGATGTCGCGATGAATTTCTCAGCATTAACACAT 2538  
Qy 2521 GATTGATCGAGAAAAATCAATGCGCATCCACATTTTAAAGGCTCATTTAAACCTTATTTT 2580  
Db 2539 GATTGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAGGCTCATTTAAACCTTATTTT 2598  
Qy 2581 AATGCAATGACTTAAAGGATGAAATGTGAAGGGGCATCAAGGATGTTTATGACG 2640  
Db 2599 AATGCAATGACTTAAAGGATGAAATGTGAAGGGGCATCAAGGATGTTTATGACG 2658  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGAGCATTTTAAAGGATGAAATGTGAAGGGGCATCAAGGATGTTTATGACG 2700  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGAGCATTTTAAAGGATGAAATGTGAAGGGGCATCAAGGATGTTTATGACG 2718  
Qy 2701 ATTGATAGTGTGCAGAAATATAACACTGAGGATTTTGGTTCCAAATTTGCACTTTTAAATC 2760  
Db 2719 ATTGATAGTGTGCAGAAATATAACACTGAGGATTTTGGTTCCAAATTTGCACTTTTAAATC 2778  
Qy 2761 TTAGAAAGAAAAACCGCCCATGTTTAAATAAACATCGACCCCTGACTTATATGCTTTGG 2820  
Db 2779 TTAGAAAGAAAAACCGCCCATGTTTAAATAAACATCGACCCCTGACTTATATGCTTTGG 2838  
Qy 2821 GAACGAAAAATTACAATGGAACAAATGAACAAATTTGAAAGTCAAAAAAGAGGAGAAATATA 2880  
Db 2839 GAACGAAAAATTACAATGGAACAAATGAACAAATTTGAAAGTCAAAAAAGAGGAGAAATATA 2898  
Qy 2881 CCTGTTAAACAGTTTCAATTTAATAGTATTAACCTCTATAA 2919  
Db 2899 CCTGTTAAACAGTTTCAATTTAATAGTATTAACCTCTATAA 2937

RESULT 5  
ABT44090  
ID ABT44090 standard; DNA; 2916 BP.  
XX  
AC ABT44090;  
XX  
XX  
DT 17-OCT-2003 (first entry)  
XX  
XX  
DE Pasteurella multocida hyaluronan synthase DNA.  
KW  
KW Hyaluronic acid; glycosaminoglycan; hyaluronan synthase; antirheumatic;  
KW UDP-glucose 6-dehydrogenase; UDP-glucose pyrophosphorylase; orthopaedic;  
KW UDP-N-acetylglucosamine; ophthalmological; dermatological; joint surgery;  
KW eye; rheumatology; dermatology; adhesion; development; cell motility;  
KW cancer; angiogenesis; wound healing; ds; gene.  
XX  
OS Pasteurella multocida.  
XX

PN WO2003054163-A2.  
XX  
PD 03-JUL-2003.  
XX  
PF 20-DEC-2002; 2002WO-US041067.  
XX  
PR 21-DEC-2001; 2001US-0342644P.  
XX  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
XX  
PI Sloma A, Behr R, Widner W, Tang M, Sternberg D, Brown S;  
XX P-PSDB; ABJ72189.  
DR WPI; 2003-559139/52.  
XX P-PSDB; ABJ72189.  
PT Producing a hyaluronic acid (e.g. for use in eye and joint surgery,  
PT orthopedics, rheumatology or dermatology) comprises culturing a  
PT Bacillus host cell and recovering the hyaluronic acid from the  
PT cultivation medium.  
XX  
PS Claim 132; Page 186-190; 218pp; English.  
XX  
CC The invention relates to a novel method which comprises producing a  
CC hyaluronic acid via culturing a Bacillus host cell under conditions  
CC suitable for production of the hyaluronic acid and subsequently  
CC recovering the hyaluronic acid from the cultivation medium. The most  
CC abundant heteropolysaccharides of the body are the glycosaminoglycans, of  
CC which hyaluronic acid is an example. A number of enzymes are involved in  
CC the biosynthesis of hyaluronic acid including hyaluronan synthase, UDP-  
CC glucose 6-dehydrogenase, UDP-glucose pyrophosphorylase and UDP-N-  
CC acetylglucosamine. The molecules of the invention demonstrate  
CC ophthalmological, antirheumatic and dermatological activities, whilst the  
CC method itself may be useful for producing a hyaluronan in a recombinant  
CC host cell. The hyaluronan generated may be used in eye and joint surgery,  
CC orthopaedics, rheumatology or dermatology and may exhibit further uses  
CC within the fields of adhesion, development, cell motility, cancer,  
CC angiogenesis and wound healing. The current sequence is that of the DNA  
CC of the invention which encodes a protein that plays a role in the  
CC synthesis of hyaluronic acid  
XX  
SQ Sequence 2916 BP; 1067 A; 481 C; 506 G; 862 T; 0 U; 0 Other;  
Query Match 99.8%; Score 2914.4; DB 9; Length 2916;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGAATACATTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
DB 1 ATGNATACATTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
QY 61 AAATTTTGAAGTCGGCGGAAATCTATGACGGAATAATGTTGAATTCCAATTACC 120  
DB 61 AAATTTTGAAGTCGGCGGAAATCTATGACGGAATAATGTTGAATTCCAATTACC 120  
QY 121 AAATGCAAGAAATCTCTCAGCACATCTCTGTTAAATTCAGCACATCTCTCTGTAAT 180  
DB 121 AAATGCAAGAAATCTCTCAGCACATCTCTGTTAAATTCAGCACATCTCTCTGTAAT 180  
QY 181 AAAGAAAGAAATCTGATGTTTGCAGTAGTCGCTTAGATATTGCAACACAACTGTTACTT 240  
DB 181 AAAGAAAGAAATCTGATGTTTGCAGTAGTCGCTTAGATATTGCAACACAACTGTTACTT 240  
QY 241 TCCACGTAATAAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAATAATAGG 300  
DB 241 TCCACGTAATAAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAATAATAGG 300  
QY 301 AAATTCCTCCTCAGAGAAATCTGAAATGCGGAGTAAAGCGGTCGCGCTTGTACCA 360  
DB 301 AAATTCCTCCTCAGAGAAATCTGAAATGCGGAGTAAAGCGGTCGCGCTTGTACCA 360  
QY 361 AAAGATTTTCCCAAGACTCTGGTTTATAGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
DB 361 AAAGATTTTCCCAAGACTCTGGTTTATAGCGCTTTTACCTGATCATGTTAATGATTTTACA 420

QY 421 TGGTACAAAAAGCGAAAGAAAGACTTGGGCATAAAACTTGAACATCAACATGTTGGTCTT 480  
DB 421 TGGTACAAAAAGCGAAAGAAAGACTTGGGCATAAAACTTGAACATCAACATGTTGGTCTT 480  
QY 481 TCTATTATCGTTTACCAATTCATTCGACCGCAATTTTATCGATTACATTTAGCCCTGTTTA 540  
DB 481 TCTATTATCGTTTACCAATTCATTCGACCGCAATTTTATCGATTACATTTAGCCCTGTTTA 540  
QY 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTACAGATGATGGTAGTCAGAA 600  
DB 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTACAGATGATGGTAGTCAGAA 600  
QY 601 GATCTATCACCGATCATTTGCGCAATATGAAATTAATTTGGATATTCGCTACGTACAGAA 660  
DB 601 GATCTATCACCGATCATTTGCGCAATATGAAATTAATTTGGATATTCGCTACGTACAGAA 660  
QY 661 AAGATTAACGTTTTCAGCCAGTCCGCTCGGATATGGGATTCAGCTTACGCAAAATAT 720  
DB 661 AAGATTAACGTTTTCAGCCAGTCCGCTCGGATATGGGATTCAGCTTACGCAAAATAT 720  
QY 721 GACTTTATGGCTTACTCGACTGTGATATGGCCCAATTCATTTATGGTTTCATTTCTTAT 780  
DB 721 GACTTTATGGCTTACTCGACTGTGATATGGCCCAATTCATTTATGGTTTCATTTCTTAT 780  
QY 781 GTTCAGAGCTATTAGAAAGATGATTTAAACAATCATTTGGTCCAAAGAAATATACATCAT 840  
DB 781 GTTCAGAGCTATTAGAAAGATGATTTAAACAATCATTTGGTCCAAAGAAATATACATCAT 840  
QY 841 ACACACATATTTGACCCCAAGAGACTTCTTAATAACCGGAGTTTCTGTAATCATTTACCA 900  
DB 841 ACACACATATTTGACCCCAAGAGACTTCTTAATAACCGGAGTTTCTGTAATCATTTACCA 900  
QY 901 GAAGTGAAAAACCAATAATAGTGTTCGCCGCAAAAGGGAGGAAACAGTTTCTCGATTGG 960  
DB 901 GAAGTGAAAAACCAATAATAGTGTTCGCCGCAAAAGGGAGGAAACAGTTTCTCGATTGG 960  
QY 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCGTTT 1020  
DB 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCGTTT 1020  
QY 1021 TTTGCGGCGGTAATGTTGCTTTCGCTTAAATAATCGCTTAAATAATTCGTTTCTTTGAT 1080  
DB 1021 TTTGCGGCGGTAATGTTGCTTTCGCTTAAATAATCGCTTAAATAATTCGTTTCTTTGAT 1080  
QY 1081 GAGGAATTTAATCACTCGGGTGGAGAGATGTGGAAATTTGGATATCGCTTATTCGGTTAC 1140  
DB 1081 GAGGAATTTAATCACTCGGGTGGAGAGATGTGGAAATTTGGATATCGCTTATTCGGTTAC 1140  
QY 1141 GGTAGTTTCTTTTAAACATTTATGATGGCATTTATGGCTACCATCAAGAGCCACAGGTAA 1200  
DB 1141 GGTAGTTTCTTTTAAACATTTATGATGGCATTTATGGCTACCATCAAGAGCCACAGGTAA 1200  
QY 1201 GAAATGAAACCGATCGTGAAGCGGAAAAATATTTAGCTCGATATTTATGAGAGAAAG 1260  
DB 1201 GAAATGAAACCGATCGTGAAGCGGAAAAATATTTAGCTCGATATTTATGAGAGAAAG 1260  
QY 1261 GTCCCTTATATCTATAGAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320  
DB 1261 GTCCCTTATATCTATAGAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320  
QY 1321 TTATGTTTCAATTTATATCCAGCTTATTAJCTGTGCAAACTATTTCAAGCGTTGCGTAGAT 1380  
DB 1321 TTATGTTTCAATTTATATCCAGCTTATTAJCTGTGCAAACTATTTCAAGCGTTGCGTAGAT 1380  
QY 1381 AGTGACCTGAATCAGACTGTTTGTGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1440  
DB 1381 AGTGACCTGAATCAGACTGTTTGTGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1440  
QY 1441 GATTAATACCTTAGAGTAGTATCAATAGCTTTTATGGTAAATTCCTAGGGTACGCATCATG 1500  
DB 1441 GATTAATACCTTAGAGTAGTATCAATAGCTTTTATGGTAAATTCCTAGGGTACGCATCATG 1500

Qy 1501 TCTAAACCAATGGCGAATAGCCTCAGCATCAATGCGAGCGTTCTTTGCTAAAGGT 1560  
Db 1501 TCTAAACCAATGGCGAATAGCCTCAGCATCAATGCGAGCGTTCTTTGCTAAAGGT 1560  
Qy 1561 TATTACATTTGGGAGTTAGATTTCAGATGATTATCTTGAGCCCTGATGCGAGTTGAACCTGTGT 1620  
Db 1561 TATTACATTTGGGAGTTAGATTTCAGATGATTATCTTGAGCCCTGATGCGAGTTGAACCTGTGT 1620  
Qy 1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTATACCACTAAATAGAAACGTC 1680  
Db 1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTATACCACTAAATAGAAACGTC 1680  
Qy 1681 AATCCGATGTAGCTTAATCGCTAAATGGTTACAAATTTGGCCAGAAATTTTCACGAGAAAA 1740  
Db 1681 AATCCGATGTAGCTTAATCGCTAAATGGTTACAAATTTGGCCAGAAATTTTCACGAGAAAA 1740  
Qy 1741 CTCAACACGGCTATGATTGCTCACACCTTTTGAATGTTTACAGATTTAGAGCTTTGGCATTTA 1800  
Db 1741 CTCAACACGGCTATGATTGCTCACACCTTTTGAATGTTTACAGATTTAGAGCTTTGGCATTTA 1800  
Qy 1801 ACTGATGGATTCAATGAAAAAATTTGAAATGCCGTAGACTATGACATGTTCTCTCAAACTC 1860  
Db 1801 ACTGATGGATTCAATGAAAAAATTTGAAATGCCGTAGACTATGACATGTTCTCTCAAACTC 1860  
Qy 1861 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAAAATCTGCTATAACCCGTGTTATACATGGT 1920  
Db 1861 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAAAATCTGCTATAACCCGTGTTATACATGGT 1920  
Qy 1921 GATAACACATCAATTTAGAAATCTGGCATTCAAAGAAAAACCAATTTTGGTTGTTAGTCAAT 1980  
Db 1921 GATAACACATCAATTTAGAAATCTGGCATTCAAAGAAAAACCAATTTTGGTTGTTAGTCAAT 1980  
Qy 1981 CAGTCATTAAATAGACAGGATCAATCTTAAATATATATGACGAATTTGATGATTTAGAT 2040  
Db 1981 CAGTCATTAAATAGACAGGATCAATCTTAAATATATATGACGAATTTGATGATTTAGAT 2040  
Qy 2041 GAAAGTAGAAAGTATATTTTCAATAAACCCCTGAATATCAAGAGAGATTGATATCTTA 2100  
Db 2041 GAAAGTAGAAAGTATATTTTCAATAAACCCCTGAATATCAAGAGAGATTGATATCTTA 2100  
Qy 2101 AAAGATATTAATAATCATCCAGAAATTAAGATGCCAAATCGCAGTCAGTATTTTATATCCC 2160  
Db 2101 AAAGATATTAATAATCATCCAGAAATTAAGATGCCAAATCGCAGTCAGTATTTTATATCCC 2160  
Qy 2161 AATACATTTAAACGGCTTAGTGAAGAAAACTAAACAAATATTTTGAATATAAATAAATA 2220  
Db 2161 AATACATTTAAACGGCTTAGTGAAGAAAACTAAACAAATATTTTGAATATAAATAAATA 2220  
Qy 2221 TTCGTTATTGTTTACATGTTGATGAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db 2221 TTCGTTATTGTTTACATGTTGATGAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Qy 2281 CTAGCCTTCTATCATATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
Db 2281 CTAGCCTTCTATCATATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
Qy 2341 ACGAGTAATAGATTAAATAAAACCTGAGCGCATTTTAAAGTAATATTAATAAATTAAGTCAG 2400  
Db 2341 ACGAGTAATAGATTAAATAAAACCTGAGCGCATTTTAAAGTAATATTAATAAATTAAGTCAG 2400  
Qy 2401 TTAATCTAAATTTGTAATACATCAATTTTTGATATCATGACAGCCTATTCTTAAATAAT 2460  
Db 2401 TTAATCTAAATTTGTAATACATCAATTTTTGATATCATGACAGCCTATTCTTAAATAAT 2460  
Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGCGCATGAATTTCTCAGCATTTAACACAT 2520  
Db 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGCGCATGAATTTCTCAGCATTTAACACAT 2520  
Qy 2521 GATTGGATCGAGAAAAATCAATGCGCATCCACATTTAAAAAGCTCATTTAAACCTTATTTT 2580  
Db 2521 GATTGGATCGAGAAAAATCAATGCGCATCCACATTTAAAAAGCTCATTTAAACCTTATTTT 2580  
Qy 2581 AATGACATGACTTTAAAAAGTATGATGTGAAGGGGCATCACAGGTATGTTTATGACG 2640

Db 2581 AATGACATGACTTTAAAAAGTATGATGTGAAGGGGCATCACAGGTATGTTTATGACG 2640  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGTCATCACATCTTGCCAGTCA 2700  
Db 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGTCATCACATCTTGCCAGTCA 2700  
Qy 2701 ATTGATAGTGTGCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAATC 2760  
Db 2701 ATTGATAGTGTGCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAATC 2760  
Qy 2761 TTAGAAAAAGAAAAACCGCCCATGATTTTAAATAAAACATCGACCTGACTTATATGSCCTTGG 2820  
Db 2761 TTAGAAAAAGAAAAACCGCCCATGATTTTAAATAAAACATCGACCTGACTTATATGSCCTTGG 2820  
Qy 2821 GAACGAAAAATTTACAAATGCGACAAATGAACAAATTTGAAAGTCAAAAAAGAGGAGAAATATA 2880  
Db 2821 GAACGAAAAATTTACAAATGCGACAAATGAACAAATTTGAAAGTCAAAAAAGAGGAGAAATATA 2880  
Qy 2881 CCTGTTAAACAAAGTTCATTATTAATAGTATTAACCTCTA 2916  
Db 2881 CCTGTTAAACAAAGTTCATTATTAATAGTATTAACCTCTA 2916

RESULT 6  
AAA27449  
ID AAA27449 standard; cDNA; 2979 BP.  
XX  
AC AAA27449;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE P. multocida chondroitin synthase coding sequence.  
XX  
KW Chondroitin synthase; CS; enzyme; hyaluronic acid; ulcer;  
KW tissue abrasion; viscoelastic replacement; bioadhesive; ss.  
XX  
OS Pasteurella multocida.  
FH Key Location/Qualifiers  
FT CDS 61..2958  
FT /\*tag= a  
FT /product= "PmCS"  
XX  
FN W0200027437-A2.  
XX  
PD 18-MAY-2000.  
XX  
PF 10-NOV-1999; 99WO-US026501.  
XX  
PR 11-NOV-1998; 98US-0107929P.  
PR 01-APR-1999; 99US-00283402.  
XX  
PA (OKLA ) UNIV OKLAHOMA STATE.  
XX  
PI Deangelis PL;  
XX  
DR WPI; 2000-376319/32.  
DR P-PSDB; AAY96213.  
XX  
PT Novel method for the enzymatic transfer of sugar molecules to an  
PT acceptor, useful for synthesis of e.g. polysaccharide bioadhesives or  
PT drug delivery systems, including hybrid molecules.  
PS Claim 16; Page 86; 86pp; English.  
XX  
CC The present sequence is the coding sequence of the Pasteurella multocida  
CC chondroitin synthase PmCS. PmCS catalyses glycosaminoglycan  
CC polymerisation to produce chondroitin: a linear polysaccharide which has  
CC viscoelastic properties which makes it useful for a number of  
CC applications. Chondroitin can be used with hyaluronic acid (HA) to coat  
CC medical devices e.g. catheters and sensors to reduce tissue abrasion. In  
CC addition, they can be used as bioadhesives for haemostatic sealing and

CC	healing of wounds and surgical incisions; and as biomaterials that	
CC	provide sustained delivery of encapsulated drugs, to wounds, ulcers,	
CC	injuries or surgical sites	
XX		
SQ	Sequence 2979 BP; 1129 A; 466 C; 497 G; 887 T; 0 U; 0 Other;	
	Query Match 77.8%; Score 2271.2; DB 3; Length 2979;	
	Best Local Similarity 86.5%; Pred. No. 0;	
	Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;	
Qy	1 ATGAATACATTTATCACAAGCAATATAAGCATATATAACAGCAATAGACTCAATATAGCACTC 60	
Db	61 ATGAATACATTTATCACAAGCAATATAAGCAATATAAGCAATAGACTCAATATAGCACTC 120	
Qy	61 AAATTTATTTGAAGTCGGCGGAATCTATGCGAGGAAATTTGTAATTTCAAAATACC 120	
Db	121 AAATTTATTTGAAGTCGCTGMAACCTACGGGCGGAAAAATTCGTTGAATTCGAATATAC 180	
Qy	121 AAATGCAAGAAAACTCTCAGCAGCATCTTCTGTAAATTCAGCAGCATCTTCTTCTGTAAT 180	
Db	181 AAATGTAAGAAAACTCTCGACCAATTC-----TTATGTAAGT 219	
Qy	181 AAAGAAGAAAAAGTCAATTTTGGCATAGTCGTTAGATATATGCAACAACTGTTACTT 240	
Db	220 GAAGATAAAAAAACAAGTGTTCGATAGCTCAITTAGATATCGCAACACAGCTCTTACTT 279	
Qy	241 TCCAAAGTAAAAAATTTAGTACTTCTGACTCGGAAAAAACAAGTTTAAAAAATAAATGG 300	
Db	280 TCCAAAGTAAAAAATTTAAGTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG 339	
Qy	301 AAATGTCCTCACTGAGAAGAAATCTGAAATGCGGAGGTAAAGAGCGCTCGCCCTGTACCA 360	
Db	340 AAATCTATCACTCGGGAAGAAATTCGGAGAACCGAGAAATCAGAAAGTGGAACTAGTACCC 399	
Qy	361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTACCTGATCATGTTAAATGATTTTACA 420	
Db	400 AAAGATTTTCCTAAGATCTTGTCTTCTGCTCCATTTGCCAGATCATGTTAAATGATTTTACA 459	
Qy	421 TGGTACAAAAGCGAAGAAAGACTTGGCATATAAAACCTGAACATCAACATGTTGGTCTT 480	
Db	460 TGGTACAAAAGTTCGAAAAAAGCTTAGGTATAAAGCGCTGTAAGAAATATCGGTCTT 519	
Qy	481 TCTATTTATCGTTTACAACTTCAATCGACGACCAATTTTATCGATTACATTTAGCCCTGTTTA 540	
Db	520 TCTATTTATTTCCCTACATTTAATCGTAGCGGTATTTTATAGATATAAGCTTAGCCCTGTTG 579	
Qy	541 GTAAACCAAAAAACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600	
Db	580 GTCAATCAGAAAAACAACTACCCATTTGAAGTCGTTGTCAGATGATGGTAGTAAGGAA 639	
Qy	601 GATCTATCACCGATCATTCGCCAATATGAAATATAATTTGGATATATTCGCTACGTACAGCA 660	
Db	640 AACTTACTTACCATTGTGCAAAATATACGAAACAAACCTTGACATAAAGTATGTAAAGCAA 699	
Qy	661 AAAGATAACGGTTTTCAGCCAGTCGCGCTCGGAATATGGGATTTAGCTTAGCAAAATAT 720	
Db	700 AAAGATTTATGAGATACAAATTTGTGTGCGAGTCAGAACTTAGGTTTACGTACAGCAAGTAT 759	
Qy	721 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAAAATFCCATTTATGGGTTCATTTCTTAT 780	
Db	760 GATTTGTCTCGATTTAGACTTCGATATGGCACCACAAATTTATGGGTTCATTTCTTAT 819	
Qy	781 GTTCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTTCGAAGAAATATACATCGAT 840	
Db	820 CTTACAGAACTATTAGAAGCAATGATATTTGTTTAAATTTGACCTTAGAAAAATATGTGGAT 879	
Qy	841 ACACACATATTGACCCAAAGACTTCTTAATAACGCGAGTTTGTCTGAATCATTTACCA 900	
Db	880 ACTCAATATTATCCGCAAGCAAAATTTCTTTACAGATFCCATATTTAATAGNATCATTACCT 939	
Qy	901 GAAGTGAACCAATAATAGTGTTCGCCGAAAAAGGGAAGCAAGTCTTCTCGGATGG 960	
Db	940 GAAACCGCTACAAATAACAAATCTTCGATTACATCAAAAGGAAATATATATCGTTGGATTGG 999	

Qy	961 CGCTTAGACAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTTCGCTTTT 1020	
Db	1000 AGATTAGAACATTTCAAAAAAACCGATAATCTAGCTCTATGTGATTCTCCGTTTCGTTAT 1059	
Qy	1021 TTTCCGCGGGTAATGTTGCTTAAAGATGCTTAAATATGCTTAAATATGCTTTCGTTT 1080	
Db	1060 TTTTTCGCGGTAAATGTTGCAATTTTCTTAAAGATGCTTAAATATGCTTTCGTTT 1119	
Qy	1081 GAGGAATTTAATCACTCGGGTGGAGAAGATGTGAAATTTGGATATCGCTTATTCGCTTAC 1140	
Db	1120 GAAGAAATTTAATCATTTGCGGGGCGAAGATGTAGAAATTTGGTTACAGATTTATTTGCCAAA 1179	
Qy	1141 GGTAGTTTCTTTTAAAGCTATTGATGGCATTTATGCGCTTACCAATCAAGAGCCACCAAGGTAAA 1200	
Db	1180 GGCTGTTTTTCAGAGTAATTTGACGGCGGAATGGCCATCCATCAAGAACCACCTGGTAAA 1239	
Qy	1201 GAAATGAACCGATCGTGAAGCGGGAAGAAATATTTAGCTCGATATTTATGAGAGAAAG 1260	
Db	1240 GAAATGAACCGAGCTGGTAAAGTATTTAGCTTTAAATTTGCTGAAAGAAAG 1299	
Qy	1261 GTCCCTTATATCTATAGAAAACTTTTACCAATGAAGATTCGCATATCAATAGAGTACCT 1320	
Db	1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAGATTCACATATTTCTAGATACCT 1359	
Qy	1321 TTAGTTTCAATTTATATCCCAAGCTTTATAACTGTGCAAACTATATTTCAACGTTGGGTAGAT 1380	
Db	1360 TTAGTTTCTATTTATATCCCGCTTTATAACTGTGCAAAATATATTTCAAGATGTGTAGAT 1419	
Qy	1381 AGTCACATGAATCAGACTGTTGTTGATCTCGAGTTTGTATTTGTAACGATGGTTCAACA 1440	
Db	1420 AGTCTCTTAATCAAACTGTTGTCGATCTCGAGGTTGTATTTGTAACGATGGTTCAACA 1479	
Qy	1441 GATTAATCTTTAGAGTGCATCAATAGCTTTTATGTAATATCTTAGGTTAGCATCATG 1500	
Db	1480 GATAATACCTTTAGAGTGCATCAATAGCTTTTATGTAATATCTTAGGTTAGCATCATG 1539	
Qy	1501 TCTAAACCAAAATGCGGAATAGCCTCAGCATCAATGCAGCGCTTTCTTTTGTAAAGGT 1560	
Db	1540 TCTAAACCAAAATGCGGAATAGCCTCAGCATCAATGCAGCGCTTTCTTTTGTAAAGGT 1599	
Qy	1561 TATTACATGGCGAGTTAGATTTCAGATGATTTCTTAGACCTGATGCGATGTAACGTGT 1620	
Db	1600 TATTACATGGCGAGTTAGATTTCAGATGATTTCTTAGACCTGATGCGATGTAACGTGT 1659	
Qy	1621 TTAAGAGATTTTAAAGATATAACGCTAGCTGTTTATACCACCTAAATAGAAACGTC 1680	
Db	1660 TTAAGAGATTTTAAAGATATAACGCTAGCTGTTTATACCACCTAAATAGAAACGTC 1719	
Qy	1681 AATCCGATGTTAGCTTAAATCGCTAATGTTTACAAATGCGCCAGAAATTTTTCAGGAGAAA 1740	
Db	1720 AATCCGATGTTAGCTTAAATCGCTAATGTTTACAAATGCGCCAGAAATTTTTCAGGAGAAA 1779	
Qy	1741 CTCACACCGCTATGATTGCTCACCATTTTGAAGATGTTTCAGATTTAGAGCTTTGGCATTTA 1800	
Db	1780 CTCACACCGCTATGATTGCTCACCATTTTGAAGATGTTTACGATTTAGAGCTTTGGCATTTA 1839	
Qy	1801 ACTGATGATTTCAATGAAAAAATGAAATGCGGTAGACTATGACATGTTCTCTCAACCTC 1860	
Db	1840 ACGGATGATTTCAACGAAAAATTTGAAAAACGCGGTGATTTAGCATGTTCTCTTAACTC 1899	
Qy	1861 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAAATCTGCTATAACCGGTGTTTATACATGGT 1920	
Db	1900 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAAATCTGCTATAACCGGTGTTTATACATGGT 1959	
Qy	1921 GATAACACATCAATTTAAGAACTTGGCATTCAAAAAGAAAAACCATTTTGTGTAGTCAAT 1980	
Db	1960 GATAACACATCCATTTAAGAACTTGGCATTCAAAAAGAAAAACCATTTTGTGTAGTCAAT 2019	
Qy	1981 CAGTCATTTAAATAGCAAGGCATACCTTATATTAATATGAGAAATTTGATCATTTAGAT 2040	
Db	2020 CAGTCATTTAAATAGCAAGGCATCAATTTATTAATATGACAAAATTTGATGATTTAGAT 2079	

Qy 2041 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2100  
Dy |||||||  
Qy 2080 GAAAGTAGAAGTATATCTTCATATAAACCCCTGAATATCAAGAAGAAATGGATATGTTA 2139  
Dy |||||||  
Qy 2101 AAAGATATTTAAATCATCCAGAAATAAGATGCCAAAATCGCAGTCAGTATTTTATCCCC 2160  
Dy |||||||  
Qy 2140 AAAGATCTTAAACTCATTTCAAATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCC 2199  
Qy 2161 AATACATATAACGGCTTAGTGAAAAAACTAAACAATATTATTGAATATAATAAAAAATATA 2220  
Dy |||||||  
Qy 2200 AATACATATAACGGCTTAGTGAAAAAACTAAACAATATTATTGAATATAATAAAAAATATA 2259  
Qy 2221 TTGGTTATTTGTTCTACATGTTGATAAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2280  
Dy |||||||  
Qy 2260 TTGGTTATTTTCTACATGTTGATAAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2319  
Qy 2281 CTAGCCTTTCTATCATATAAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2340  
Dy |||||||  
Qy 2320 TTGGCTTTCTATCATATAGCACCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2379  
Qy 2341 ACGAGTAATAGATAATAAAAACTGAGCGGCAATTTAAGTAATATAATAAATTAAAGTCAG 2400  
Dy |||||||  
Qy 2380 ACGAGTAATAGATAATAAAAACTGAGCGCAATTTAAGTAATATAATAAATTAAAGTCAG 2439  
Qy 2401 TTAATCTAAATCTGTAATACATCATTTTTCATATATCATGACAGCCTATTTCGTTAAAAAT 2460  
Dy |||||||  
Qy 2440 TTAATCTAAATCTGTAATACATCATTTTTCATATATCATGACAGCCTATTTCGTTAAAAAT 2499  
Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGCGATGAATTTCTCAGCATTAACACAT 2520  
Dy |||||||  
Qy 2500 GACAGCTATGCTTATATGAAAAAATATGATGTCGCGATGAATTTCTCAGCATTAACACAT 2559  
Qy 2521 GATTGGATCGAGAAAAATCAATCGCGATCCACATTTTAAAAAGCTCATTTAAACCTTATTTT 2580  
Dy |||||||  
Qy 2560 GATTGGATCGAGAAAAATCAATCGCGATCCACATTTTAAAAAGCTCATTTAAACCTTATTTT 2619  
Qy 2581 AATCACAATGACTTAAAGAATGATGAATGTAAGGGGCGATCACAAGGTATGTTTATGACG 2640  
Dy |||||||  
Qy 2620 AATGACAAATGACTTAAAGAATGATGAATGTAAGGGGCGATCACAAGGTATGTTTATGAAG 2679  
Qy 2641 TATCGGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTCAATCATCATCTTGGCAGTCA 2700  
Dy |||||||  
Qy 2680 TATCGGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTCAATCATCATCTGCGCAATCA 2739  
Qy 2701 ATTGATAGTGCAGAAATATAAACAATGAGATATTTGGTTCCAAATTTGCACTTTTAAATC 2760  
Dy |||||||  
Qy 2740 ATTGATAGTGCAGAAATATAAACAATGAGATATTTGGTTCCAAATTTGCACTTTTAAATC 2799  
Qy 2761 TTAGAAAAGAAAACCGGCCATGTTTAAATAAAACATCGACCCCTGACTTATATGCTTTGG 2820  
Dy |||||||  
Qy 2800 TTAGAAAAGAAAACCGGCCATGTTTAAATAAAACATCGACCCCTGACTTATATGCTTTGG 2859  
Qy 2821 GAACGAAAATTTAATGAGCAAAATGAACAAATTTGAAAGTGAAGGAGGAGGAGAAAATATA 2880  
Dy |||||||  
Qy 2860 GAACGAAAATTTAATGAGCAAAATGAACAAATTTCAAAGTGAAGGAGGAGGAGAAAATATC 2919  
Qy 2881 CCTGTTAAAGGTTCAATTAATTAATAGTATAACTCTATAAA 2920  
Dy |||||||  
Qy 2920 CCCGTTAAAGGTTCAATTAATTAATAGTATAACGCTATAAA 2959

RESULT 7  
ABA05097  
ID ABA05097 standard; DNA; 2979 BP.  
XX  
AC ABA05097;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Pasteurella multocida chondroitin synthase gene #1.  
XX  
KW Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer;  
eye application; joint application; moisturiser; drug delivery;

XX  
OS Pasteurella multocida.  
XX  
FH Key Location/Qualifiers  
FT 61..2945  
FT /\*tag= a  
FT /product= "chondroitin synthase"  
XX  
PN W0200180810-A2.  
XX  
PD 01-NOV-2001.  
XX  
PP 25-APR-2001; 2001WO-US013395.  
XX  
PR 25-APR-2000; 2000US-0199538P.  
XX  
PA (DANG/) DE ANGELIS P L.  
XX  
PI De Angelis PL;  
XX  
DR WPI; 2002-049237/06.  
DR P-PSDB; AAM47335.  
XX  
PT New chondroitin synthase gene obtained from Pasteurella multocida, useful  
as hyaluronan polysaccharide substitute in medial or cosmetic  
applications, e.g. for eye or joint applications, for moisturizer or  
wound dressings.  
XX  
PS Claim 4; Page 117-118; 125pp; English.  
XX  
CC The present invention relates to the coding sequence of the Pasteurella  
multocida chondroitin synthase. A chondroitin polysaccharide may be used  
as a hyaluronan polysaccharide substitute in medial or cosmetic  
applications, for example in eye or joint applications, for moisturiser  
or wound dressings. The enzyme may be used in covalently coupled  
specific drugs, proteins or toxins to the structurally modified  
chondroitin for general or targeted drug delivery or radiological  
procedures, covalently cross linking the hyaluronic acid itself or to  
other supports to achieve a gel or other three dimensional biomaterial  
with stronger physical properties, and covalently linking hyaluronic acid  
to a surface to create a biocompatible film or monolayer. The present  
sequence is one version of the coding sequence of the invention  
XX  
SQ Sequence 2979 BP; 1129 A; 466 C; 497 G; 887 T; 0 U; 0 Other;  
Query Match 77.8%; Score 2271.2; DB 6; Length 2979;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;  
Qy 1 ATGATATCATATCACAGCAATTAAGCATATATAACAGCAATGACTATCAATTAGCACTC 60  
Dy |||||||  
Qy 61 ATGATATCATATCACAGCAATTAAGCATATATAACAGCAATGACTATCAATTAGCACTC 120  
Dy |||||||  
Qy 61 AAATTATTTGAAAGTCCGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAATATCC 120  
Dy |||||||  
Qy 121 AAATTATTTGAAAGTCTGCTGAAACCTAGCGGGGAAATCGTTGAATTCGAATATATC 180  
Qy 121 AAATGCAAGAAAAAATCTTCAGCACATCTTCTGTTAAATTCAGCACATCTTCTGTAAT 180  
Dy |||||||  
Qy 181 AAATGTAAGAAAAAATCTTCGACCAATTC-----TTATGTAAGT 219  
Qy 181 AAAGAAGAAAAAATGTAATGTTTGGGATAGTCGGTAGATATTGCAACACACTGTTACTT 240  
Dy |||||||  
Qy 220 GAAGATAAAAAAACAAGTGTTCGATAGTCAATAGATATCGCAACACAGCTCTTACTT 279  
Qy 241 TCCAACTGTAATAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300  
Dy |||||||  
Qy 280 TCCAACTGTAATAAATTTAATCTTATCCGATCAGAAAAAACAACAGTTTAAAAAATAAATGG 339  
Qy 301 AAATGCTCTAGAGAGAAATCTGAAATATCGGAGGTAAAGAGCGTTCGCCCTTTGTACCA 360  
Dy |||||||  
Qy 340 AAATCTATCACTCGGAAAAAATCGAGAACGCAAAATCAGAAAGGTGGAACCTAGTACCC 399

QY	361	AAAGATTTTCCCAAGATCTGGTTTTAGCGCCTTTTACCTGTGATCATGTTAAATGATTTTACA	420
DB	400	AAAGATTTTCCCTAAAGATCTTGTCTTCTCCATTCGCCAGATCATGTTAAATGATTTTACA	459
QY	421	TGGTACAAAAGCGGAAGAAAGACTTGGCATAAAACTTGAACATCAACATGTTGGTCTT	480
DB	460	TGGTACAAAATCGAAAAAAGACTTGGTATTAAGCCTGTAAATGAAGATATCGGTCTT	519
QY	481	TCTATTATCGTTACACATTTCAATCGACCGCAATTTTATCGATTACATTTAGCCTGTTTA	540
DB	520	TCTATTATTATCTACATTTAATCGTAGCCGTATTTTATAGATATAACGTTAGCCTGTTTG	579
QY	541	GTAACCAAAAAACACATTTACCGTGTGAAGTTATCGTGACAGATCATGTTAGTACAGAA	600
DB	580	GTCATACAGAAAAACAACTACCATTTGAAGTCTGTTGTCAGATGATGTTAGTAGGAA	639
QY	601	GATCTATCACCGATCATTTCCGCAATATGAATAATAAATTTGGATATTCGCTACGTCAGACAA	660
DB	640	AACCTACTTACCATTTGCAAAATACGAACAACAACTTGACATAAAGTATGTAAGACAA	699
QY	661	AAAGATAACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATTAGCCTTAGCCAAATAT	720
DB	700	AAAGATTATGGATATCAATTTGTGTCAGTCAGAACTTAGTGTACGTACAGCAAAAGTAT	759
QY	721	GACTTTATTGGCTTACTCGACTGTGATATCGCGCCAAATCCATTTATGGGTTCAATCTTAT	780
DB	760	GATTTTGTCTCGATTCCTAGACTCGGATATGGCACCAACAATATATGGGTTCAATCTTAT	819
QY	781	GTTTCAGAGCTATTAGAAGATGATGATTTAAACAATCAATTTGGTCCAGAAAAATACATCGAT	840
DB	820	CTTACAGACTTTTGAAGACATGATTTGTTTAAATTCGACCTAGAAAAATATGTTGAT	879
QY	841	ACACAACATATTTGACCCAAAGACTTTTAAATAACCGGATTTGCTTGAATCAATTACCA	900
DB	880	ACTCATAATATTACCGCAGAACAACTCTTAAACGATCCATTAATTAATAGAATCACTACCT	939
QY	901	GAAGTGAACCAATATAGTTTGGCGCAAAAGGGGAAGGAAACAGTTTCTCTGGATTTGG	960
DB	940	GAACCCGCTACAAATAACAATCTCTCGATTACATCAAAAGAAATATATCGTTGGATTTGG	999
QY	961	CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCGCTTATCCGATTCGCTTTCCGTTTT	1020
DB	1000	AGATTAGAACATTTCAAAAAACCGATATCTACGTCTATGATTTCTCGTTTCGTTAT	1059
QY	1021	TTTGGCGGGTAAATGTTGCTTTTCGCTTAAAAATAGGCTTAAATAAATCCGTTTCTTTGAT	1080
DB	1060	TTTGTTCGGGTAAATGTTGCTTTTCTTAAAGAAATGGCTTAAATAAGTAGTTGGTTGCTAT	1119
QY	1081	GAGGAATTTAATCATCTGGGTGGAGAGATGTGGAATTTGATATCGCTTATTTCCGTTAC	1140
DB	1120	GAAGAAATTTAATCATTTGGGGGGGGGAGATGTAGAAATTTGGTTACAGATTTATTGCCAA	1179
QY	1141	GGTAGTTTCTTTAAACCTATTATGATGGCATTTATGGCCTACCATCAAGAGCCACCAAGSTAAA	1200
DB	1180	GGCTGTTTTTTTCAGAGTAAATTTGACGGCGGAATGGCCATCCATCAAGAACCACTGGTAAA	1239
QY	1201	GAAAAATGAACCGATTCGTGAAGCGGGAAAAATATTACGCTCGATATTATTAGAGAAAAAG	1260
DB	1240	GAAAAATGAACAGAACCGAGCTGGTAAAAAGTATTACGCTTAAAAATTTGTGAAGAAAAAG	1299
QY	1261	GTCCCTTATATCTATAGAAAACTTTTACCATAGAGATTCGCGATATCAATAGAGTACCT	1320
DB	1300	GTACCTTATCATCTATAGAAAGCTTTTACCAATAGAGATTCACATATTATAGAAATACCT	1359
QY	1321	TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTTGGGTAGAT	1380
DB	1360	TTAGTTTCTAATTTATATCCCGCTTATAACTGTGCAATTTATTTCAAGATGTGTAGAT	1419
QY	1381	AGTGCACTGAATFACAGCTGTTGTTGATCTCGAGGTTTGTATTTGTAAAGATTTTCAACA	1440
DB	1420	AGTGCTCTTAATCAAACTGTTGTGATCTCGAGGTTTGTATTTGTAAAGATTTTCAACA	1479

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Db |||||||CGATCGAGAAATCAATGCGCATCCACCATTAAAGCTGATTAACCTATTTT 2619
Qy |||||||AATGACAAATGACTTTAAAGAGTATGAATGCTGAAGGGGCATCACAAGGTATGTTTATGACG 2640
Db |||||||AATGACAAATGACTTTAAGAGTATGAATGCTGAAGGGGCATCACAAGGTATGTTTATGAG 2679
Qy |||||||TATGCGGTAGCGCATGAGCTTCTGACGATTAATGAAGAGTATGAATGCTGCGCATCA 2700
Db |||||||TATGCGGTAGCGCATGAGCTTCTGACGATTAATGAAGAGTATGAATGCTGCGCATCA 2739
Qy |||||||ATTGATAGTGTGCGAGATATAACACTGAGATATTTGGTTCCAAATTTGCACTTTTAAATC 2760
Db |||||||ATTGATAGTGTGCGAGATATAACACTGAGATATTTGGTTCCAAATTTGCACTTTTAAATC 2799
Qy |||||||TTAGAAAAGAAAACCGGCCATGTATTTAAATAAACATCGACCTGACTTATATGCTTTGG 2820
Db |||||||TTAGAAAAGAAAACCGGCCATGTATTTAAATAAACATCGACCTGACTTATATGCTTTGG 2859
Qy |||||||GAACGAAAATTTACAAATGAGCAAAATGAACAAATTTGAAAGTGCAGAAAGAGGAGAAATATA 2880
Db |||||||GAACGAAAATTTACAAATGAGCAAAATGAACAAATTTGAAAGTGCAGAAAGAGGAGAAATATC 2919
Qy |||||||CCTGTTAACAAGTTTCATTTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 2920
Db |||||||CCCGTTAACAAGTTTCATTTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 2959
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## RESULT 8

```
ID ADP75648 standard; DNA; 2979 BP.
XX AC
XX ADP75648;
XX DT
XX DE 12-AUG-2004 (first entry)
XX DE Pasteurella multocida hyaluronidase coding sequence #1.
XX DE polymer production; hyaluronidase coding sequence #1.
XX DE hyaluronidase coding sequence #1.
XX DE hyaluronidase coding sequence #1.
XX DE Pasteurella multocida.
XX DE WO2003029261-A2.
XX DE 10-APR-2003.
XX DE 12-JUL-2002; 2002WO-US022386.
XX DE 13-JUL-2001; 2001US-0305263P.
XX DE 22-JAN-2002; 2002US-0350642P.
XX DE 08-MAY-2002; 2002US-00142143.
XX DE (DEAN/) DEANGELIS P L.
XX DE Deangelis PL;
XX DE WPI; 2003-532558/50.
XX DE P-PSDB; ADP75649.
```

Producing polymer, e.g. hyaluronidase or chondroitin polymer, by providing a functional acceptor, a synthase capable of elongating the acceptor and sugars such that the synthase elongates the acceptor to provide polymer.

Claim 1; SEQ ID NO 1; 538pp; English.

The invention comprises a method for producing a polymer, especially a hyaluronidase (HA) or chondroitin (CD) polymer composed of less than 150 sugars. The method involves providing a functional acceptor, and providing a synthase capable of elongating the functional acceptor, and providing sugars such that the synthase elongates the functional acceptor to provide the polymer. The method of the invention is useful for

CC producing a hyaluronidase or chondroitin polymer composed of 1-150 sugars. The present DNA sequence encodes a Pasteurella multocida hyaluronidase or chondroitin polymer.

CC hyaluronidase or chondroitin polymer.

XX

SQ Sequence 2979 BP; 1129 A; 466 C; 497 G; 887 T; 0 U; 0 Other;

Query Match 77.8%; Score 2271.2; DB 11; Length 2979;

Best Local Similarity 86.5%; Pred. No. 0;

Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;

Qy 1 ATGAATACATTTATCAAGCAATATAAGCATATAACAGCAATGACTATCAATTAGCACTC 60

Db 61 ATGAATACATTTATCAAGCAATATAAGCATATAACAGCAATGACTATGAATTAGCACTC 120

Qy 61 AAATATTTGAAAGTTCGGGGAATCTATGAGCGGAAATTTGTTGAAATTTCAATTTACC 120

Db 121 AAATATTTGAGAGTCTGCTGAAGCTAGCGGCGAAATTCGTTGAATTTCAATTTATC 180

Qy 121 AAATGCAAGAAAGAACTCTCAGCACATCTCTCTGTTAATTCAGCACATCTCTCTGTAAT 180

Db 181 AAATGTAAGAAAGAACTCTCGACCAATTC-----TTATGTAAGT 219

Qy 181 AAAGAAAGAAAGTCAATTTTTCGATAGTTCGTTAGATATTCGACACAACTGTTACTT 240

Db 220 GAAGATAAAGAAAGAACTCTCTGATAGTTCGTTAGATATTCGACACAACTGTTACTT 279

Qy 241 TCCAAAGTAAAGAAATTTAGTACTTTCTGACTCGGAAAGAAAGTTCGTTAAAGTAAAGT 300

Db 280 TCCAAAGTAAAGAAATTTAGTACTTTCTGATAGTTCGTTAGATATTCGACACAACTGTT 339

Qy 301 AAATGCTCACTGAGAAAGAACTCTGAAAGTTCGAGGAGTAAAGCGGCTGCTGTTACCA 360

Db 340 AAATGCTCACTGAGAAAGAACTCTGAAAGTTCGAGGAGTAAAGCGGCTGCTGTTACCA 399

Qy 361 AAAGATTTTCCAAAGTTCGTTTTCGATAGTTCGTTAGATATTCGACACAACTGTTACTT 420

Db 400 AAAGATTTTCCAAAGTTCGTTTTCGATAGTTCGTTAGATATTCGACACAACTGTTACTT 459

Qy 421 TGGTAAAGAAAGGAAAGAAAGTTCGTTTTCGATAGTTCGTTAGATATTCGACACAACTGTT 480

Db 460 TGGTAAAGAAAGTTCGTTTTCGATAGTTCGTTAGATATTCGACACAACTGTTACTT 519

Qy 481 TCTATTATTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCG 540

Db 520 TCTATTATTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCG 579

Qy 541 GTAAACCAAGAAAGGAAAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCG 600

Db 580 GTCAATCAGAAAGGAAAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCG 639

Qy 601 GATCTATCAGGATTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCG 660

Db 640 AACTTACTTACCAATTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCG 699

Qy 661 AAGATATTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCG 720

Db 700 AAGATATTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCG 759

Qy 721 GACTTTATTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCG 780

Db 760 GATTTTCTCGATTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCG 819

Qy 781 GTTCAGAGCTATTTAGAGATGATTTTAAAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCG 840

Db 820 CTTACAGAACTATTTAGAGATGATTTTAAAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCG 879

Qy 841 ACACAACTATTTAGAGATGATTTTAAAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCG 900

Db 880 ACTCATATTTATTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCG 939

Qy 901 GAACTGAAAGGAAAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCG 960

Db 940 GAAACCGCTACAAATTAAGATGATTTTAAAGTTCGTTTTCGATAGTTCGTTTTCGATAGTTCG 999

QY 961 CGCTTAGAACCAATTCGAAAAACAGAAAATCTCCGCTTATCCGATTCGCTTTTCGTTTT 1020  
DB 1000 AGATTAGAACATTTCAAAAAACCGATAATCTACGTCTATGATTCCTCGGTTCTGTTAT 1059  
QY 1021 TTTGCGGGGTAATGTGTTCTTCGCTTAAAAAATCGCTTAAATAATCCGGTTTCTTTGAT 1080  
DB 1060 TTTGTTGCGGTAATGTGTTGCAATTTCTAAAGAAATGGCTTAAATAAGTAGGTGTTGTCGAT 1119  
QY 1081 GAGGAATTTAATCACTGGGGTGAGAGATGTGGAATTTGGATATCGCTTATTCGTTAC 1140  
DB 1120 GAAGAAATTTAATCAATTTGGGGGGCGGAAGATGTGGAATTTGGTTACAGAAATTTTGCCAAA 1179  
QY 1141 GGTAGTTCTTTTAAACATTTATGATCGCATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1200  
DB 1180 GGCTGTTTTTTTCAGAGTAATTTGACGGGGAATGGCCATCCATCAAGAACCCCTGGTAAA 1239  
QY 1201 GAAAAATGAACCGATCGTGAACGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1260  
DB 1240 GAAATGAACAGAACGGGAACTGGTAAAGTATTACGCTTAAATAATGTGAAAGAAAAG 1299  
QY 1261 GTCCCTTATATCTATAGAAAATTTTACCAATAGAAGATTCCGATATCAATAGATACCT 1320  
DB 1300 GTACCTTACATCTATAGAAGCTTTTACCAATAGAAGATTTCATATTTCATAGAAATACCT 1359  
QY 1321 TTAGTTTCAATTTATATCCAGCTTATRACTGTGCAAACTATATTCAAGTTGCGTAGAT 1380  
DB 1360 TTAGTTTCTTATTTATATCCCGCTTATTAACCTGTGCNAATTTATTTCAAGATGTGTAGAT 1419  
QY 1381 AGTGCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTGAACGATGGTTCAACA 1440  
DB 1420 AGTGTCTTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTGTGAACGATGGTTCAACA 1479  
QY 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGTGTAATAATCTTAGGGTAGCATCATG 1500  
DB 1480 GATAATACCTTAGAAGTGATCAATAAGCTTTATGTGTAATAATCTTAGGGTAGCATCATG 1539  
QY 1501 TCTTAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGACAGCGTTTCTTTTCTTAAAGGT 1560  
DB 1540 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGACAGCGTTTCTTTTCTTAAAGGT 1599  
QY 1561 TATTACATTTGGGCGAGTTAGATTAGATGATTTCTTTGAGCCTGATGTCAGTTGAACCTGTG 1620  
DB 1600 TATTACATTTGGGCGAGTTAGATTAGATGATTTCTTTGAGCCTGATGTCAGTTGAACCTGTG 1659  
QY 1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680  
DB 1660 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1719  
QY 1681 AATCCGGATGGTAGCTTAATCGCTAATGTTACNAATTTGGCCAGAAATTTTTCAGAGAAA 1740  
DB 1720 AATCCGGATGGTAGCTTAATCGCTAATGTTACNAATTTGGCCAGAAATTTTTCAGAGAAA 1779  
QY 1741 CTCACAAACGCTATGATGCTCACCACCTTTAGAACTTTTACGATTTAGAGCTTTGGCATTTA 1800  
DB 1780 CTCACAAACGCTATGATGCTCACCACCTTTAGAACTTTTACGATTTAGAGCTTTGGCATTTA 1839  
QY 1801 ACTGATGGATTCAATGAAGAAAATTTGAAAATGCGGTAGACTATGACATGTTCTTCAAACCTC 1860  
DB 1840 ACGGATGGATTTTAAACGAAAATATTGAAAACGCGGTGGAATTTAGACATGTTCTTAAACCTC 1899  
QY 1861 AGTGAAGTTGGAAAAATTTTAAACATCTTAATTAATCTGCTATTAACCGCTGTTATACATGGT 1920  
DB 1900 AGTGAAGTTGGAAAAATTTTAAACATCTTAATTAATCTGCTATTAACCGCTGTTATACATGGT 1959  
QY 1921 GATAACACATCAATTAAGAACTTTGGCATTTCAAAGAAAACCATTTTGTGTAGTCAAT 1980  
DB 1960 GATAACACATCAATTAAGAACTTTGGCATTTCAAAGAAAACCATTTTGTGTAGTCAAT 2019  
QY 1981 CAGTCAATTAATAGACAAGGCATTAATTTAATTAATGACGAATTTGATGATTTAGAT 2040  
DB 2020 CAGTCAATTAATAGACAAGGCATTAATTTAATTAATGACAAAATTTGATGATTTAGAT 2079

QY 2041 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2100  
DB 2080 GAAAGTAGAAGTATATCTTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTA 2139  
QY 2101 AAGATATTTAAATCATCCAGAAATAAGAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2160  
DB 2140 AAGATCTTTAAATCATTTCAAAATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCC 2199  
QY 2161 AATACATTTAAACGGCTTAGTGAAAAAACTAAACAATATTATTGAATATAATAAAAAATA 2220  
DB 2200 AATACATTTAAACGGCTTAGTGAAAAAACTAAACAATATTATTGAATATAATAAAAAATA 2259  
QY 2221 TTCGTTATTTGTTTACATGTTGATAAGAAATCATCTTACACCAGATATCAAAAAAGAAATA 2280  
DB 2260 TTCGTTATTTTACATGTTTGAAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2319  
QY 2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATTAATGATATCTCATATTAC 2340  
DB 2320 TTGGCTTTCTATCATAGCACCAAGTGAATATTTTACTAAATTAATGATATCTCATATTAC 2379  
QY 2341 ACGAGTAATAGATTAAATAAAAACTGAGGCGCATTTTAAGTAATATTAAATTAAGTCAG 2400  
DB 2380 ACGAGTAATAGATTAAATAAAAACTGAGGCGCATTTTAAGTAATATTAAATTAAGTCAG 2439  
QY 2401 TTAATCTAAATTTGTGAATACATCATTTTGTGATAATCATGACAGCCTATTGTTAAAAAT 2460  
DB 2440 TTAATCTAAATTTGTGAATACATCATTTTGTGATAATCATGACAGCCTATTGTTAAAAAT 2499  
QY 2461 GACAGCTATGCTTATATGAAAAAATATGATCTCGCATGAATTTCTCAGCATTTAACACAT 2520  
DB 2500 GACAGCTATGCTTATATGAAAAAATATGATCTCGCATGAATTTCTCAGCATTTAACACAT 2559  
QY 2521 GATTGGATCGAGAAAATCAATCGCATCCACCATTTTAAAAAGCTGATTAAAAACCTATTTT 2580  
DB 2560 GATTGGATCGAGAAAATCAATCGCATCCACCATTTTAAAAAGCTGATTAAAAACCTATTTT 2619  
QY 2581 AATGCAATGACTTTAAAAAGTATGAATGTGAAAGGGGATCAAAAGGTATGTTTATGAGC 2640  
DB 2620 AATGCAATGACTTTAAAAAGTATGAATGTGAAAGGGGATCAAAAGGTATGTTTATGAGC 2679  
QY 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTATTAAAGAGTCAATCAGCATCTTGCCAGTCA 2700  
DB 2680 TATGCGCTAGCGCATGAGCTTCTGACGATTATTAAAGAGTCAATCAGCATCTTGCCAGTCA 2739  
QY 2701 ATTGATAGTGTGCCAGAAATAAACAATCAGGATATTTGTTTCCAAATTTGCACTTTTAAATC 2760  
DB 2740 ATTGATAGTGTGCCAGAAATAAACAATCAGGATATTTGTTTCCAAATTTGCACTTTTAAATC 2799  
QY 2761 TTAGAAAAAGAAAACCGGCCATGTATTTTAAATAAACATCGACCTGATATATGCTTGG 2820  
DB 2800 TTAGAAAAAGAAAACCGGCCATGTATTTTAAATAAACATCGACCTGATATATGCTTGG 2859  
QY 2821 GAACGAAAATTTCAATGAGCAAAATGAACAAATTTGAAGTGCAAAAGAGGAGAAAATATA 2880  
DB 2860 GAACGAAAATTTCAATGAGCAAAATGAACAAATTTGAAGTGCAAAAGAGGAGAAAATATA 2919  
QY 2881 CCTGTTTAAACAGTTCATTTATTAATAGTATACTTATAAA 2920  
DB 2920 CCCGTTTAAACAGTTCATTTATTAATAGTATAACGCTATAAA 2959

## RESULT 9

ADP75667  
ID ADP75667 standard; DNA; 2271 BP.

XX ADP75667;

XX AC

XX 12-AUG-2004 (first entry)

XX

DE Pasteurella multocida truncated hyaluronic acid synthase gene #11.

XX polymer production; hyaluronic acid polymer; chondroitin polymer;

XX hyaluronic acid synthase; gene; ds; enzyme.

KW

XX	Pasteurella multocida.
OS	WO2003029261-A2.
PN	
XX	
PD	10-APR-2003.
XX	
PF	12-JUL-2002; 2002WO-US022386..
XX	
PR	13-JUL-2001; 2001US-0305263P.
PR	23-JAN-2002; 2002US-030642P.
PR	08-MAY-2002; 2002US-00142143..
XX	(DEAN/) DEANGELIS P L.
PA	Deangelis PL;
P1	WPI; 2003-532558/50.
XX	
DR	Producing polymer, e.g. hyaluronic acid or chondroitin polymer, by providing a functional acceptor, a synthase capable of elongating the acceptor and sugars such that the synthase elongates the acceptor to provide polymer.
PT	
PT	
PT	
PT	
XX	Disclosure; SEQ ID NO 20; 538pp; English.
XX	The invention comprises a method for producing a polymer, especially a hyaluronic acid (HA) or chondroitin (CD) polymer composed of less than 150 sugars. The method involves providing a functional acceptor, and providing a synthase capable of elongating the functional acceptor, and providing sugars such that the synthase elongates the functional acceptor to provide the polymer. The method of the invention is useful for producing a hyaluronic acid or chondroitin polymer composed of 1-150 sugars. The present DNA sequence encodes a truncated Pasteurella multocida hyaluronic acid synthase of the invention.
CC	
XX	Sequence 2271 BP; 812 A; 384 C; 404 G; 671 T; 0 U; 0 Other;
SQ	
Query Match	77.7%; Score 2267.8; DB 11; Length 2271;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 2269; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Qy	1 ATGAATACATTATCACAAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
Db	1 ATGAATACATTATCACAAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
Qy	61 AAATTTATTTGAAAAGTCGGCGGAAATCTATGACGGAATAATTTGTGAATTTCAAATTACC 120
Db	61 AAATTTATTTGAAAAGTCGGCGGAAATCTATGACGGAATAATTTGTGAATTTCAAATTACC 120
Qy	121 AAATGCAGAAGAAAACTCTCAGACATCTTCTGTTTAATTCAGCACATCTTTCTGTAAT 180
Db	121 AAATGCCAAGAAAACTCTCAGACATCTTCTGTTTAATTCAGCACATCTTTCTGTAAT 180
Qy	181 AAAGAAGAAAAAGTCAATGTTTGCGTAGTFCGGTTAGATATTTGCAACAACACTGTACTT 240
Db	181 AAAGAAGAAAAAGTCAATGTTTGCGTAGTFCGGTTAGATATTTGCAACAACACTGTACTT 240
Qy	241 TCCAACGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300
Db	241 TCCAACGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300
Qy	301 AAATTCCTCACTCAGAGAAATCTGAAATGCGGAGTAAAGCGGTGCGCCCTGTACCA 360
Db	301 AAATTCCTCACTCAGAGAAATCTGAAATGCGGAGTAAAGCGGTGCGCCCTGTACCA 360
Qy	361 AAAAGATTTTCCCAGAAAGTCTGGTTTTAGCGCCCTTTTACCTGATCATGTTAAATGATTTACA 420
Db	361 AAAAGATTTTCCCAGAAAGTCTGGTTTTAGCGCCCTTTTACCTGATCATGTTAAATGATTTACA 420
Qy	421 TGSTACAAAAGCGAAAGAACACTTGGCATATAAAACCTTGAAACATCAATCTTGGCTTT 480
Db	421 TGSTACAAAAGCGAAAGAACACTTGGCATATAAAACCTTGAAACATCAATCTTGGCTTT 480







1141 GGTAGTTCTTTAAACCTATTGATGGCATATATGCGCTTACCATCAAGACCAACAGGTAA 1200  
 1180 GGCTGTTTTTCAGAGTAATTTGACGGCGGAATGCGATACCATCAAGAACCAACCTGGTAAA 1239  
 1201 GAAATGAAACCGATCGTGAACGGGAAANAATATTAGCTCGATATATTACAGAGAAAG 1260  
 1240 GAAATGAAACAGACCGGAGCTGGTAAAGTATTACGCTTAAATTTGTGAAGAAAG 1299  
 1261 GTCCCTTATCTATAGAAAATTTTACCATAAGAGATTCGCATATCAATAGAGTACCT 1320  
 1300 GTACCTTACATCTATAGAAAGCTTTTACCATAAGAGATTCGCATATCAATAGATACCT 1359  
 1321 TTAGTTTCAATTTATATCCAGCTTATAAATCTGTCGAACTATATTCACAGTTGCGTAGAT 1380  
 1360 TTAGTTTCTATTTATATCCCGCTTATAAATCTGTCGAAATATAATCAAGATGTTAGAT 1419  
 1381 AGTCACTGAATCAGACTGTTGTTGATCTCAGGTTTGTATTTCTAAGATGTTTCAACA 1440  
 1420 AGTCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1479  
 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGTTAATATCTAGGTTACGCATCATG 1500  
 1480 GATAATACCTTAGAAGTGATCAATAAGCTTTATGTTAATATCTAGGTTACGCATCATG 1539  
 1501 TCTAAACCAATGCGGAATAGCCTCAGCATCAAAATGCGAGCTTTCTTTTGTAAAGGT 1560  
 1540 TCTAAACCAATGCGGAATAGCCTCAGCATCAAAATGCGAGCTTTCTTTTGTAAAGGT 1599  
 1561 TATTACATGGGAGTTAGATTTCAGATGATTATCTTGAGGCTGATGCAATGGAATGTT 1620  
 1600 TATTACATGGGAGTTAGATTTCAGATGATTATCTTGAGGCTGATGCAATGGAATGTT 1659  
 1621 TTAAGAAGATTTTAAAGATGATAAAGCTAGCTGTTGTTTATACACCTAATAGAAACCTC 1680  
 1660 TTAAGAAGATTTTAAAGATGATAAAGCTAGCTGTTGTTTATACACCTAATAGAAACCTC 1719  
 1681 AATCCGGATGTTAGTTAATCGCTAATGTTTACAAATGCGCAGAAATTTTCAAGAGAAAA 1740  
 1720 AATCCGGATGTTAGTTAATCGCTAATGTTTACAAATGCGCAGAAATTTTCAAGAGAAAA 1779  
 1741 CTCAACCGCTATGATGCTCACCATTATAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1800  
 1780 CTCAACCGCTATGATGCTCACCATTATAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1839  
 1801 ACTGATGATTCAATGAAATAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
 1840 ACGATGATTTTAAGCAAAATATTGAAACCGCGTGATATGACATGTTCTTAAACTC 1899  
 1861 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAATCTGCTATAACCGGTGTTATACATGGT 1920  
 1900 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAATCTGCTATAACCGGTGTTATACATGGT 1959  
 1921 GATAACACATCAATTTAAGAACTTGGCATTTCAAGAGAAACCAATTTTGTGTAGTCAAT 1980  
 1960 GATAACACATCAATTTAAGAACTTGGCATTTCAAGAGAAACCAATTTTGTGTAGTCAAT 2019  
 1981 CAGTCATTAAATAGACAGGCACTATTATATATATATGACGAATTTGATGATTTAGAT 2040  
 2020 CAGTCATTAAATAGACAGGCACTATTATATATATATGACGAATTTGATGATTTAGAT 2079  
 2041 GAAAGTAGAAGTATATTTTCAATAAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
 2080 GAAAGTAGAAGTATATCTTCAATAAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2139  
 2101 AAAGATATTAATCATCTCAGATTAAGATGCGCAAAATCGCAGTCAGTATTTTATCTCC 2160  
 2140 AAAGATCTTAAACTCATTTCAAAATAAAGATGCGCAAAATCGCAGTCAGTATTTTATCTCC 2199  
 2161 AATACATTTAAACGGCTTAGTGAAAAAATCTTAAACATATTTTGAATATAATAAATAATA 2220  
 2200 AATACATTTAAACGGCTTAGTGAAAAAATCTTAAACATATTTTGAATATAATAAATAATA 2259

2221 TTGTTATTGTTCTCATCATGTTGATAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2280  
 2260 TTGTTATTATTCTCATCATGTTGATAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2319  
 2281 CTAGCCTTCTTATCATATAAATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
 2320 TTGCTTCTTATCATATAAGCACCAGTGAATATTTTACTAAATATGATATCTCATATTAC 2379  
 2341 ACAGTAATAGATTAATAAATACTGAGGCGCATTTAAGTAAATATTAATAAATTAAGTCAG 2400  
 2380 ACAGTAATAGACTAATAAATACTGAGGCGCATTTAAGTAAATATTAATAAATTAAGTCAG 2439  
 2401 TTAATCTTAATTTGCTAATACATCATTTTGTAAATATCATGACAGCTTATTCGTTTAAAT 2460  
 2440 TTAATCTTAATTTGCTAATACATCATTTTGTAAATATCATGACAGCTTATTCGTTTAAAT 2499  
 2461 GACAGCTATGCTTATATGAAAAATATGATGTCGCGCATGAAATTTCTCAGCATTAACACAT 2520  
 2500 GACAGCTATGCTTATATGAAAAATATGATGTCGCGCATGAAATTTCTCAGCATTAACACAT 2559  
 2521 GATTGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAGGCTGATTTAAACCTATTTT 2580  
 2560 GATTGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAGGCTGATTTAAACCTATTTT 2619  
 2581 AATGACATGACTTAAAGATGATGAATGTAAGAGGCGCATCAAGGTATGTTTATGACG 2640  
 2620 AATGACATGACTTAAAGATGATGAATGTAAGAGGCGCATCAAGGTATGTTTATGACG 2679  
 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGTATCATCATCTTGCAGTCA 2700  
 2680 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGTATCATCATCTTGCAGTCA 2739  
 2701 ATTGATAGTGTCCAGAAATAACACAGAGATTTTGGTTCGAATTTTGCACCTTTTAAATC 2760  
 2740 ATTGATAGTGTCCAGAAATAACACAGAGATTTTGGTTCGAATTTTGCACCTTTTAAATC 2799  
 2761 TTAGAAAAAGAAACCGGCGCATGTTTAAATAAACAATCGACCTGACTTATATGCTTTGG 2820  
 2800 TTAGAAAAAGAAACCGGCGCATGTTTAAATAAACAATCGACCTGACTTATATGCTTTGG 2859  
 2821 GAACGAAAAATTAACAATCGCAAAATGAACAAATTTGAAAGTGCAAAAAGAGGAGAAATATA 2880  
 2860 GAACGAAAAATTAACAATCGCAAAATGAACAAATTTGAAAGTGCAAAAAGAGGAGAAATATA 2919  
 2881 CCGTTTAAACAGTTTCAATTTAATAATAGTAACTCTATAAA 2920  
 2920 CCGTTTAAACAGTTTCAATTTAATAATAGTAACTCTATAAA 2959

RESULT 12  
 AEA04966  
 ID AEA04966 standard; DNA; 2979 BP.  
 XX AEA04966;  
 AC AEA04966;  
 XX  
 DT 11-AUG-2005 (first entry)  
 XX  
 DE Chondroitin synthase, PmCS, coding sequence, SEQ ID 4.  
 XX Chondroitin synthase; polysaccharide; gene; ds.  
 XX Pasteurella multocida.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 CDS 61..2958  
 FT /\*tag= a  
 FT /product= "PmCS"  
 XX  
 PN US2005124046-A1.  
 XX  
 PD 09-JUN-2005.  
 XX  
 PF 16-JUL-2002; 2002US-00197153.

XX 10-NOV-1999; 99US-00437277.  
XX (DEAN/) DEANGELIS P L.  
XX Deangelis PL;  
XX WPI: 2005-417007/42.  
DR P-PSDB; AEA04965.  
DR GENBANK; AF195517.  
XX  
PT Elongating a functional acceptor (e.g. hyaluronic acid or chondroitin),  
PT useful in polysaccharide polymer grafting, comprises providing hyaluronic  
PT acid synthase, UDP-GlcUA and/or UDP-GlcNAc sugars to elongate the  
PT functional acceptor.  
XX  
PS Disclosure; SEQ ID NO 4; 41pp; English.  
XX  
PS The present invention relates to a method for elongating a functional  
CC acceptor. The method comprises providing a hyaluronic acid (HA) synthase  
CC (PmHAS; AEA04963) capable of elongating the functional acceptor and  
CC providing UDP-GlcUA and UDP-GlcNAc sugars such that the hyaluronic acid  
CC synthase elongates the functional acceptor. PmHAS adds sugars to the  
CC nonreducing end of a growing polymer chain. The PmHAS sequence is  
CC significantly different from the other known HA synthases; there appears  
CC to be only two short potential sequence motifs (AEA04967 and AEA04968) in  
CC common between PmHAS and the other HA synthases. The method is useful in  
CC polysaccharide polymer grafting, which may be utilized in the development  
CC of biotechnological medical improvements. These may be used for producing  
CC hybrid polysaccharides or for forming polysaccharide coatings. Also  
CC disclosed is chondroitin synthase (PmCS; AEA04965) and its coding  
CC sequence (AEA04966) from Pasteurella multocida. Type A P. multocida  
CC produces a HA capsule [GlcUA-GlcNAc repeats] and possesses the PmHAS  
CC enzyme. On the other hand, Type P P. multocida produce a chondroitin or  
CC chondroitin-like polymer capsule [GlcUA-GalNAc repeats] using PmCS.  
CC Either HA or chondroitin chains can serve as acceptors for PmCS as both  
CC acceptors serve well for PmHAS.  
XX  
SQ Sequence 2979 BP; 1130 A; 466 G; 495 C; 888 T; 0 U; 0 Other;  
Query Match 77.6%; Score 2266.4; DB 14; Length 2979;  
Best Local Similarity 86.4%; Pred. No. 0;  
Matches 2523; Conservative 0; Mismatches 376; Indels 21; Gaps 1;  
QY 1 ATGAATACATTATCAACGAATATAAGCATATAACAGCAATGACTATCAATAGCACTC 60  
DB 61 ATGAATACATTATCAACGAATATAAGCATATAACAGCAATGACTATCAATAGCACTC 120  
QY 61 AAATTATTGAAAGTCGGGAAATCTATGACGGAAATTTGTTGAAATTCAAATATACC 120  
DB 121 AAATTATTGAGAAAGTCGCTGAAACCTACGGCGAAATATCGTTGAAATTCNAATATC 180  
QY 121 AAATGCAAAAGAAATCTCTCAGCACATCTCTCTGTTTAATTCAGCACATCTCTCTGTAAT 180  
DB 181 AAATGTAAGAAATCTCTCGACCAATTC-----TTATGTAAGT 219  
QY 181 AAGAAGAAAGAAAGTCAATGTTTCGGATAGTCGCTTAGATATTCGACACACAACTGTACTT 240  
DB 220 GAAGATAAAAGAAAGTGTTCGGATAGCTCATTTAGATATCGCAACACAGCTCTTACTT 279  
QY 241 TCCAACGTAAAGAAATAGTACTTCTGACTCGGAAAGAAACACGTTTAAAGAAATATGCG 300  
DB 280 TCCAACGTAAAGAAATTAACCTCTATCCGAATCAGAAAGAAACAGTTTAAAGAAATATGCG 339  
QY 301 AAATTGCTCACTCAGAAAGAAATCTGAAATTCGGAGGTAAAGAGCGTTCGCGCTTGTACCA 360  
DB 340 AAATCTATCACTCGGAAAGAAATCGGAGACGCAAGAAATCAGAAAGGTGGAACCTAGTACCC 399  
QY 361 AAGAAGTTTTCCAAAGATCTGTTTTAGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
DB 400 AAGAAGTTTTCTAAAGATCTGTTCTTGTCTCCATTCAGATCATGTTAATGATTTTACA 459  
QY 421 TGGTACAAAGCAAGAAAGAAAGACTTTGGCATAAACCTGAACATCAACATGTTGCTCTT 480

DB 460 TGGTACAAAGCAAGAAAGAAAGCTTAGGTATAAGCCTGTAAATTAAGAAATATCGGTCTT 519  
QY 481 TCTATTATCGTTTACAAACATTCATCAATCGACCAAGCAATTTTATCGATTACATTAAGCCTGTTTA 540  
DB 520 TCTATTATATCTTACATTTAATCGTAGCCGTATTTAGATATAACCGTTAGCCTGTTTG 579  
QY 541 GTAAACCAAAACACATTTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGAA 600  
DB 580 GTCAATCAGAAACAAACATCCCATTTGAAGTCGTTGTTGAGATGATGGTAGTAAGAA 639  
QY 601 GATCTATCACCGATCATTCGCCAATATGAAATTAATTTGGAATATTCGCTACGTACAGACA 660  
DB 640 AACTTACTTACCATTTGCAAAATATACGAAACAAACCTTTGACATAAAGTATGTAGACAA 699  
QY 661 AAAGATACGGTCTTCAAGCCAGTCCGCTCGGAATATGGGATTAACGTTTAGCAAAATAT 720  
DB 700 AAAGATATGATATCAATTTGTGCACTCAGAAACTTAGGTTTACGTACAGCAAGTAT 759  
QY 721 GACTTTATTTGCTTACTCGACTGTGATATGGGCAAAATCCATTTATGGTTTCATCTTTAT 780  
DB 760 GATTTTGTCTCGATTTCTAGACTGCGATATGCGACCAACAAATTTATGGTTTCATCTTTAT 819  
QY 781 GTTCAGAGCTATTAGAAAGATGATTTAAACAATCATTTGTCACCAAGAAATACATCGAT 840  
DB 820 CTTACAGAACTATTAGAAAGACATGATTTGTTTAAATTTGGACCTAGAAATATATGTGGAT 879  
QY 841 ACACAACATATTGACCCAAAAGACTTCTTAATTAACGGGAGTTTCTTGAATCATTTACCA 900  
DB 880 ACTATAATATTACCGCAAGAAATCTTCTTAACGATCCATTTAATTAAGATCCTACTCT 939  
QY 901 GAAATGAAACCAATAATAGTGTTCGCCCAAAAGGGGAAAGGAACAGTTTCTCTGATGG 960  
DB 940 GAAACCGCTACAAATTAACATCTTCGATTTACATCAAAAGGAAATATATCTGTTGATGG 999  
QY 961 CGCTTAGAACCAATTCGAAACAAACAGAAATCTCCGCTTATCGGATTCGCTTTCCGTTT 1020  
DB 1000 AGATTAGAACATTTCAAAAGAAACCGATTAATCTACGCTCTATGTGATTTCTCCGTTCTGTTAT 1059  
QY 1021 TTTTCGGCGGGTAAATGTTGCTTTTCGCTAAAGAAATGCTTAAATTAATTCGTTTCTTTGAT 1080  
DB 1060 TTTAGTTCGGGTAATGTTGCTATTTTCTTAAGAAATGCTTAAATTAAGTAGTTGTTGTCAT 1119  
QY 1081 GAGGAATTTAATCACTCGGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTCGCTTAC 1140  
DB 1120 GAAGAAATTTAATCATTTGGGGGCGCAAGATGTAGAATTTGGTTACAGATTTATTTGCCAAA 1179  
QY 1141 GGTAGTCTTTTAAACCTATTGATGGCATTTATGGCTTACCATTCAAGAGCCACAGGTAAA 1200  
DB 1180 GGCTGTTTTTTCAGAGTAATTTGACCGCGGAATGGCATACCATCAAGAACCCACCTGGTAAA 1239  
QY 1201 GAAATGAAACCGATCGTGMAGCGGMAAAATATTTAGCTCGATATTATAGAGAAAAAG 1260  
DB 1240 GAAATGAAACAGACGCGGAAGCTGTTAAAGTATTACGCTTAAATTTGTAAGAAAG 1299  
QY 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT 1320  
DB 1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAAGATTCACATATTTCATAGAAATCCT 1359  
QY 1321 TTAGTTTCAATTTATATCCAGCTTATAAATCTGTGMAAATATATTCAAGCTTTCGCTAGAT 1380  
DB 1360 TTAGTTTCTTATTTATATATCCCGCTTATAAATCTGTGCAAAATTTATTTCAAGAGATGTGAT 1419  
QY 1381 AGTGCACTGAATCAGACTGTTGCTGCTCGAGGTTTGTATTGTTGTAACCATGTTTCAACA 1440  
DB 1420 AGTGCTCTTAATCAAACTGTTGCTGATCTCGAGGTTTGTATTGTTGTAACCATGTTTCAACA 1479  
QY 1441 GATAATACCTTAGAAGTGTATCAATAGCTTTTATGGTAATAATCCCTAGGGTAGCGATCATG 1500  
DB 1480 GATAATACCTTAGAAGTGTATCAATAGCTTTTATGGTAATAATCCCTAGGGTAGCGATCATG 1539  
QY 1501 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAATATGACGCGTTTCTTTTGTCTAAAGGT 1560

Db 1540 TCTAAACCAATGGCGNATAGCCTCAGCATCAAAATGCAGCGGTTTCTTTTGCTAAAGGT 1599  
Qy 1561 TATTACATTGGCGAGTTAGATTTCAGATGATTTATCTTGAGCCTGATGCAAGTTGAACCTGTGT 1620  
Db 1600 TATTACATTGGCGAGTTAGATTTCAGATGATTTATCTTGAGCCTGATGCAAGTTGAACCTGTGT 1659  
Qy 1621 TTTAAAGAAATTTTAAAGATATAAACGCTAGCTTGTGTTTATACACCTAATAGAAAAGTC 1680  
Db 1660 TTTAAAGAAATTTTAAAGATATAAACGCTAGCTTGTGTTTATACACCTAATAGAAAAGTC 1719  
Qy 1681 AATCCGATGTAGCTTAATCGCTAAATGGTTTACAATTTGGCCAGAGAAATTTTACAGAGAAAAA 1740  
Db 1720 AATCCGATGTAGCTTAATCGCTTAATGGTTTACAATTTGGCCAGAGAAATTTTACAGAGAAAAA 1779  
Qy 1741 CTCAACACGGCTATGATTGCTCACCACCTTTTGAAGATGTTTACGATTTAGAGCTTGGCATTTA 1800  
Db 1780 CTCAACACGGCTATGATTGCTCACCACCTTTTGAAGATGTTTACGATTTAGAGCTTGGCATTTA 1839  
Qy 1801 ACTGATGATTAATGAAAGAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
Db 1840 ACGGATGGATTTAAACGAAATATTTGAAACCGCGTGGATTATGACATGTTCTCTTAAACTC 1899  
Qy 1861 AGTGAAGTTGAAAATTTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTTACATGGT 1920  
Db 1900 AGTGAAGTTGAAAATTTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTTACATGGT 1959  
Qy 1921 GATAACACATCAATTAAGAAAATCTTGGCATTCAAAAGAAAAACCAATTTTGGTTGTAGTCAAT 1980  
Db 1960 GATAACACATCAATTAAGAAAATCTTGGCATTCAAAAGAAAAACCAATTTTGGTTGTAGTCAAT 2019  
Qy 1981 CAGTCATTAATAGACAGGATACCTTATTATTAATTTATGACGAATTTGATGATTTAGAT 2040  
Db 2020 CAGTCATTAATAGACAGGATACCTTATTATTAATTTATGACGAATTTGATGATTTAGAT 2079  
Qy 2041 GAAAGTGAAGATATATTTTCAATAAACCCTGAAATATCAAGAGAGATTGATATCTTA 2100  
Db 2080 GAAAGTGAAGATATATCTTCAATAAACCCTGAAATATCAAGAGAAATGATATTTTA 2139  
Qy 2101 AAAGATCTTAAATCAATTCAAAATAAAGATGCGCAAAATCGCAGTCAGTATTTTCTATCCC 2160  
Db 2140 AAAGATCTTAAATCAATTCAAAATAAAGATGCGCAAAATCGCAGTCAGTATTTTCTATCCC 2199  
Qy 2161 AATACATTAACCGCTTAGTGAAAAAATAAACAATATTATTGATATATAATAAATAATA 2220  
Db 2200 AATACATTAACCGCTTAGTGAAAAAATAAACAATATTATTGATATATAATAAATAATA 2259  
Qy 2221 TTGCTTATTTGTTTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db 2260 TTGCTTATTTTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2319  
Qy 2281 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2340  
Db 2320 TTGGCTTTCTATCAATGACCAAGTGAATATTTTACTAAATAATGACATCTCATATTAC 2379  
Qy 2341 ACGAGTAATAGATTAATAAATACTGAGCGGCAATTTAAGTAATATAATAAATTAAGTCAG 2400  
Db 2380 ACGAGTAATAGATTAATAAATACTGAGCGCAATTTAAGTAATATAATAAATTAAGTCAG 2439  
Qy 2401 TTTAAATCTAAATTTGTAATACATCATCTTTTGTATATCATGACAGCTATTCGTTAAATAAT 2460  
Db 2440 TTTAAATCTAAATTTGTAATACATCATCTTTTGTATATCATGACAGCTATTCGTTAAATAAT 2499  
Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTTCTCAGCATTTAACACAT 2520  
Db 2500 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTTCTCAGCATTTAACACAT 2559  
Qy 2521 GATTGGATCGAGAAAATCAATCGCGCATCCACCATTTTAAAGCTCATTTAAACCTTATTTT 2580  
Db 2560 GATTGGATCGAGAAAATCAATCGCGCATCCACCATTTTAAAGCTCATTTAAACCTTATTTT 2619  
Qy 2581 AATGACATGACTTTAAAGATGATGAATGTGAAAGGGGATCACAAGGTATGTTTATGACG 2640  
Db 2620 AATGACATGACTTTAAAGATGATGAATGTGAAAGGGGATCACAAGGTATGTTTATGACG 2679

Qy 2641 TATGCGCTAGCGCATGAGCTTCTGAGATTTATTAAGAGAGTCATCATCTTGCAGTCA 2700  
Db 2680 TATGCGCTACCGCATGAGCTTCTGAGATTTATTAAGAGAGTCATCATCTTGCAGTCA 2739  
Qy 2701 ATTGATAGTGTGCGAGATATAACACTGAGGATATTTGGTTCCAAATTTGCACCTTTTAATC 2760  
Db 2740 ATTGATAGTGTGCGAGATATAACACTGAGGATATTTGGTTCCAAATTTGCACCTTTTAATC 2799  
Qy 2761 TTAGAAAAAGAAAAACCGGCCATGATTATTAATAAACATCGACCTGACTTTATATGCTTTGG 2820  
Db 2800 TTAGAAAAAGAAAAACCGGCCATGATTATTAATAAACATCGACCTGACTTTATATGCTTTGG 2859  
Qy 2821 GAACGAAATTTACAATGAGCAAAATGAACAAATTTGAAAGTCCAAAAGAGAGAGAAATATA 2880  
Db 2860 GAACGAAATTTACAATGAGCAAAATGAACAAATTTGAAAGTCCAAAAGAGAGAGAAATATA 2919  
Qy 2881 CCTGTTAAACAAGTTTCATTATTATTAATAGTATTAACCTCTATAA 2920  
Db 2920 CCGTTAAACAAGTTTCATTATTATTAATAGTATTAACCGCTATAA 2959

RESULT 13  
AEA04964  
ID AEA04964 standard; DNA; 2112 BP.  
XX  
AC AEA04964;  
XX AC  
DT 11-AUG-2005 (first entry)  
XX  
DE Hyaluronic acid synthase, PmHAS, coding sequence, SEQ ID 2.  
XX  
KW Hyaluronic acid synthase; polysaccharide; gene; ds.  
XX  
OS Pasteurella multocida.  
XX  
FH Key Location/Qualifiers  
FT CDS l. 2112  
FT /\*tag= a  
FT /product= "PmHAS"  
XX  
PN US2005124046-A1.  
XX  
PD 09-JUN-2005.  
XX  
PF 16-JUL-2002; 2002US-00197153.  
XX  
PR 10-NOV-1999; 99US-00437277.  
XX  
PA (DEAN/) DEANGELIS P L.  
XX  
PI Deangelis PL;  
XX  
DR WPI; 2005-417007/42.  
DR P-ESDB; AEA04963.  
DR GENBANK; AF036004.  
XX  
PT Elongating a functional acceptor (e.g. hyaluronic acid or chondroitin),  
PT useful in polysaccharide polymer grafting, comprises providing hyaluronic  
PT acid synthase, UDP-GlcUA and/or UDP-GlcNAc sugars to elongate the  
PT functional acceptor.  
XX  
PS Claim 4; SEQ ID NO 2; 4lpp; English.  
XX  
CC The present invention relates to a method for elongating a functional  
CC acceptor. The method comprises providing a hyaluronic acid (HA) synthase  
CC (PmHAS; AEA04963) capable of elongating the functional acceptor and  
CC providing UDP-GlcUA and UDP-GlcNAc sugars such that the hyaluronic acid  
CC synthase elongates the functional acceptor. PmHAS adds sugars to the  
CC nonreducing end of a growing polymer chain. The PmHAS sequence is  
CC significantly different from the other known HA synthases: there appears  
CC to be only two short potential sequence motifs (AEA04967 and AEA04968) in  
CC common between PmHAS and the other HA synthases. The method is useful in

CC polysaccharide polymer grafting, which may be utilized in the development  
CC of biotechnological medical improvements. These may be used for producing  
CC hybrid polysaccharides or for forming polysaccharide coatings. The  
CC present sequence is the coding sequence for PmHAS.

XX	SQ	Sequence 2112 BP; 746 A; 358 C; 387 G; 621 T; 0 U; 0 Other;	
		Query Match 72.3%; Score 2110.4; DB 14; Length 2112;	
		Best Local Similarity 100.0%; Pred. No. 0;	
		Matches 2111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	ATGATAATATATCAAGCAATATAAGCATATAACAGCAATGACTATCAATAGCACTC 60	
Db	1	ATGATAATATATCAAGCAATATAAGCATATAACAGCAATGACTATCAATAGCACTC 60	
Qy	61	AAATATTGTAAGTCGGCGGAATCTATGGACGGAATTTGTTGAATTTCAATATACC 120	
Db	61	AAATATTGTAAGTCGGCGGAATCTATGGACGGAATTTGTTGAATTTCAATATACC 120	
Qy	121	AAATGCAAGAAAACTCTCAGCACATCTCTGTTAAATTCAGCACATCTTCTGTAAT 180	
Db	121	AAATGCAAGAAAACTCTCAGCACATCTCTGTTAAATTCAGCACATCTTCTGTAAT 180	
Qy	181	AAAGAAAGAAAAAGTCAATGTTTGGATAGTCGGTTAGATATTGCAACACAACTGTACTT 240	
Db	181	AAAGAAAGAAAAAGTCAATGTTTGGATAGTCGGTTAGATATTGCAACACAACTGTACTT 240	
Qy	241	TCCAAAGTAAAAAATAGTACTTCTGAGCTCGGAAAAAACAAGTAAAAAATAATGG 300	
Db	241	TCCAAAGTAAAAAATAGTACTTCTGAGCTCGGAAAAAACAAGTAAAAAATAATGG 300	
Qy	301	AAATGTCACAGAGAAATCTGAAATGCGAGGTAAGAGCGCTCGCCCTGTACCA 360	
Db	301	AAATGTCACAGAGAAATCTGAAATGCGAGGTAAGAGCGCTCGCCCTGTACCA 360	
Qy	361	AAAGATTTTCCAAAGATCTGTTTGGCGCTTTTACCTGATCATGTTAATGATTTTACA 420	
Db	361	AAAGATTTTCCAAAGATCTGTTTGGCGCTTTTACCTGATCATGTTAATGATTTTACA 420	
Qy	421	TGGTACAAAAGCGAAAGAAAGACTTGGGCATATAAAACCTGAAACATCAATGTTGCTCTT 480	
Db	421	TGGTACAAAAGCGAAAGAAAGACTTGGGCATATAAAACCTGAAACATCAATGTTGCTCTT 480	
Qy	481	TCTATTATCGTTACACATTCATCGACGAGCAATTTTATCGATTACATTTAGCCTGTTTA 540	
Db	481	TCTATTATCGTTACACATTCATCGACGAGCAATTTTATCGATTACATTTAGCCTGTTTA 540	
Qy	541	GTAAACCAAAAAACATTTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600	
Db	541	GTAAACCAAAAAACATTTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600	
Qy	601	GATCTATACCGATCATTCGCAATATGAAATAAATTTGGATATTGCGTACGTACAGCAA 660	
Db	601	GATCTATACCGATCATTCGCAATATGAAATAAATTTGGATATTGCGTACGTACAGCAA 660	
Qy	661	AAAGATAACGGTTTTCAAGCCAGTCGCGTCCGGAATATGGATATCGCTTACGCAATAT 720	
Db	661	AAAGATAACGGTTTTCAAGCCAGTCGCGTCCGGAATATGGATATCGCTTACGCAATAT 720	
Qy	721	GACTTTATTGGCTTACTCGACTGTGATATGGCGCCAAATCCATTTATGGGTTTCAATCTTAT 780	
Db	721	GACTTTATTGGCTTACTCGACTGTGATATGGCGCCAAATCCATTTATGGGTTTCAATCTTAT 780	
Qy	781	GTTGCAGAGCTATTAGAAGATGATATTTAAACAATCAATTTGGTCCAGAAAAATACATCGAT 840	
Db	781	GTTGCAGAGCTATTAGAAGATGATATTTAAACAATCAATTTGGTCCAGAAAAATACATCGAT 840	
Qy	841	ACACACATATTGACCCAAAAGACTTCTTAATAAAGCGAGTTTGGCTTGAATCATTTACCA 900	
Db	841	ACACACATATTGACCCAAAAGACTTCTTAATAAAGCGAGTTTGGCTTGAATCATTTACCA 900	
Qy	901	GAAGTCAAAACCAATTAATAGTTTGGCGCAAAAGGGAAGCAAGTCTCTCGGATTTGG 960	
Db	901	GAAGTCAAAACCAATTAATAGTTTGGCGCAAAAGGGAAGCAAGTCTCTCGGATTTGG 960	

Db	901	GAAGTCAAAACCAATTAATAGTTTGGCGCAAAAGGGAAGCAAGTCTCTCGGATTTGG 960	
Qy	961	CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCGCTTATCCGATTCGCTTTCCGTTTT 1020	
Db	961	CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCGCTTATCCGATTCGCTTTCCGTTTT 1020	
Qy	1021	TTTCGGCGGGTAATGTTGCTTTTCGCTTAAAAATGGCTTAAATTAATCCGGTTCTTTGAT 1080	
Db	1021	TTTCGGCGGGTAATGTTGCTTTTCGCTTAAAAATGGCTTAAATTAATCCGGTTCTTTGAT 1080	
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Db	1141	GGTAGTTTCTTTAAAACTATTGATGGCAATTATGGCTTACCAATCAAGACCCACAGTAAA 1200	
Qy	1201	GAAATGAAACCGATCGTGAAGCGGAAAAATATTACGCTCGATATTATGAGAGAAAAG 1260	
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QY 2101 AAGATATTTAAA 2112  
Db 2101 AAGATATTTAAA 2112

## RESULT 15

ADP75718  
ID ADP75718 standard; DNA; 2112 BP.  
XX  
AC ADP75718;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Pasteurella multocida polymer production method-related DNA sequence #2.  
XX  
KW polymer production; hyaluronic acid polymer; chondroitin polymer; enzyme;  
XX gene; ds.  
XX  
OS Pasteurella multocida.  
XX  
PN WO2003029261-A2.  
XX  
PD 10-APR-2003.  
XX  
PF 12-JUL-2002; 2002WO-US022386.  
XX  
PR 13-JUL-2001; 2001US-0305263P.  
PR 22-JAN-2002; 2002US-0350642P.  
PR 08-MAY-2002; 2002US-00142143.  
XX  
XX (DEAN/) DEANGELIS P L.  
PA  
XX  
PI Deangelis PL;  
XX  
XX WPI; 2003-532558/50.  
XX  
PT Producing polymer, e.g. hyaluronic acid or chondroitin polymer, by  
providing a functional acceptor, a synthase capable of elongating the  
acceptor and sugars such that synthase elongates the acceptor to provide  
polymer.  
XX  
PS Disclosure; SEQ ID NO 71; 538pp; English.  
XX  
XX The invention comprises a method for producing a polymer, especially a  
hyaluronic acid (HA) or chondroitin (CD) polymer composed of less than  
150 sugars. The method involves providing a functional acceptor,  
CC providing a synthase capable of elongating the functional acceptor, and  
CC providing sugars such that the synthase elongates the functional acceptor  
to provide the polymer. The method of the invention is useful for  
CC producing a hyaluronic acid or chondroitin polymer composed of 1-150  
CC sugars. The present Pasteurella multocida DNA sequence was used in the  
CC exemplification of the invention.  
XX  
SQ Sequence 2112 BP; 745 A; 359 C; 387 G; 621 T; 0 U; 0 Other;  
Query Match 72.2%; Score 2108.8; DB 11; Length 2112;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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Qy 901 GAAGTGAACCAATAATAGTTGTTGCCGCAAAAGGGGAAGGAACAGTTTCTCTGGATTGG 960
Db 901 GAAGTGAACCAATAATAGTTGTTGCCGCAAAAGGGGAAGGAACAGTTTCTCTGGATTGG 960
Qy 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1020
Db 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1020
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Job time : 1590 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 05:22:16 ; Search time 10317 Seconds  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues  
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_est2:  
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4: gb\_hc:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_gss1:  
10: gb\_gss2:  
11: gb\_gss3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	96.4	3.3	1378	10	AG350209
6	94.2	3.2	2157	10	CL081966
7	92	3.2	1060	10	CW937448
8	90.6	3.1	1324	10	AG376784
9	90.2	3.1	1313	7	CK997149
10	89.8	3.1	1239	10	CW953278
11	89.8	3.1	1539	10	AG340947
12	89.4	3.1	1390	10	AG347224
13	87.6	3.0	1260	10	CL491610
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19	86.6	3.0	1169	11	CNS06RQ
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ALIGNMENTS

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DEFINITION  
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VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999  
Drosophila melanogaster genome survey sequence T7 end of BAC:  
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly); genomic survey sequence.  
AL069706  
AL069706.1 GI:4949849  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1101)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosier at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source

1. .1101  
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/clone\_lib="RPCI-98"  
/note="end : T7"

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QY 2527 ATCGAGAAATCAATGCGCATCCACATTTAAAAAGCTCATTTAAACATTTTAAATGAC 2586
Db 1002 ATTAANAATATATATAANTATATAATAAAAAATATAAAAAATATAAAAAATATAAATAT 1061
QY 2587 AATGACTTAAAAAGTATGAATGTGAAGGGGCATCACAAGGTATGTTTATGACGTATGCG 2646
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RESULT 3
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LOCUS
DEFINITION
TcB38_1_B02_T7 Tribolium BAC library Tribolium castaneum genomic,
genomic survey sequence.
ACCESSION
CW952279
VERSION
CW952279.1 GI:56735316
KEYWORDS
GSS.
SOURCE
Tribolium castaneum (red flour beetle)
ORGANISM
Tribolium castaneum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Tenebrionidae; Tribolium.
```

```
REFERENCE
Savard J. and Tautz, D.
Tribolium castaneum BAC-ends sequencing project
Unpublished (2003)
Contact: Savard, J.
Abteilung für Evolutionsgenetik, AG Tautz
Institut für Genetik, Universität zu Köln
Weyertal 121, 50931 Köln, Germany
Tel: 49 221 470 6911
Fax: 49 221 470 5975
Email: savard@uni-koeln.de
Class: BAC ends.
Location/Qualifiers
1. .891
/organism="Tribolium castaneum"
/mol_type="genomic DNA"
/strain="GA-2"
/db_xref="taxon:7070"
/clone_lib="Tribolium BAC library"
/notes="Vector: pBACe3.6; Site 1: EcoR1; Site 2: EcoR1;
Library constructed by Exelixis Inc."
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FEATURES
source
3.4%; Score 100.2; DB 10; Length 891;
Best Local Similarity 46.8%; Pred. No. 6.5e-10;
Matches 315; Conservative 0; Mismatches 358; Indels 0; Gaps 0;
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ORIGIN
Query Match
Beet Local Similarity 46.8%; Pred. No. 6.5e-10;
Matches 315; Conservative 0; Mismatches 358; Indels 0; Gaps 0;
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QY 1863 TGAAGTTGGAAAAATTTAAACATCTTAAATAAAATCTGCTATACCGTGTATTACATGGTGA 1922
Db 792 TAATATTATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 733
QY 1923 TAACACATCAATTAAGAACTTTGGCATTCAAAAGAAAAACCATTTTGTGTAGTCAATCA 1982
Db 732 TAATAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 673
QY 1983 GTCAATTAATAACACAGGCATCACTTATTAATAATTTATGACGAATTTTGTATGATTTAGATGA 2042
Db 672 TAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 613
QY 2043 AAGTAGAAGATATATTTTCAATAAAGCGCTGAATATCAAGAGAGATTTGATTTCTTAAA 2102
Db 612 TAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 553
QY 2103 AGATATTAAATCATCCAGATATAAGATGCCAAATCGCAGTCAGTATTTTATCCCAA 2162
Db 552 TAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 493
QY 2163 TACATTAAACGGCTTTAGTGAAAAAACTAAACCAATTTATTTGAATATATAAAAAATATAT 2222
Db 492 TAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 433
QY 2223 CGTTATTGTTCTCATGTTGATAAGATCATCTTTACACAGATATCAAAAAGAAATACT 2282
Db 432 TAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 373
QY 2283 AGCCTTCTCATTAACATCAAGTGAATTTTACTTAATAATATGATATCTCATATTACAC 2342
Db 372 TAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 313
QY 2343 GAGTAATAGATTAATAAAAACTGAGCGCATTTTAAGTAATATTTAATAAATAAGTCAGTT 2402
Db 312 TAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 253
QY 2403 AAATCTAAATTTGTAATACATCATTTTGTGATAATCATGACAGCCTTATTCGTTGTTAAAATGA 2462
Db 252 TAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 193
QY 2463 CAGCTATGCTTATATGAAAAAATATGATGCGGCATGAATTTCTCAGCATTAACACATGA 2522
Db 192 TAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 133
QY 2523 TTGGATCGAGAA 2535
Db 132 AAAAAAAGATA 120
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RESULT 4
CW973509
LOCUS
DEFINITION
A1AA-aaas9f06.b1 Ancylostoma caninum whole genome shotgun library
(A1AAGS 001) Ancylostoma caninum genomic, genomic survey sequence.
ACCESSION
CW973509
VERSION
CW973509.1 GI:56776238
KEYWORDS
GSS.
SOURCE
Ancylostoma caninum (dog hookworm)
ORGANISM
Ancylostoma caninum
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatidae; Ancylostomatidae; Ancylostomatidae; Ancylostoma.
REFERENCE
1 (bases 1 to 889)
Mitreva, M., McCarter, J. P., Pape, D., Ritter, E., Tsagarelshvili, R.,
Ronko, I., Martin, J., Wyllie, T., Dante, M., Meyer, R., Messina, D.,
Waterson, R. H., Clifton, S. W. and Wilson, R.
Genome Survey sequences from the parasitic nematode Ancylostoma
caninum
Unpublished (2004)
Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
```

```

Fax: 314 286 1810
Email: nenatode@watson.wustl.edu
Genomic DNA provided by John Hawdon (mtmjmh@gwumc.edu) DNA
sequenced by Washington University Genome Sequencing Center
Class: shotgun.

FEATURES
    source
        1..889
            /organism="Ancylostoma caninum"
            /mol_type="genomic DNA"
            /strain="Baltimore"
            /db_xref="taxon:29170"
            /dev_stage="Adult"
            /lab_host="GS10"
            /clone_lib="Ancylostoma caninum whole genome shotgun
            library (A1AGSS 001)"
            /note="vector: pOTW13; Site 1: BstX1; Site 2: BstX1;
            Ancylostoma caninum genomic DNA was randomly sheared,
            end-repaired and size fractionated to enrich for 2-4 kb
            fragments. Genomic DNA was provided by John Hawdon
            (mtmjmh@gwumc.edu) at George Washington University.
            Sequencing by Washington University Genome Sequencing
            Center, St. Louis, MO."

ORIGIN
    Query Match      3.3%; Score 96.6; DB 10; Length 889;
    Best Local Similarity 46.5%; Pred. No. 3.6e-09;
    Matches 312; Conservative 0; Mismatches 359; Indels 0; Gaps 0;

Qy 1813 AATGAAAAAATGGAATGCGGTAGACATATGACATGTTCCCTCAAACTCAGTGAAGTTGGA 1872
Db 14 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 73

Qy 1873 AAATTTAAACATCTTAATAAAATCGCTATTAACCGGTGTTATACATGGTGATAACACATCA 1932
Db 74 AGTAATAATAATAATAATAATAATAATAATAACAGTAATAATAATAATAATAATAATAA 133

Qy 1933 ATTAAGAACTTGGCATTCAAAAGAAACCAATTTTGTGTGAGTCATCGATTAATAAT 1992
Db 134 AATAATAATAATAATAATAATAATAATAACAGTAATAATAATAATAATAATAATAATAA 193

Qy 1993 AGACAAGGCATACTATTATAATTTATGACGAATTTTGATGATTTTAGTAAGTAGAAAG 2052
Db 194 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 253

Qy 2053 TATATTTTCAATAAAACCGGTGAATATCAAGAAGAGATTGATATCTTTAAAGATATTAA 2112
Db 254 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 313

Qy 2113 ATCATCCAGATAAGATGCCAAATCGCAGTCAGTATTTTTTATCCCAATACATTAAAC 2172
Db 314 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 373

Qy 2173 GGCTTAGTGAATAAATACTTAAATTTATTTGAAATATAATAATAATAATAATAATAATTCGTTATTGTT 2232
Db 374 GATAATAATAATAACAATAATAATAATAATAATAATAATAATAATAATAATAATAA 433

Qy 2233 CTACATGTTGTAAGAATCATCTTACACCATATCAAAAAGAAATCTAGCCTTCTAT 2292
Db 434 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 493

Qy 2293 CATAAACATCAAGTGAATTTTACTAATAATATGATATCTCATATTACACAGTAATAAGA 2352
Db 494 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 553

Qy 2353 TTAATAAAACCTGAGCGCCATTTAAGTAATAATTAATAATAATTAAGTCAGTTAAATCTAAAT 2412
Db 554 AGTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 613

Qy 2413 TGTGAATACATCATTTTGTGATAATCATGACAGCCTATTCGTTAAAAATGACAGCTATGCT 2472
Db 614 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 673

Qy 2473 TATATGAAAA 2483
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Db 674 AATAATAATAA 684

RESULT 5
AG350209/c
LOCUS      1378 bp      DNA      linear      GSS 18-DEC-2004
DEFINITION Mus musculus molossinus DNA, Clone.MSMg01-146M02.TJ, genomic survey
            sequence.
VERSION    AG350209
KEYWORDS   AG350209.1 GI:47923519
SOURCE     GSS.
ORGANISM   Mus musculus molossinus (Japanese wild mouse)
MUS musculus molossinus
Bukaryoka; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarctontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1
AUTHORS    Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,
            Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and
            Shiroishi, T.
TITLE      Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
JOURNAL    Genome Res. 14 (12), 2439-2447 (2004)
PUBMED     15574823
REFERENCE  2 (bases 1 to 1378)
AUTHORS    Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE      Direct Submission
JOURNAL    Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT    Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@tc.riken.jp).
            Taikuba Institute, Bio Resource Center.
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@tc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector      : pBACe3.6
R.Site 1    : EcoRI
R.Site 2    : EcoRI.
FEATURES    Location/Qualifiers
            source
                1..1378
                    /organism="Mus musculus molossinus"
                    /mol_type="genomic DNA"
                    /sub_species="molossinus"
                    /db_xref="taxon:57486"
                    /clone="MSMg01-146M02.TJ"
                    /sex="male"
                    /tissue_type="mixture of kidney and spleen"
                    /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN
    Query Match      3.3%; Score 96.4; DB 10; Length 1378;
    Best Local Similarity 47.7%; Pred. No. 4e-09;
    Matches 350; Conservative 0; Mismatches 376; Indels 8; Gaps 2;

Qy 1873 AAATTTAAACATCTTATAAAATCTGCTATAACCGGTATTATACATGGTGATAACACATCA 1932
Db 1178 AATATTTAAAAATAAAAAATTAATAATAATAAAAAATATAAAAAATATAAAAAATAAAA 1119

Qy 1933 ATTAAGAACTTGGCATTCAAGAGAAACCAATTTTGTGTGAGTCATCGATTAATAAT 1992
Db 1118 AAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 1059

Qy 1993 AGACAAGGCATACTATTATAATAATTTGATGATTTTAGATGAAGTAGAAAG 2052
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Db 1058 AAAAAAAAAATATAAAAAAAAAATTTAA-----AAATTAATAATAATAATAATAATAATAATA 1006

Qy 2053 TATATTTTCAATAAAACCGCTGATATACAGACAGATTCATATCTTTAAAGATTTAAA 2112

Db 1005 AAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAA 946

Qy 2113 ATCATCCAGATAAAGATGCCAAATCGCAGTCAGTATTTTTTATCCCAATACATTAAC 2172

Db 945 AATAATAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA 886

Qy 2173 GGCTTAGTGAATAAACTAAACAAATATTATTGAATATATAAAAAATAATTCGTTATTGTT 2232

Db 885 AATAAAAAATATATAATTTATATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA 826

Qy 2233 CTACATGTTGATAGAATCATCTTACACCATATCAAAAAAGAAATACTAGCCTTCTAT 2292

Db 825 AAAAAATTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 766

Qy 2293 CATAAACATCAAGTGAATATTTTACTTAATAATGATATCTCATATTACACGAGTAATAGA 2352

Db 765 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 706

Qy 2353 TTAATAAAAACTGAGCGCATTTAAGTAAATATTATAATAATTAAAGTCAGTTAAATCTAAAT 2412

Db 705 ATATAAAAAATAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 646

Qy 2413 TGTGAATACATCTTTTGTGATATCATGACAGCCTATTCGTTAAAAATGACAGCTATGCT 2472

Db 645 AAAAAATAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 587

Qy 2473 TATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACATGATGGATCGAG 2532

Db 586 AAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 527

Qy 2533 AAAATCAATGCCATCCACCACTTTAAAAAGCTCAATTAATAACTTATTTTAATGACAAATGAC 2592

Db 526 AAAAAATAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 467

Qy 2593 TTAATAAGTATGAA 2606

Db 466 TTAATAATAATAATA 453

RESULT 6

CL081966/c

LOCUS

DEFINITION

CH216-165D13 Sp5.1 CH216 Xenopus tropicalis genomic clone

CH216-165D13, genomic survey sequence.

ACCESSION

CL081966

VERSION

CL081966.1

KEYWORDS

GSS.

SOURCE

Xenopus tropicalis (western clawed frog)

ORGANISM

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoides; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE

1 (bases 1 to 2157)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

AUTHORS

A physical map of the xenopus tropicalis genome

TITLE

Unpublished (2003)

JOURNAL

Contact: Richard K Wilson

COMMENT

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Insert Length: 175000 Std Error: 0.00

Seq primer: Sp5 atctgccgttcgatcct

Class: BAC ends

High quality sequence start: 341

High quality sequence stop: 412.

FEATURES

Location/Qualifiers

1..2157

/organism="Xenopus tropicalis"

/mol\_type="genomic DNA"

/strain="Nigerian frog"

/db\_xref="taxon:8364"

/clone="CH216-165D13"

/sex="male"

/cell\_line="Stock 248 F7A2, inbred N7"

/clone\_lib="CH216"

/notes="Vector: pFARBAC2.1; CHORI-216 Xenopus tropicalis BAC library"

ORIGIN

Query Match 3.28; Score 94.2; DB 10; Length 2157;

Best Local Similarity 47.1%; Pred. No. 1.2e-08;

Matches 384; Conservative 0; Mismatches 428; Indels 3; Gaps 3;

Qy 1801 ACTGATGCTCAATGAAAAAATTTGAAAAATGCCGTAGCATATGACATGTTCTCTCAAACTC 1860

Db 1583 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1524

Qy 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAAATAAAATCTGCTATTAACCGTGTATTACATGGT 1920

Db 1523 AATAAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1464

Qy 1921 GATTAACATCAATTAAGAAACTTTGGCATTCAAAAGAA-AAACCATTTTGTGTAGTCAA 1979

Db 1463 TAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1404

Qy 1980 TCAGTCATTAATAAGACAAAGGCATACTTATTATAATTTATGACGAATTTGATGATTTAGA 2039

Db 1403 TATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1344

Qy 2040 TGAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTT 2099

Db 1343 CAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1284

Qy 2100 AAAAGATATTA-AAATCATCCAGATTAAGATGCCAAATCGCATGCTAGTATTTTTTATC 2158

Db 1283 AAAAAATAACATAAAAAATAAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 1224

Qy 2159 CCAATACATTAACCGCTTAGTGAATAAATACTAAACAAATATTATTGATATATAATAATA 2218

Db 1223 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1164

Qy 2219 TATTGCTTATTGTTCTACATGTTGATAAGAAATCATCTTTACACCATATCAAAAAAGAA 2278

Db 1163 ACTATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1104

Qy 2279 TACTAGCCTTCTATCATATAACATCAAGTGAATATTTTACTAAATTAATGATATCTCATATT 2338

Db 1103 AAATAATAAAAAATAAAAAATA-AAATAATAATAAAAAAATAAAAAAATAAAAAAATAAAAA 1045

Qy 2339 ACACGAGTAATAGATTAATAATAAATACTGAGGCGCATTTAAGTAAATATTATAATAATTAA 2398

Db 1044 AAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 985

Qy 2399 AGTTAAATCTAAATTTGTGAATACATCATTTTGTGATAATCATGACAGCCTATTCGTTAAAA 2458

Db 984 ATAAAAAATAAAAAATAATAAAAAATAATAATAATAAAAAATAATAATAATAATAATA 925

Qy 2459 ATGACAGCTATGCTTATATGAAAAAATAATGATGTCGGCATGAATTTCTCAGCATTAACAC 2518

Db 924 AAAAAATAAAAAATAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 865

Qy 2519 ATGATTGGATCGAGAAATCAATGCGCATCCACCATTTTAAAAAGCTCATTTAAAACTTATT 2578

Db 864 AAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 805

Qy 2579 TTAATGACAAATGACTTTAAAAAGTATGAATGTGAAA 2613

Db 804 TATAATAAAAAAATAAAAAATAAAAAAATAAAAAATAAAAAATAAAAAATAATAATAATA 770

CW937448  
LOCUS CW937448 1060 bp DNA linear GSS 20-DEC-2004  
DEFINITION TcB16.2\_H03\_SP6 Tribolium BAC library Tribolium castaneum genomic,  
genomic survey sequence.  
ACCESSION CW937448  
VERSION CW937448.1 GI:56720061  
KEYWORDS GSS.  
SOURCE Tribolium castaneum (red flour beetle)  
ORGANISM Tribolium castaneum  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
Tenebrionidae; Tribolium.  
1 (bases 1 to 1060)  
Savard, J. and Tautz, D.  
Tribolium castaneum BAC-ends sequencing project  
UNPUBLISHED (2003)  
CONTACT: Savard, J.  
Abteilung für Evolutionsgenetik, AG Tautz  
Institut für Genetik, Universität zu Köln  
Weyertal 121, 50931 Köln, Germany  
Tel: 49 221 470 6911  
Fax: 49 221 470 5975  
Email: savard@uni-koeln.de  
Class: BAC ends.  
FEATURES  
source  
1..1060  
/organism="Tribolium castaneum"  
/mol\_type="genomic DNA"  
/strain="GA-2"  
/db\_xref="taxon:7070"  
/clone\_lib="Tribolium BAC library"  
/note="vector: pBACes.6; Site\_1: EcoRI; Site\_2: EcoRI;  
Library constructed by Exelixis Inc."  
ORIGIN  
Query Match 3.2%; Score 92; DB 10; Length 1060;  
Best Local Similarity 44.5%; Pred. No. 3.2e-08;  
Matches 470; Conservative 0; Mismatches 572; Indels 15; Gaps 3;  
Qy 1872 AAAATTTAAACATCTTAAATAAATCTGCTATAACCGTGTATTACATGGTGATACACATC 1931  
Db 10 AAAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 69  
Qy 1932 AATTAAAGAACTTGCATTCAAAGAGAAAACCAATTTTGTGTAGTCAATCAGTCATTTAA 1991  
Db 70 AAATAATAAATAAAGAAAAATTTAAAAAATAAAGATAATGAAAAAATTAATCAATNAATTC 129  
Qy 1992 TAGACAAGGCATACCTTATTATTAATATGACGAATTTTCATGATTTAGATGAAGTAGAAA 2051  
Db 130 AACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 189  
Qy 2052 GTATATTTTCAAT-----AAACCGCTGAATATCAAGAGAGATTCATCTTAAAG 2104  
Db 190 ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 249  
Qy 2105 ATATTAATAATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTTATCCCAATA 2164  
Db 250 AAATATAAATTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 309  
Qy 2165 CATTAAACCGCTTAGTGAATAAATACTAAACAATATTATTGAATATAATAAATAAATAATTCG 2224  
Db 310 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATT 369  
Qy 2225 TTATTTGTTCTACATGTTGTAAGATCATCTTTACACCATATATCAAAAGAAATACTAG 2284  
Db 370 ATAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 429  
Qy 2285 CTTCTATCATAAACATCAAGTGAATATTTTACTAAATAAATGAATATCTCATATTACAGA 2344  
Db 430 AAATAAATGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 489  
Qy 2345 GTAATAGATTAAATAAATACTGAGCGCATTTTAAGTAATATTAAATAAATAAAGTCAGTTAA 2404

Db 490 AAAATATAAGATATAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 549  
Qy 2405 ATCTAAATTTGTAATACATCAITTTTTTGATATATCATGACGCCCTATTGCTTTAAAAATGACA 2464  
Db 550 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 609  
Qy 2465 GCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTTAAACATCATGATT 2524  
Db 610 AAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 669  
Qy 2525 GGATCCGAGAAAATCAATGCGCATCCACCAITTTAAAAAGCTCATTTAAAACTTTATTTTAAATG 2584  
Db 670 ATAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 723  
Qy 2585 ACAATGACTTAAAAAGTATGATGTGAAGGGGCATCACAGGTATGTTTATGACGTATG 2644  
Db 724 AAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 783  
Qy 2645 CGCTAGCGCATGAGCTTCTGACGATTTAAACAAGTCATCATCTTGCAGTCAATTG 2704  
Db 784 AAGAAAAATAATAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 843  
Qy 2705 ATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCTCAATTTGCACATTTTAACTCTTAG 2764  
Db 844 TAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 903  
Qy 2765 AAAAGAAAAACCGGCATGATTTTAAATAAACAATCGACCCCTGACTTATATATGCTTGGGAAC 2824  
Db 904 TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 963  
Qy 2825 GAAAATTTACAAATCGACAAATGAACA--AATTGAAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAG 2882  
Db 964 GAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1023  
Qy 2883 TGTTACACAGTTCATTATTAATAGTATATACTCTATAA 2919  
Db 1024 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1060  
RESULT 8  
LOCUS AG376784/c 1324 bp DNA linear GSS 21-DEC-2004  
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-184109.T7, genomic survey  
sequence.  
ACCESSION AG376784  
VERSION AG376784.1 GI:47987989  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus (Japanese wild mouse)  
ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,  
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and  
Shiroishi, T.  
Contribution of Asian mouse subspecies Mus musculus molossinus to  
genomic constitution of strain C57BL/6J, as defined by BAC-end  
sequence-SNP analysis  
Genome Res. 14 (12), 2439-2447 (2004)  
15574823  
JOURNAL  
PUBMED  
REFERENCE 2 (bases 1 to 1324)  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan  
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the mouse BAC library MSMg01. For BAC  
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
Tsukuba Institute, Bio Resource Center.  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1



Db 674 TAATATTATAATAATAATTTTATTAATTAATTAATTAATTTATATTTATTTATTTA 733  
Qy 2095 ATCTTAAAGATATTAATAATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTT 2154  
Db 734 TTATAAATTAATTAATAAATTTTATTTATTTATTTTAAATAAATAAATAAATAAT 793  
Qy 2155 TATCCCAATACATTAAGCGGCTTAGTGAAGAACTAAACAAATATTTTGAATATAATAA 2214  
Db 794 AAAATTATTAATAAATAAATAATATAAATAAATAATTAATTAATTAATAATAATTTA 853  
Qy 2215 AATATATTCGTTATTTGTTACATGTTGATAAGAAATCATCTTACACAGATAT---CAA 2270  
Db 854 TAATTTAAATTTTAAATTTTAAATTTTATTAATAAATTTTAAATAATTTTAAATTA 913  
Qy 2271 AAAAGAAATACAGCTCTTATCATATAAACATCAAGTGAATATTTTACTAAATAATGATAT 2330  
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Qy 2331 CTCATATACAGAGTAAATAGATTAATAAATAAGCGGCGGATTTAAGTAAATTAATAA 2390  
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Db 1034 TTTATTTTAAATTAATAATTTTAAATAAATAAATTTTNTTTTATTTAA 1086

RESULT 10  
LOCUS CW953278 1239 bp DNA linear GSS 20-DEC-2004  
DEFINITION TGB39.2\_C10\_SP6 Tribolium BAC library Tribolium castaneum genomic,  
genomic survey sequence.

ACCESSION CW953278  
VERSION CW953278.1 GI:56736315

KEYWORDS GSS.  
SOURCE Tribolium castaneum (red flour beetle)

ORGANISM Tribolium castaneum  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
Tenebrionidae; Tribolium.  
1 (bases 1 to 1239)

REFERENCE Savard, J. and Tautz, D.  
AUTHORS Tribolium castaneum BAC-ends sequencing project  
TITLE Abteilug fur Evolutionsgenetik, AG Tautz  
JOURNAL Institut fur Genetik, Universitat zu Koln  
COMMENT Unpublished (2003)  
Contact: Savard, J.  
Weyertal 121, 50931 Koln, Germany  
Tel: 49 221 470 6911  
Fax: 49 221 470 5975  
Email: savard@uni-koeln.de  
Class: BAC ends.

FEATURES  
source Location/Qualifiers  
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/note="Vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
Library constructed by Exelixis Inc."

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Query Match 3.1%; Score 89.8; DB 10; Length 1239;  
Beet Local Similarity 46.0%; Pred. No. 9,1e-08;  
Matches 341; Conservative 0; Mismatches 397; Indels 3; Gaps 1;  
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Qy 1933 ATTAAGAACTGGCATTCAAAGAAACCATTTTGTGTAGTCATCATTAAT 1992

Db 529 TATAAATAAATTTTAAATAAATAATGAAAATCATATAAACTGATCAAAAAATAAT 588  
Qy 1993 AGCAAGGCATTAACCTTATTAATTAATGACGAATTTTGATGATTTAGATGAAGTAGAAG 2052  
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Qy 2113 ATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTATCCCAATACATTAAC 2172  
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Db 1186 TAAATAAATAAATAAATAAATAAATA 1206

RESULT 11  
LOCUS AG340947/c 1539 bp DNA linear GSS 18-DEC-2004  
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-134C16.T7, genomic survey  
sequence.

ACCESSION AG340947.1 GI:47914257  
VERSION AG340947

KEYWORDS Mus musculus molossinus (Japanese wild mouse)  
SOURCE Mus musculus molossinus

ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,  
AUTHORS Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriawaki, K. and  
Shiroishi, T.  
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to  
genomic conetitution of strain C57BL/6J, as defined by BAC-end  
sequence-SNP analysis

JOURNAL Genom Res. 14 (12), 2439-2447 (2004)  
PUBMED 15574823

REFERENCE 2 (bases 1 to 1539)  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

TITLE Direct Submission  
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical



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source 1. 1390
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/clone="MSMg01-142K18.T7"
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ORIGIN
Query Match 3.1%; Score 89.4; DB 10; Length 1390;
Best Local Similarity 43.7%; Pred. No. 1.1e-07;
Matches 437; Conservative 0; Mismatches 562; Indels 1; Gaps 1;

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Dy 1352 AATAAAATATTAGATATTAAATAGAAATTTATAAAAAATAGGAATATAAGATAAAGAATC 1293
Qy 1873 AAATTTAAACATCTTAATAAAATCTGTATTAACCGTGTATTACATGTTGATGATAACACATCA 1932
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dy 1292 AAATAAAATATAAGTACAAAAAATANATAAGAAAAAAGTGMAAGAAAGACAGAAAGAAAGA 1233
Qy 1933 ATTAAGAACTTGGCATTTCAAGAGAAACCAATTTTGTGTAGTCAATCGTCAATTTAAAT 1992
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dy 1232 TAGACAAAAGGATCATATAATACAAAATATAAAAAAGTAAAAAATAAATGAATAAAAA 1173
Qy 1993 AGACAAGGCATAACTTATTATAATTTATGACAAATTTTGATGATTTTAGATGAAGTAGAAAG 2052
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Dy 1172 AAATAAAACAAAATAAAAAATTAATAAAACAAATATAAATAATGAAGTAAAGGAAGAA 1113
Qy 2053 TATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTTGATATCTTTAAAGATATTAAA 2112
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Dy 1112 AATATTAAACAGAAATAAAATAATAATAAAGAA-ATAAAAAAATAAAAAAATAAATAAAT 1054
Qy 2113 ATCATCAGATAAGATGCCAAATCGCAGTCAGTATTTTTTATCCCATACATTAAC 2172
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Dy 933 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 874
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Dy 873 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 814
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Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dy 813 ATAATAATAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 754
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Qy 2652 CATGAGCTTCTGAGCATTTATTAAAGAGTCAATCTTCCCATCTTCCCATCTTATGATGCTG 2712
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Db 513 AAAACAAAAAATAATATATAAAACAAAGACAGAGGAAGATAAAAAACGACAGACAAA 454
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Qy 2773 ACCGGCCATGTTATTTAATAAAACATCGCCCTGACTTATA 2812
Dy 393 TCACTAAATTAACAAATAAATATATATACAGACCTATA 354

RESULT 13
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SAIL_559_B08.v3 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_559_B08.v3, genomic survey sequence.
CL491610
CL491610.1 GI:45976650
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1260)
Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Macwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
12468722
Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS823639; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged
FEATURES
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/clone_lib="SAIL Collection"
/notes="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

Query Match 3.0%; Score 87.6; DB 10; Length 1260;
Best Local Similarity 43.8%; Pred. No. 2.6e-07;
Matches 358; Conservative 0; Mismatches 454; Indels 6; Gaps 1;

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Dy 373 ANNTAATTAATAATTTAAATTAATAATTAATAATTAATAATTTATTNAAAAAATAA 432
Qy 1856 AACTCAGTGAAGTTGAAAAATTTAAACATCTTTAATAAAATCTGCTATAACCGGTATTAC 1915
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dy 433 TAATAAAATAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAANN 492
Qy 1916 ATGCTGATACACATCAATTTAAGAACTGGCAATTCAAAAGAAAAACCATTTTGTGTAG 1975
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dy 493 ANANTATTATTAAATNAAAAAATAAATAAATAAATAAATAAATAAATAAATAAANNNTTA 552
Qy 1976 TCAATCAGTCATTAAATAGACAAGGCATACTTATTATAATTATGACGAATTTGATGATT 2035
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Ancylostoma caninum genomic DNA was randomly sheared,  
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fragments. Genomic DNA was provided by John Hawdon  
(mtmjmh@gwumc.edu) at George Washington University.  
Sequencing by Washington University Genome Sequencing  
Center, St. Louis, MO."

Query Match 3.0%; Score 87.4; DB 10; Length 735;  
Best Local Similarity 47.1%; Pred. No. 2.7e-07;  
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DB 82 AAT 141  
QY 1993 AGACAAGCATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 2052  
DB 142 AAT 201  
QY 2053 TATATTTCAATAAAACCGCTGAATATCAAGAGAGATTGATATCTTAAAGAGATATTAA 2112  
DB 202 AAT 261  
QY 2113 ATCATCCAGATTAAGATGCCAAATCGCAGTCAGTATTTTTTATCCCAATACATTAAC 2172  
DB 262 AAT 321  
QY 2173 GGTCTTAGTGAATAAACTAAACAATTAATTTGAATAATAATAATAATAATAATAATAATAAT 2232  
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QY 2233 CTACATGTTGATGAACAATCACTTACACAGATATCAAAAAGAAATAGTACGCTTCTAT 2292  
DB 382 AAT 441  
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DB 442 AAT 501  
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ORIGIN

RESULT 15  
AG347098/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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Mus musculus molossinus DNA, clone:MSMg01-142102.T7, genomic survey  
sequence.  
AG347098  
AG347098.1 GI:47920408  
GSS.  
Mus musculus molossinus (Japanese wild mouse)

DB 553 NANTAAAAATTTAAATAATATTANAAAAATNNAAAAATAATNAAAAAATAAANTTTAAAA 612  
QY 2036 TAGATGAAGTAGAAGTATATTTTCATATAAACCGCTGAATATCAAGAGAGATTGATA 2095  
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QY 2096 TCTTAAAAATATTAATAATCATCCAGATTAAGATGCCAAATCGCAGTCAGTATTTTT 2155  
DB 673 ATAAAAATATATTTAATAATATATAAATAA-----AAAATAATTAATAAAAAAAA 726  
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DB 727 AAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 786  
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QY 2276 AAATCTAGCTTCTATCATATAACATCAAGTGAATATTTTACTAATAATGATATCTCAT 2335  
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DB 907 AAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 966  
QY 2396 GTCAGTTAAATCTAAATTTGATGATCATATTTTGTGATTAATCATGACGCTTATTCGTTA 2455  
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QY 2456 AAAATGACAGCTATGCTTATATGAAAAAATATGATGCGCATGAATTTCTCAGCATTA 2515  
DB 1027 AAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 1086  
QY 2516 CACATGATGATCGAGAAAAATCAATGCGCATCCACATTTAAAGCTCATTAATAACTT 2575  
DB 1087 TAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 1146  
QY 2576 ATTTAATGACATGACTTAAAAAGTATGAATGTGAAA 2613  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES

CW960936 735 bp DNA linear GSS 21-DEC-2004  
AIAA-aac14d08.b1 Ancylostoma caninum whole genome shotgun library  
(AIAAGSS 001) Ancylostoma caninum genomic, genomic survey sequence.  
CW960936  
CW960936.1 GI:56761663  
GSS.  
Ancylostoma caninum (dog hookworm)  
Ancylostoma caninum  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.  
1 (bases 1 to 735)  
Mitrevu,M., McCarter,J.P., Pape,D., Ritter,E., Tsagareishvili,R.,  
Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D.,  
Waterston,R.H., Clifton,S.W. and Wilson,R.  
Genome Survey sequences from the parasitic nematode Ancylostoma  
caninum  
Unpublished (2004)  
Contact: Mitrevu M  
Washington University in St. Louis  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: nematode@watson.wustl.edu  
Genomic DNA provided by John Hawdon (mtmjmh@gwumc.edu) DNA  
sequenced by Washington University Genome Sequencing Center  
Class: shotgun.  
Location/Qualifiers

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

# REFERENCE AUTHORS

1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,  
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and  
Shiroishi, T.

**TITLE**  
Contribution of Asian mouse subspecies *Mus musculus molossinus* to  
genomic constitution of strain C57BL/6J, as defined by BAC-end  
sequence-SNP analysis

**JOURNAL**  
Genome Res. 14 (12), 2439-2447 (2004)

## PUBMED

15574823

2 (bases 1 to 1268)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

**REFERENCE**  
Direct Submission

**TITLE**  
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan  
(E-mail: hattori@psc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

**COMMENT**  
Clones are derived from the mouse BAC library MSMg01. For BAC  
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
Tsukuba Institute, Bio Resource Center,  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: abe@rtc.riken.jp

PRIMERS

Sequencing : T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : ECoRI

R.Site 2

Location/Qualifiers

1. .1268

/organism="Mus musculus molossinus"

/mol\_type="genomic DNA"

/sub\_species="molossinus"

/db\_xref="taxon:57486"

/clones="MSMg01-142102.T7"

/sex="male"

/tissue type="mixture of kidney and spleen"

/clone\_lib="MSMg01 Mouse Male BAC Library"

## FEATURES

source

## ORIGIN

Query Match 3.0%; Score 87.4; DB 10; Length 1268;  
Best Local Similarity 45.1%; Pred. NO. 2.8e-07;  
Matches 439; Conservative 0; Mismatches 526; Indels 9; Gaps 3;

Qy 1948 ATTCAAAAGAAAACCACTTTTGGTGTAGTCAATCAGTCATTAAATAGACAAGGCATAACT 2007

Db 1246 AATAAAATAANTATAAATTAATTTATAAATAAATTAATAAATAAATAAATAAATAAATAA 1187

Qy 2008 TATTATAATTATGACGAATTTGATGATTTA-GATGAAAGTAGAAAGTATATTTTCAATAA 2066

Db 1186 AAATATAATAAATTAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1127

Qy 2067 AACCGCTGAATATCAAGAAGAGATTGATATCTTAAAGATATTAAATATCAATCCAGAATAA 2126

Db 1126 ATTAATAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1067

Qy 2127 AGATGCCAAATCGGAGTCAGTATTTTTTTATCCCAATACATTAACGGCTTAGTGAAAAA 2186

Db 1066 ATATAAAATAAAAAAATTTATAAATAAATTAATAAATAAATAAATAAATAAATAAATAA 1007

Qy 2187 ACTAAACAATATTTTGAATATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2246

Db 1006 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 947

Qy 2247 GAATCATCTTACACCAGATATCAAAAAAGAAATACTAGCCTTCTATCATATAAACAATCAAGT 2306

Db 946 ATTTTAATAATAAAAAATTTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 894

Qy 2307 GAATATTTTACTAAATAATGATATCTCATATTTACAGAGTAATAGATTTAATAAAAACTGA 2366

Db 893 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 834

Qy 2367 GCGCATTTTAAAGTAATATTAAATAAATAAAGTCAGTTAAATCTAAATTTGTAATACATCAT 2426

Db 833 TTTATATATAAATTTAAATAATATTATAAANAANAANAATAAATAAATAAATAAATAAATAA 774

Qy 2427 TTTTGATATCATGACAGCGCTATTTCGTTAAANAATGACAGCTATGCTTATATGAAAAATA 2486

Db 773 ATATTTTATAAAAAATAAATTTATTTAAATAAATTTAAATAAATAAATAAATAAATAAATAA 714

Qy 2487 TGATGCGGCATGAATTTCTCAGCATTAACACATGATTGGATCGAGAAAAATCAATGCGCA 2546

Db 713 AATAATAAANAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 654

Qy 2547 TCACCATTTTAAAAAGCTCATTTAAAACTTTATTTTAAATGACAAATGACTTAAAAAGTATGAA 2606

Db 653 TATATAATAAANAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 594

Qy 2607 TGTGAAGGGGCATCAAGGTATGTTTATGACGTATGCCGTAGCGCATGAGCTTCTGAC 2666

Db 593 ATAAAAATATAAATTAATAAATAAANAATAAANAATAAATAAATAAATAAATAAATAAATAA 534

Qy 2667 GATTATTAAAGAAGTCATCACATCTTGCAGTCAATTTGATAGTGTGCCAGAAATATAACAC 2726

Db 533 ATAAAAANAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 474

Qy 2727 TGAGGATATTTGGTTCCAAATTTGCACCTTTTAAATCTTAGAAAAAGAAACCGGCCATGTATT 2786

Db 473 TAAATATAATTTTAAATTTAAAAANAANAANAANAANAATAAAGAGTAAAAATAAATAAATTAGGTATT 414

Qy 2787 TAATAAAACATCGACCCCTGACTTATATGCGCTTGGGAACGAAATTTACAATGGACAATGA 2846

Db 413 TAATAAAA-AAAAATATTTTATTTTNTTTTAAAAANAANAANAATAAATAAATAAATAAATAA 355

Qy 2847 ACAAAATTGAAAGTGCAAAAGAGGAGAAATAATATACCTGTTTAAACAAGTTTCATTATTATATAG 2906

Db 354 TAAATAAATAAANAATAAANAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 295

Qy 2907 TATAACTCTATAAA 2920

Db 294 TATAATTTTAAATA 281

Search completed: January 8, 2006, 12:56:35

Job time : 10323 secs

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QY 1979 ATCAGTCATTAATAGACAGGCGATACCTATTATATATGACGAACTTGTGATTAG 2038  
 Db 16946 TTTATGAGAAAATATAATATAATATTATTA-----ATATGATCATTAATATTATA 16892  
 QY 2039 ATGAAAGTAGAAGATATATTTTCAATAAAAACGCTGAATATCAGAAGAGATTGATCT 2098  
 Db 16891 TAAATAGTATTTTATTAATAAATAAATAATATTTGATTAATAAATAATAGTAAATGTAT 16832  
 QY 2099 TAAAGATTAATAATCATCCGAATTAAGATGCCAAAATGCCAGTCAGTATTTTATC 2158  
 Db 16831 ATAAATTTGACACAATATTAATATATATATATTAATTAATGAATGATATACAAATTTATAT 16772  
 QY 2159 CCAATACATTAACGCGCTAGTGAATAAACTAAACATATTAATGATTAATAATAATA 2218  
 Db 16771 ATAAATTTGATTTTATTAATCTCGATTAATAAATAATTTTATATATAAATAATATA 16712  
 QY 2219 TATTCGTTATGTTCTACATGTTGATAGAAATCATCTTAACACAGATCAAAAAAGAA 2278  
 Db 16711 GTGATTATATAAATATATTTATTAATTAATGATTAAGATTAATAATAAATAATA 16652  
 QY 2279 TACTAGCCTTCTATCAATAACATCAAGTAAATTTTACTAATAATAGTATCTATAT 2338  
 Db 16651 ATATAAATAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 16592  
 QY 2339 ACACAGATTAATGATTAATAAATACTGAGGCGATTTAGTAAATTAATAATTAAGTC 2398  
 Db 16591 TAAATAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 16532  
 QY 2399 AGTTAAATCTAAATTTGTAATACATCATTTTGAATATCATGACAGCTATTCGTTAAA 2458  
 Db 16531 CAACATATGCTAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 16472  
 QY 2459 ATGACAGCTATGCTATATGAAAAAATATGATGTCGCAATGAAATTTCTCAGCATTAAC 2518  
 Db 16471 ATGTTAATTAATCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 16412  
 QY 2519 ATGATTGATCGAAGAAATCAATGGCATCCACCATTTAAAAAGTCATTAATACTTAT 2578  
 Db 16411 AAGAAATTAATCAATTAATAAATAATGAAATTAATTAATAAAGTCTATGCGATTTATACA 16352  
 QY 2579 TTAATGACATGACTTAATAAAGATATGTAAGGAGGCGATCAAGGTATGTTATGA 2638  
 Db 16351 ATATATGATTAATAAATAATTTTATTAATAATTTCTCTAATGAATTAATGACATA 16292  
 QY 2639 CGTANGCGCTAGCGCATGAGCTTCTGACATTAATAAGAGTCAATCAATCTTGCCAGT 2698  
 Db 16291 TAAAAATTAACAGTCGAATATTTTATTAATTAATTAATTAATTAATTAATTAATGA 16232  
 QY 2699 CAATTGATAGTGCAGAAATTAACACGAGAGATTTTGTCCAATTTGCACTTTAA 2758  
 Db 16231 TACCTAATATGATTTTATTAATAATTAATTAATTAATTAATTAATTAATTAATTA 16172  
 QY 2759 TCTTGAAGAAAGAAA 2773  
 Db 16171 TTTTAAGAAATTAATA 16157

Search completed: January 8, 2006, 13:05:34  
 Job time : 533 secs

Db 11693 TCTTCTCAAAACAAATGCTGGGTTGAGATACCGCTAAATTTGGTGTATCCGTTGCAC 11634  
Qy 1556 AAGGTTATTACATTTGGGACATTTAGATTCAGATTCATTTGAGCGCTGATCAGTTGA 1613  
Db 11633 GGGGACATGATATCATTTGTTGATCCGATGATTAATGCGATTCAGATTAATATTTGA 11576

## RESULT 14

US-08-998-416-1137/C

Sequence 1137, Application US/08998416

Patent No. 6239264

GENERAL INFORMATION:

APPLICANT: Philippen, Peter

APPLICANT: Pohlmann, Rainer

APPLICANT: Steiner, Sabine

APPLICANT: Mohr, Christine

APPLICANT: Wendland, Jürgen

APPLICANT: Knechtle, Philipp

APPLICANT: Reblschung, Corinne

TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSEYII

NUMBER OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 1152

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6239264artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: No. 6239264th Carolina

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998,416

FILING DATE: 24-DEC-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CH 0016/97

FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Weigle, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 1137:

SEQUENCE CHARACTERISTICS:

LENGTH: 636 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: PAG1692RP

US-08-998-416-1137

Query Match 2.5%; Score 71.8; DB 3; Length 636;

Best Local Similarity 47.5%; Pred. No. 5.1e-07;

Matches 252; Conservative 0; Mismatches 272; Indels 7; Gaps 1;

Qy 1960 AACATTTTGTGTGTCATGATCATTAATAGCAAGCATTAAGTATTAATATATAT 2019  
Db 564 AATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 505  
Qy 2020 GACGAATTTGATGATTTAGATGAAAGTAAAGTATTTTCAATTAACCGCTGAAT 2079  
Db 504 TAAATATTAATTAATTAAGTAAAGTAAATTAATTTTAATTAATTTCTTAATTA 445  
Qy 2080 CAAAGAGATGATTAATCTTAAAGATTAATTAATTAATTAATTAATTAATTA 2139

Db 444 GATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 385  
Qy 2140 GCAGTCAGATTTTATTTTATCCCAATATCAATTAACGGCTTAGTGAAGAACTTAACATAT 2199  
Db 384 ATTACAAATATTTA-----AATTAATTAATTTTATTAATTAATTAATTAATTAAT 332  
Qy 2200 ATTGAATTAATTAATTAATTAATTAATTTGTTATGTTCTACAGTGTGAATGAATCATCTTACA 2259  
Db 331 AATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 272  
Qy 2260 CCAGATATCAAAAAAGAAATCTAGCTTATCATTAACATCAAGTGAATATTTTACTA 2319  
Db 271 AATTAATTAATTAATTAATTAATTAATTTTAATTAATTAATTAATTAATTAATTA 212  
Qy 2320 AATAATGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2379  
Db 211 AGTATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 152  
Qy 2380 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2439  
Db 151 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 92  
Qy 2440 GACAGCTATTCGTTAAAAATGACAGCTATGCTTAATTAATTAATTAATTAATTAAT 2490  
Db 91 GATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 41

## RESULT 15

US-09-662-254B-23/C

Sequence 23, Application US/09662254B

Patent No. 6933145

GENERAL INFORMATION:

APPLICANT: Moyer, Richard W.

APPLICANT: Li, Yi

APPLICANT: Bawden, Alison Louise

TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous

TITLE OF INVENTION: Vertebrate Cells

FILE REFERENCE: UF-221C1X1

CURRENT APPLICATION NUMBER: US/09/662,254B

CURRENT FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: 09/086,651

PRIOR FILING DATE: 1998-05-29

PRIOR APPLICATION NUMBER: 60/224,479

PRIOR FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn version 3.1

SEQ ID NO 23

LENGTH: 50000

TYPE: DNA

ORGANISM: Amsacta moorei entomopoxvirus

US-09-662-254B-23

Query Match 2.4%; Score 71; DB 3; Length 50000;

Best Local Similarity 42.5%; Pred. No. 3.5e-06;

Matches 440; Conservative 0; Mismatches 590; Indels 5; Gaps 1;

Qy 1739 AACTCAACCGCTATGATGCTCAACACTTGAAGTTCACGATTAAGCTTGCGATT 1798  
Db 17186 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 17127  
Qy 1799 TAACGATGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1858  
Db 17126 TAAATTTATTAAGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 17067  
Qy 1859 TCAGTGAAGTGAAGAAATTTTAACATCTTAATTAATCTGATTAACCGTATTAACATG 1918  
Db 17066 TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 17007  
Qy 1919 GTGATTAACATCAATTAATTAAGAACTTGCAATTAAGAAATTAATTAATTAATTA 1978  
Db 17006 TATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 16947

NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 2344  
LENGTH: 2529  
TYPE: DNA  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-2344

Query Match 2.5%; Score 72.6; DB 3; Length 2529;  
Best Local Similarity 52.5%; Pred. No. 5.4e-07;  
Matches 159; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 1332 AGTTCAATTTATATCCAGCTTATTAACGTGCAAACTATATTCACAGTTGGGTAGTAG 1382  
DB 33 AGTGCAGTCATGTGACCCGCTATTAACGTAGAAACCTTATTTAGAAAGGCACTTATATG 92  
QY 1383 TGCACATGATCAGACTGTGTGATCTGAGGTTTGTATTTGTAACGATGCTTCAACAGA 1442  
DB 93 TTGAAAAACCAACATGGAAGAAATGAAATCTTAATTAATGATGCGCTTACTGA 152  
QY 1443 TAATACCTTAGAAGTATCATTAAGTTTATGTATTAATCCTAGGGTACGATCATGTC 1502  
DB 153 TTAATGTCAAAAAATTAATTAAGAAATTCACAAAGATGATCCAGTTTCGGGTTTCAA 212  
QY 1503 TAAACCAATGGCGGAATAGCCTCAGATCAAAATGCAAGCCGTTCTTTGCTTAAAGTTA 1562  
DB 213 TGTAAAAAATGGGGAAATGGAAAAAGCTTTAACTTGGGTTTTCAGAAAGCAAAAGTGA 272  
QY 1563 TTACATTTGGGAGTTAGATTCAGATGATTAATCTTGAAGCTGATGCAAGTGAATGTGTTT 1622  
DB 273 GATATATTTGCGAATTTGAAAGTAGCATTAATGATGATTCATGAGCGCTTATAGCGTTTATA 332  
QY 1623 AAA 1625  
DB 333 CAA 335

RESULT 12  
US-09-627-122-21/C  
Sequence 21, Application US/09627122  
Patent No. 6472521  
GENERAL INFORMATION:  
APPLICANT: Uhlmann, Eugen  
APPLICANT: Greiner, Beate  
APPLICANT: Unger, Bernhard  
APPLICANT: Gothe, Gislinde  
APPLICANT: Schwerdel, Marc  
TITLE OF INVENTION: OLIGONUCLEOTIDES FOR THE INHIBITION OF HUMAN eg5  
FILE REFERENCE: 02481.1678  
CURRENT APPLICATION NUMBER: US/09/627,122  
CURRENT FILING DATE: 2000-07-27  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 21  
LENGTH: 5340  
TYPE: DNA  
ORGANISM: Plasmodium falciparum  
US-09-627-122-21

Query Match 2.5%; Score 72.6; DB 3; Length 5340;  
Best Local Similarity 46.4%; Pred. No. 6.9e-07;  
Matches 237; Conservative 0; Mismatches 274; Indels 0; Gaps 0;

QY 1914 ACATGATGATTAACATCAATTAAGAACTTGGCATTCAAAAGAAAAACATTTTGTGT 1973  
DB 1101 AAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1042  
QY 1974 AGTCATCACTGCTTAATTAATGACAAAGGCATTAATTAATTAATTAATTAATTAATTA 2033  
DB 1041 AAATTAATCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 982  
QY 2034 TTTAGATGAAGTAAGTAATTTTCAATTAATTAATTAATTAATTAATTAATTAATTA 2093

DB 981 AAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 922  
QY 2094 TATCTTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2153  
DB 921 TTAATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 862  
QY 2154 TTATCCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2213  
DB 861 TTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 802  
QY 2214 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2273  
DB 801 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 742  
QY 2274 AGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2333  
DB 741 AGATCAAGGTGATCATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 682  
QY 2334 ATATTACAGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2393  
DB 681 ATACTTGAAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 622  
QY 2394 AATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2424  
DB 621 TATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 591

RESULT 13  
US-09-634-238-29/C  
Sequence 29, Application US/09634238  
Patent No. 6544772  
GENERAL INFORMATION:  
APPLICANT: Glenn, Matthew  
APPLICANT: Havukkala, Ilkka J.  
APPLICANT: Bloksberg, Leonard, N.  
APPLICANT: Lubbers, Mark W.  
APPLICANT: Dekker, James  
APPLICANT: Christenson, Anna C.  
APPLICANT: Holland, Ross  
APPLICANT: O'Toole, Paul W.  
APPLICANT: Reid, Julian R.  
APPLICANT: Coolbear, Timothy  
TITLE OF INVENTION: Polynucleotides, materials incorporating  
FILE REFERENCE: 11000.1043U  
CURRENT APPLICATION NUMBER: US/09/634,238  
CURRENT FILING DATE: 2000-08-08  
NUMBER OF SEQ ID NOS: 422  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 29  
LENGTH: 13825  
TYPE: DNA  
ORGANISM: Lactobacillus rhamnosus  
US-09-634-238-29

Query Match 2.5%; Score 72.4; DB 3; Length 13825;  
Best Local Similarity 52.7%; Pred. No. 1.1e-06;  
Matches 157; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 1316 TACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1375  
DB 11873 TGCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 11814  
QY 1376 TAGATAGTCACTGAATCAAGCTGTGTGATCTGAGGTTTGTATTTGTAACGATGTT 1435  
DB 11813 TAGACAGTTTAATTTGGCAACATACGTCAATTAATTAATTAATTAATTAATTAATTA 11754  
QY 1436 CAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1495  
DB 11753 CGGCAACCGTTACATGTCATTAATTTGTAATTAATTAATTAATTAATTAATTAATTAATTA 11694  
QY 1496 TCATGCTTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1555



US-09-900-038A-3

Query Match	2.8%;	Score 80.6;	DB 3;	Length 6865;
Best Local Similarity	53.3%;	Pred. NO. 1.1e-08;		
Matches 170;	Conservative	0;	Mismatches 149;	Indels 0;
			Gaps	0;

Qy	1332	TAGTTTCATTATTAATCCAGCTTAATACGTGCAAACTATATTCAGAGTTGGCTAGATA	1381
Db	3998	TTGTTTCTATCGTTTATACCTATATTCAACTCGGAAGCATATCTTAAAGAAAGCCGCAT	4057
Qy	1382	GTGCACTGAATCAGACTGTGTGTGATCTCGAGGTTTGATATTTGTACAGATGGTTCACAG	1441
Db	4058	CCGTCCTCAACAGACTATTCATTGATGAATGAAGATTAATCTGATTAATATGATCACTG	4117
Qy	1442	ATATATACCTTAGAATGTGATCATAAGCTTTATGTAAATATCTGAGGTACGATCATGT	1501
Db	4118	ATATATATGTGAGAAATTTGTGATTAATTTATCTCAAAAAGACATCGCATCTGTGATTTTC	4177
Qy	1502	CTAAACCAATGCGCGAATAGCCTCAGCATCAATGACGCGTTTCTTTTGCTAAAGGTT	1561
Db	4178	ATAAAAAAAATGGAAGGGGATCTTGGCGAAGAACCTAGGCTTGATTAATCAACAGCGC	4237
Qy	1552	ATTACATTGGCGAGTTAGATTCAATGATTAATCTTGAGCCTGATGCAAGTTGAACTGTGT	1621
Db	4238	AATTCATTAACGTTTGATGATAGTGAATTTTGTAGCAACGAATTAATTAATGAAATATGT	4297
Qy	1622	TAAAGAAATTTTAAAGA	1640
Db	4298	TAAAAAATTTAATCACTGA	4316

```

RESULT 8
US-09-134-000C-2987
; Sequence 2987: Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucet-Stein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6012
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2987
;
; LENGTH: 993
;
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2987

```

Query Match 2.6%; Score 77; DB 3; Length 993;  
Best Local Similarity 52.3%; Pred. No. 3.7e-08;  
Matches 170; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY	1316	TACCTTTAGTTCAATTATATATCCAGCTTATACGTGCAACTATATTCAGAGTTGCG	1375
Db	20	TGCCCAAAATTGTATTATTGTTCGTATACAAATGAGAAAAATATTAGAAAAAATGTG	79
QY	1376	TAGATAGTGCATGCATCAGACTGTGTTGTGATCTCGAGTTGTGATTTGTACAGATGTT	1435
Db	80	TACGCTCTATTTAGCTCAACGTTACTGACTTTGAATTAATCTGTGGACGATGGCT	139
QY	1436	CAACAGATATACCTTAGAGTGATCAATAGCTTTATGTATATATCTTAGGGTAGCA	1495
Db	140	CTCCAGACAGTTCTGGAGCAATGTGTGATCAATTTCTCGAACAAAGATCAACGGGTAAAG	199
QY	1496	TCATGTCTAAACCAATGCGGGAATAGCCTAGCATCAAAAGCGCGTTCTTTTGCTA	1555
Db	200	TTATTCATTAAGAAATGGTGGGCTTAGCGATGCTCGTATATGCTGGAAATTGAAATAGCA	259
QY	1556	AAGGTTATTCATTTGGGCAAGTAGATTGAGATGATTTATCTTGAGCCGATGACAGTTGAAC	1615

Db 260 CAGGAGATATTATTAGTTCCTAGACTGATGATTCATTGCACATGATATGATGAC 319

Qy 1616 TGTGTTAAAGAAATTTTAAAGA 1640

Db 320 TATTATATACAAATATCGTAAAGA 344

RESULT 9  
US-08-998-416-186/c  
; Sequence 186, Application US/08998416

```

1  APPLICANT:  Philippson, Peter
2  APPLICANT:  Pohlmann, Rainer
3  APPLICANT:  Steiner, Sabine
4  APPLICANT:  Mohr, Christine
5  APPLICANT:  Wendland, Jurgen
6  APPLICANT:  Knechtle, Philipp
7  APPLICANT:  Reibschung, Corinne
8  TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSEYI
9  TITLE OF INVENTION:  AND USES THEREOF
10 NUMBER OF SEQUENCES:  1152
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE:  No. 6239264artis Corporation
13 STREET:  3054 Cornwallis Road
14 CITY:  Research Triangle Park
15 STATE:  No. 6239264tn Carolina
16 COUNTRY:  USA
17 ZIP:  27709
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE:  floppy disk
21 COMPUTER:  IBM PC compatible
22 OPERATING SYSTEM:  PC-DOS/MS-DOS
23 SOFTWARE:  PatentIn Release #1.0, Version #1.30
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER:  US/08/998,416
26 FILING DATE:  24-DEC-1997
27 CLASSIFICATION:  435
28
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER:  CH 0016/97
31 FILING DATE:  31-DEC-1996
32 ATTORNEY/AGENT INFORMATION:
33 NAME:  Meigs, J. Timothy
34 REGISTRATION NUMBER:  38,241
35 REFERENCE/DOCKET NUMBER:  PF/5-30306/A/CGC1976
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE:  919-541-8857
38 TELEFAX:  919-541-8689
39 INFORMATION FOR SEQ ID NO:  186:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH:  615 base pairs
42 TYPE:  nucleic acid
43 STRANDEDNESS:  single
44 TOPOLOGY:  linear
45 MOLECULE TYPE:  DNA (genomic)
46 ORGANISM:  PAG1074RP
47
48 US-08-998-416-186

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Query Match	2.6%;	Score 75.8;	DB 3;	Length 615;
Best Local Similarity	46.8%;	Pred. No. 6e-08;		
Matches 239;	Conservative	0;	Mismatches 272;	Indels

QY 1980 TCAGTCATTTAAATAGACAGCCATCACTTTATTAATATTAAGCAATTTGATGTTAGA 2039  
 Db 551 TATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTTATTAATTAATTAATTAATTAATA 492  
 QY 2040 TGAAGTAGAAGATATTTTCATTAACCCGCGATATCAAGACAGATTTGATCTT 2099  
 Db 491 ATTAAGAAATTTAAAGTTAAATTTTAATTAATTAATTTCTATTAATAAAGTTAAATTAATAT 432  
 QY 2100 AAAAGATATTAAATCATTCAGAAATTAAGATGCCAAATTCGCACTGATTTTTTATTC 2159

Db	8068	ATAATTTTAAATTAATTTAAATATAATATAATATAATATAAAGATTAATTAATTTTAAAGAT	8127
Qy	2037	AGATGAAGAGTAAAGATTAATTTTCAATTAACCGCTGAATATCAAGAGAGATTGATAT	20986
Db	8128	ATTTTAAAAAATAATGATTTATATATAGATGATTAATATATTCATGATAAATTAATCG	8187
Qy	2097	CTTAAAGATATTAATAATCATCCGAATAAAGATCCAAAATCGCAGTCAGTATTTT	2156
Db	8188	AAATAAAAAATTTAAATTTATTTATTTTGGAAAAATATATTAATTTAATATTTATTA	8247
Qy	2157	TCCCATATCATTAACCGCTTAGTGAACAAAACTAAACAATTTATGTAATATAAATA	2216
Db	8248	T-ATPATATATAAATGAGATCTTACCATCCGAAATTTTATTTAAATATTTATATAAT	8306
Qy	2217	TATATTCGTATTTGTTCTACATGTTG-ATAAGAAATCATCTTACACCAATATTCAAAAAG	2275
Db	8307	TAGATATTAATGATTAATATAATTTGTTATAATTTGATTTTATACAGATGTAAATATA	8366
Qy	2276	AAATACTAGCCTTCATCATATAACATCAAGGAATTTTCTAAATATAGTATCTCAT	2335
Db	8367	AAATTAATATATAAAAAATATAAAAAATGATGAAAAAATTTATCAAAAAATTTATATCTAA	8428
Qy	2336	ATTACAGAGTAATGATTAATTAATAAATCAAGCGCATTTAAGTAAATTAATAAATTA	2395
Db	8427	CAGATTA-AATTAATATATGAATATAAACAATTATATAGATTTGGTTGATTTATCATATTAAT	8485
Qy	2396	GTCAGTTAAATCTAAATATGTGAATACATTTTGTGATATCATGA	2441
Db	8486	TCATCATTAATGAATATTTTATTTATATAAATATATAAAAAAATATATA	8531

RESULT 6  
 US-09-107-532A-2527  
 Sequence 2527, Application US/09107532A  
 Patent No. 6581375  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 NUMBER OF SEQUENCES: 7310  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02354  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD-ROM ISO9660  
 COMPUTER: PC  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,532A  
 FILING DATE: 30-Jun-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/085,598  
 FILING DATE: 14 May 1998  
 APPLICATION NUMBER: 60/051571  
 FILING DATE: July 2, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Arinello, Pamela Deneke  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-012  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEFAX: (781)893-8277  
 INFORMATION FOR SEQ ID NO: 2527:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 984 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: circular

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? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Enterococcus faecium
?
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (8) LOCATION 1...964
? SEQUENCE DESCRIPTION: SEQ ID NO: 2527
US-09-107-552A-2527

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Query Match	2.8%;	Score 80.6;	DB 3;	Length 984;
Best Local Similarity	52.5%;	Pred. No. 5.5e-09;		
Matches 176;	Conservative 0;	Mismatches 159;	Indels 0;	Gaps 0;

Qy	1309	AATGAGACCTTAGTTCAATTAAATCCACCTATAATCTGCAAACTATATTCAA	1368
Db	13	AATATAATGTGTGAGATTAGTATTAATGTTCCTGTGTATAAGTTGAAAAATATTTAAGA	72
Qy	1369	CGTTGCGCATAGTAGGCAGCTGAATCAGACTGTTTGATCTCGAGGTTTGATTTGTAAAC	1428
Db	73	AAATGTGAGATTGGATTTTAGCCCAACATTACTGATTTTGAAGTTATATTAGTAGAT	132
Qy	1429	GATGGTTCAACAGATAAATACCTTAGAAGTATCAATAAGCTTTAATGTAATATCTAAG	1488
Db	133	GATGATGATCTCTGACAAATAGCGGGAAATCTGTATGATGATGCTGAAAAAGATATATCGA	192
Qy	1489	GTACGCATCATGTCTTAAACCAATATGCGGGAATAGCCTCAGCATCAATATGACCGCTTCT	1548
Db	193	GTACGTGTGATCCATTAATAAGAAACGCGCGGATTAAGCAGTGTCAAGAAATGCGCGGATTCAT	252
Qy	1549	TTTGCTAAAGTTATTTACATTGGGCACTTAATTCAGATGATTTATCTTGACCTGATGCA	1608
Db	253	GTTCGAGACGCAATATCTTAGCGTTTGTTGTACAGTGTGATTAATTTAGATGAAGATATG	312
Qy	1609	GTTGACCTGTGTTAAAAAGATTTTTTTAAAAAGATAA	1643
Db	313	TATGAAATTTGTATGGAATTTGAAAAATTCATGA	347

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/ RESULT 7
/ US-09-900-038A--3
/ Sequence 3, Application US/09900038A
/ Patent No. 6828128
/ GENERAL INFORMATION:
/ APPLICANT: Miyake, Katsuhide
/ APPLICANT: Watanabe, Masaki
/ APPLICANT: Iijima, Shinji
/ TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the same
/ FILE REFERENCE: 766.53
/ CURRENT APPLICATION NUMBER: US/09/900.038A
/ CURRENT FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: JP 2001-392
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/
/ LENGTH: 6865
/
/ TYPE: DNA
/
/ ORGANISM: Streptococcus agalactiae type Ib
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (617)..(1789)
/ NAME/KEY: CDS
/ LOCATION: (1816)..(2262)
/ NAME/KEY: CDS
/ LOCATION: (2265)..(2744)
/ NAME/KEY: CDS
/ LOCATION: (2843)..(3979)
/ NAME/KEY: CDS
/ LOCATION: (3982)..(4953)
/ NAME/KEY: CDS
/ LOCATION: (5009)..(5947)
/

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Db      1201  GAAATGAAACCGATCGTGAAGCGGAAAAATATTAACCTCGATATTATGAGAAAAG 1260
Qy      1261  GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAAGTGGCATATCAATAGACT 1320
Db      1261  GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAAGTGGCATATCAATAGACT 1320
Qy      1321  TTAGTTTCAATTTATATCCACGCTTATTAAGTGGCAAACTATATTCAGGTTCCGTA 1380
Db      1321  TTAGTTTCAATTTATATCCACGCTTATTAAGTGGCAAACTATATTCAGGTTCCGTA 1380
Qy      1381  AGTGCACCTGAATCAGACTGTTGTGATCTCGAGGTTGTGATTTGTAACAGTGTTCAC 1440
Db      1381  AGTGCACCTGAATCAGACTGTTGTGATCTCGAGGTTGTGATTTGTAACAGTGTTCAC 1440
Qy      1441  GATATATCTTATGAAAGTATCAATAGCTTTATGTAATTAATCCATAGGTTAGCATC 1500
Db      1441  GATATATCTTATGAAAGTATCAATAGCTTTATGTAATTAATCCATAGGTTAGCATC 1500
Qy      1501  TCTAAACCAATGGCGGAATAGCTCAGCATCAAAATGACGCGTTCTTTCTTAAAGT 1560
Db      1501  TCTAAACCAATGGCGGAATAGCTCAGCATCAAAATGACGCGTTCTTTCTTAAAGT 1560
Qy      1561  TATTAATTTGGGAGTTAGATTCAATGATTAATCTTGAGCTGATGACGTTGAATGTGT 1620
Db      1561  TATTAATTTGGGAGTTAGATTCAATGATTAATCTTGAGCTGATGACGTTGAATGTGT 1620
Qy      1621  TTTAAAGAAATTTTAAAGATTAAGAGCTGAGCTGTGTTATACCACTTAATGAAGCT 1680
Db      1621  TTTAAAGAAATTTTAAAGATTAAGAGCTGAGCTGTGTTATACCACTTAATGAAGCT 1680
Qy      1681  AATCGGAGTGTAGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATG 1740
Db      1681  AATCGGAGTGTAGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATG 1740
Qy      1741  CTCACACGCGCTATGATGCTGACCACTTGAATGCTTGAATGATGACGCTTGCAAT 1800
Db      1741  CTCACACGCGCTATGATGCTGACCACTTGAATGCTTGAATGATGACGCTTGCAAT 1800
Qy      1801  ACTGATGATTCATATGAAAAATTTGAAAAATGCCGTGACATGACATGTTCTCAAACT 1860
Db      1801  ACTGATGATTCATATGAAAAATTTGAAAAATGCCGTGACATGACATGTTCTCAAACT 1860
Qy      1861  AATGGAAGTGGAAAAATTTTAAACCTTTAATTAATTAATTAATTAATTAATTAAT 1920
Db      1861  AATGGAAGTGGAAAAATTTTAAACCTTTAATTAATTAATTAATTAATTAATTAAT 1920
Qy      1921  GATTAACATCAATTAAGAACTTGGCATTCAAAAAGAAAAACCAATTTGTGTAGTCA 1980
Db      1921  GATTAACATCAATTAAGAACTTGGCATTCAAAAAGAAAAACCAATTTGTGTAGTCA 1980
Qy      1981  CAGTCATTAATTAAGACAGGCGATTAATTAATTAATTAATTAATTAATTAATTA 2040
Db      1981  CAGTCATTAATTAAGACAGGCGATTAATTAATTAATTAATTAATTAATTAATTA 2040
Qy      2041  GAAAGTGAAGAAATTTTTCATATAAAACCGCGAATATCAAGAAAGATTGATCTTA 2100
Db      2041  GAAAGTGAAGAAATTTTTCATATAAAACCGCGAATATCAAGAAAGATTGATCTTA 2100
Qy      2101  AAAGATTTTAA 2112
Db      2101  AAAGATTTTAA 2112

RESULT 5
US-09-662-254B-27
; Sequence 27, Application US/09662254B
; Patent No. 6933145
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: U1, Y1
; APPLICANT: Bawden, Allison Louise
; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
; TITLE OF INVENTION: Vertebrate Cells
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; FILE REFERENCE: UF-221C1XCI
; CURRENT APPLICATION NUMBER: US/09/662, 254B
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 09/086,651
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/224,479
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patent version 3.1
; SEQ ID NO 27
; LENGTH: 32392
; TYPE: DNA
; ORGANISM: Amsacta moorei entomopoxvirus
US-09-662-254B-27

Query Match      2.8%   Score 82.4; DB 3; Length 32392;
Best Local Similarity 44.8%; Pred. No. 6.9e-09;
Matches 558; Conservative 0; Mismatches 681; Indels 7; Gaps 6;

Qy      1197  TAAAGAAATGAAACCGATCGTGAAGCGGAAAAATTTACGCTCGATATTATGAGAGA 1256
Db      7292  TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7351
Qy      1257  AAAGTCCCTTAATCTATAGAAAACCTTTACCAATAGAAAGTTGCGATATCAATAGCT 1316
Db      7352  CGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7411
Qy      1317  ACCTTAGTTCAATTTATATCCAGCTTATTAATGCTGCAAACTATTTCAAGTTGCGT 1376
Db      7412  AATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7471
Qy      1377  AGATAGTCACATGATCAGACTGTTGTGATCTCGAGGTTGTGATTTGTAACGATGTT 1436
Db      7472  AACTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7529
Qy      1437  AACAGATTAATCTTGAAGTGAATCAATAGCTTTATGTAATTAATCTAGGTTAGCAT 1496
Db      7530  GAATGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7589
Qy      1497  CATGCTAAACCAATAGCGGAATAGCGCTGACATCAATGAGCGGTTCTTTGCTAA 1556
Db      7590  AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7649
Qy      1557  AGTTATTACATTTGGGAGTTGATTCAGATGATTAATCTTGAGCGCTGATGACGTTG 1616
Db      7650  AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7708
Qy      1617  GTGTTAAAGAAATTTTAAAGATTAAGCTAGCTGTGTTATACCACTAATTAAGAA 1676
Db      7709  AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7768
Qy      1677  CGTCAATCCGATGATGAGTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTA 1736
Db      7769  AATAGCTTTGATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7828
Qy      1737  AAAACCTCAACGCGATGATGCTCACCACTTGAATGTTACAGATTAAGAGCTTGCA 1796
Db      7829  AATATGCTATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7888
Qy      1797  TTTAACTGATGATTCATGAAATAATTAATTAATTAATTAATTAATTAATTAATTA 1856
Db      7889  CTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7948
Qy      1857  ACTCAGTGAAGTTGAAAAATTTAAACCTTTAATTAATTAATTAATTAATTAATTA 1916
Db      7949  ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8007
Qy      1917  TGGTGAATACATCAATTAAGAACTTGGCATTCAAAAGAAAAACCAATTTGTGTAGT 1976
Db      8008  TAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8067
Qy      1977  CAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2036
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|||||  
Db 181 AATGTAAAGAAAACCTCGACCAATTC-----TTATGTAGT 219  
Oy 181 AAAGAGAAAAAGTCAATGTTTGGCATAGTCCGTTAGATATGGCAACACACTGTACTT 240  
Db 220 GAAAGTAAAAAAGAGTGTGGCATAGCTCATTAAGATATCGCAACACAGCTGTACTT 279  
Oy 241 TCCAAAGTAAAAAATTGTAATCTTCTGACTCGAAAAAACAAGTTAAAAATTAATGG 300  
Db 280 TCCAAAGTAAAAAATTGTAATCTTCTGACTCGAAAAAACAAGTTAAAAATTAATGG 339  
Oy 301 AAATGCTCACTGAGAGAAATCTGAAAATGCGAGTAAAGACGCGCTGCTTACCA 360  
Db 340 AAATCTATCACTGGGAAAAAATCGAGAACGCAAAATCAGAAAGTGGAACTAGTACC 399  
Oy 361 AAAGATTTTCCCAAAAGATCTGGTTTATAGCGCTTTACCTGATCATGTTAATTTTACA 420  
Db 400 AAAGATTTTCCCAAAAGATCTGGTTTATAGCTTGCATGCGAGATCATGTTAATGATTTTACA 459  
Oy 421 TGGTCAAAAAGCGAAAGAAAGACTGGCATAAAACCTGAACATCAACATGTGCTCT 480  
Db 460 TGGTCAAAAATCGAAAAAAGCTTAGGTATAAAGCTGTAAATTAAGAAATTCGCTCTT 519  
Oy 481 TCTATTATGCTTACAAATTCATCGAACCGAATTTTATCGATTACATTTAGCTGTCTTA 540  
Db 520 TCTATTATTATCTTACATTTATATGCTAGCGGATTTTATAGATATAACGTTAGCTGTG 579  
Oy 541 GTTAAACCAAAAAACACTTACCCGTTTGAAGTTATCGTACAGATGATGTGTGTCAGGA 600  
Db 580 GTCAATCAAGAAAAACAACTACCCATTTGAAGTCGTTGTGCAAGATGATGTGTGAAGGA 639  
Oy 601 GATCTATCAGCATCATTTGCGCAATTAAGAAATTAATGGATATTCGCTACGTCAGACA 660  
Db 640 AACTTACTTACCATGTGTGCAAAAATTAAGAACTTAAGACATTAAGTATTAAGACAA 699  
Oy 661 AAAGATTAACGTTTTTCAAGCCAGTCCGCTCGAATATGGAATTAACGTTACCAAAATAT 720  
Db 700 AAAGATTAATGATATCAATTTGTGTGAGTCAGAAACTTGAAGTTTACGACCAAAAGTAT 759  
Oy 721 GACTTATATGGCTTACTCGACTGTGATATGGCGCAATTCATTTATGCTTCTTAT 780  
Db 760 GATTTGTCTCGATCTTACATGCGATATGGCACCAACAAATTAATGAGTTTCAATCTTAT 819  
Oy 781 GTTGCAGACTATTAAGATGATGATTAACAATGATGTGCAAGAAATATACATCAT 840  
Db 820 CTTACGAACTATTAAGACATGATATGTTTAAATGACATTAAGAAATATGTTGAT 879  
Oy 841 ACACAAATATTTGACCCCAAAAGACTCTTAAATTAACGCGATTTGCTTGAATCATTTACA 900  
Db 880 ACTCATATATTTACCGCAGAACATTTCTTAAAGATCCATTTTAAATGAAATCACTACCT 939  
Oy 901 GAAAGTAAAAACCAATATATAGTGTGCGCAAAAGGGAAAGAACAGTTTCTCTGATGG 960  
Db 940 GAAACGCTACAAATTAACAATCTTGCATTAATCAAAAGAAATATATGTTGATGG 999  
Oy 961 CGCTTGAACAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTCCGTTT 1020  
Db 1000 AGATTATGAACATTTCAAAAAAACGAAATCTACGCTATGATTTCTCCGTTTCTGATAT 1059  
Oy 1021 TTTGGCGGGGTAATGTTGCTTCCGTTAAAAAATGCTAAATCCGTTTCTTTGAT 1080  
Db 1060 TTTGTGCGGGTATATTTGCTATTTTCTTAAAGATGCTAAATTAATGATGTTGCTGAT 1119  
Oy 1081 GAGGAATTTAATCACTGGGTGAGAGATGTGAAATTTGATATGCTTATTCGTTTAC 1140  
Db 1120 GAAAGATTTAATCATTTGGGGGGGGAAGATGTAGAAATTTGTTACAGATTAATTTGCCAAA 1179  
Oy 1141 GGTAGTTTCTTTAAACTATTTGATGGCATTTATGGCTTACATCAAGACCAAGGTAAA 1200  
Db 1180 GCGCTTTTCTTTCAGAGTAAATTTGACGGCGGAATGGCATCCATCMAAACAACCTGTGAAA 1239  
Oy 1201 GAAAAAGAAACGATGTTGAGCGGAAAAAATATTAACGCTGATTTATGAGAGAAAG 1260  
|||||

Db 1240 GAAAAAGAAACGAAACCGGAAGCTGTGTAAGTATTACGCTTAAATTTGTGAAAAAG 1299  
Oy 1261 GTCCCTTATATCTATTAAGAAAACTTTTACCAATAGAAATTTGCATATCAATAGATCCT 1320  
Db 1300 GTACCTTACATCTATTAAGAAAGCTTTTACCAATTAAGAAATTCACATATTCATAGATACCT 1359  
Oy 1321 TTAAGTTCAATTTATATCCAGCTTATTAATCTGTGCAAACTATATTTCAACGTTGCTAGAT 1380  
Db 1360 TTAAGTTCTATTTATATCCCGCTTATTAATCTGTGCAAACTATATTTCAAAAGATGTGATAT 1419  
Oy 1381 AGTCACGATTCAGACTGTTGATCTGAGGTTTGTATTTTGTAAACGATGTTCAACA 1440  
Db 1420 AGTGTCTTAATCAAACTGTTGTGATCTGAGGTTTGTATTTGTAAAGATGTTCAACA 1479  
Oy 1441 GATAATACCTTAGAAGTATCAATTAAGCTTTATGTAATTAATCTTAGGTAACGATCATG 1500  
Db 1480 GATATATCTTAGAAGTATCAATTAAGCTTTATGTAATTAATCTTAGGTAACGATCATG 1539  
Oy 1501 TCTAAACCAATGGCGAATATGCTCAGCATCAAAATGACGCGTTTCTTTGCTTAAAGT 1560  
Db 1540 TCTAAACCAATGGCGAATATGCTCAGCATCAAAATGACGCGTTTCTTTGCTTAAAGT 1599  
Oy 1561 TATTACATTTGGCGAATTGATTCAGATGATTAATCTTGAAGCTGATGAGTTGAATCTGAT 1620  
Db 1600 TATTACATTTGGCGAATTGATTCAGATGATTAATCTTGAAGCTGATGAGTTGAATCTGAT 1659  
Oy 1621 TTAAGAAATTTTAAAGATTAACCGCTAGCTTGTGTTATACCATTAATTAAGAAACGTC 1680  
Db 1660 TTAAGAAATTTTAAAGATTAACCGCTAGCTTGTGTTATACCATTAATTAAGAAACGTC 1719  
Oy 1681 AATCGGATGGTATGATTAATGCTTAATGTTTAAATGCGCAAAATTTTACAGAGAAAA 1740  
Db 1720 AATCGGATGGTATGATTAATGCTTAATGTTTAAATGCGCAAAATTTTACAGAGAAAA 1779  
Oy 1741 CTCACAAAGGCTATGATTTGCTCAACCATTTGAAGATTTACAGATTAAGAGCTTGGATTTA 1800  
Db 1780 CTCACAAAGGCTATGATTTGCTCAACCATTTGAAGATTTACAGATTAAGAGCTTGGATTTA 1839  
Oy 1801 ACTGATGATTCATATGAAGAAAAATGAAATCCGCTAGACATATGATCTCTCAAACTC 1860  
Db 1840 ACGATGATTTTAACGAAAAATTTGAAACCCGCTGATTTATGATATGATCTCTTAAACCTC 1899  
Oy 1861 AGTGAAGTTGAAAAATTTAAACATCTTAATTAATATCTGCTATTAACCGGTATTAATCATGCT 1920  
Db 1900 AGTGAAGTTGAAAAATTTAAACATCTTAATTAATATCTGCTATTAACCGGTATTAATCATGCT 1959  
Oy 1921 GATTAACATCAATTAAGAAACTTGGCATTTCAAAAGAAACCAATTTGTGTGATGCTAAT 1980  
Db 1960 GATTAACATCAATTAAGAAACTTGGCATTTCAAAAGAAACCAATTTGTGTGATGCTAAT 2019  
Oy 1981 CAGTATTAATTAAGCAAGGCACTAATTAATTAATTAATTAAGCAATTTGATGATTTAGAT 2040  
Db 2020 CAGTATTAATTAAGCAAGGCACTAATTAATTAATTAATTAAGCAATTTGATGATTTAGAT 2079  
Oy 2041 GAAAGTAAAGTATATTTTCAATTAACCCGCTGAATATCAAGAAAGATGATATGTTA 2100  
Db 2080 GAAAGTAAAGTATATTTTCAATTAACCCGCTGAATATCAAGAAAGATGATATGTTA 2139  
Oy 2101 AAAGATTAATTAATCAATCAAGATTAAGATGCAAAATGCGAGTCAATTTTATATCC 2160  
Db 2140 AAAGATTAATTAATCAATCAAGATTAAGATGCAAAATGCGAGTCAATTTTATATCC 2199  
Oy 2161 AATACATTAATTAAGGCTTATGTAAGAAACCTAAACATATTAATGAATATTAATTAATTA 2220  
Db 2200 AATACATTAATTAAGGCTTATGTAAGAAACCTAAACATATTAATGAATATTAATTAATTA 2259  
Oy 2221 TTCGTTATTTCTTCAATGTTGATTAAGATCACTTTACACAGATATCAAAAAAGAAATA 2280  
Db 2260 TTCGTTATTTCTTCAATGTTGATTAAGATCACTTTACACAGATATCAAAAAAGAAATA 2319  
Oy 2281 CTAGCCTTCTATCAATTAACATCAAGTGAATATTTTATCAATTAATGAATATCTCATATTAC 2340  
Db 2320 TTGGCTTCTATCATTAAGCAACAGTGAATATTTTATCAATTAATGAATATCTCATATTAC 2379  
|||||



Db	2479	GACAGCTATGCTTATATGAAAAAATATGATGTGGCATGAATTTCTCAGCATTAACACAT	2538	
Qy	2521	GATTGGATCGAGAAAATCAATCGCGCATCCACATTTAAAAAGCTCATTTAAAACTTATTTT	2580	
Db	2539	GATTGGATCGAGAAAATCAATCGCGCATCCACATTTAAAAAGCTCATTTAAAACTTATTTT	2598	
Qy	2581	AATGACAAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAACAGGTATGTTTATGACG	2640	
Db	2599	AATGACAAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAACAGGTATGTTTATGACG	2658	
Qy	2641	TATCGCCTAGCGCATGAGCTTCTGACGATTATTAAAGAAGTCATCACATCTTGCCAGTCA	2700	
Db	2659	TATCGCCTAGCGCATGAGCTTCTGACGATTATTAAAGAAGTCATCACATCTTGCCAGTCA	2718	
Qy	2701	ATTGATAGTGTGCCAGATAATAACACTGAGGATATTGGTTCCAAATTTGCACATTTTAATC	2760	
Db	2719	ATTGATAGTGTGCCAGATAATAACACTGAGGATATTGGTTCCAAATTTGCACATTTTAATC	2778	
Qy	2761	TTAGAAAAAGAAAACCGGCCCATGTATTTAATAAACAATCGACCTGACTTATATGCTTTGG	2820	
Db	2779	TTAGAAAAAGAAAACCGGCCCATGTATTTAATAAACAATCGACCTGACTTATATGCTTTGG	2838	
Qy	2821	GAACGAAAATTAACAATGAGCAAAATGAACAAATTTGAAAGTGCAAAAAGAGGAGAAAAATA	2880	
Db	2839	GAACGAAAATTAACAATGAGCAAAATGAACAAATTTGAAAGTGCAAAAAGAGGAGAAAAATA	2898	
Qy	2881	CCTGTTTAAACAAGTTCATTATTAAATAGTATAACTCTATAA	2919	
Db	2899	CCTGTTTAAACAAGTTCATTATTAAATAGTATAACTCTATAA	2937	
RESULT 2				
US-10-172-527A-9				
; Sequence 9, Application US/10172527A				
; Patent No. 6951743				
; GENERAL INFORMATION:				
; APPLICANT: Weigel, Paul H				
; APPLICANT: Kumari, Keshava				
; APPLICANT: DeAngelis, Paul				
; TITLE OF INVENTION: HYALURONAN SYNTHASE GENES AND EXPRESSION THEREOF IN BACILLUS HOST				
; FILE REFERENCE: 3554.048				
; CURRENT APPLICATION NUMBER: US/10/172,527A				
; CURRENT FILING DATE: 2002-06-13				
; PRIOR APPLICATION NUMBER: 60/297,788				
; PRIOR FILING DATE: 2001-06-13				
; PRIOR APPLICATION NUMBER: 60/297,744				
; PRIOR FILING DATE: 2001-06-13				
; PRIOR APPLICATION NUMBER: 09/469,200				
; PRIOR FILING DATE: 1999-12-21				
; PRIOR APPLICATION NUMBER: 09/178,851				
; PRIOR FILING DATE: 1998-10-26				
; NUMBER OF SEQ ID NOS: 41				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 9				
; LENGTH: 2937				
; TYPE: DNA				
; ORGANISM: pasteurella multocida				
US-10-172-527A-9				
Query Match 99.9%; Score 2917.4; DB 3; Length 2937;				
Best Local Similarity 100.0%; Pred. No. 0;				
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
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Db	79	AAATTTTGGAAAGTCGGCGGAAATCTATCGACGAAAAATTTGTTGAATTTCAAATTACC	138	
Qy	121	AAATGCAAGAAAAAATCTCTCAGCACATCTCTTGTGTTAATTCAGCACATCTTTCTGTGAAT	180	

Qy	301	AAATTTGCTCACTGAGAGAAATCTGAAAATGCGGAGGTAAGAGCGGTGCGCCCTTGTTACCA	360
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Qy	781	GTTGAGAGCTATTAGAGATGATGATTTAAACAATCATTTGGTTCGAAGAAATACATCGAT	840
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Dd	859	ACACAACATATTGACCCAAAAGACTTCTTAAATAACCGAGTTTGTGTAATCATTTACCA	918
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Dd	1339	TTAGTTTCAATTTTATATCCAGCTTATAAATGTGTGCAAACTATATTCAACGTTGGTAGAT	1398

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Qy	1441	GATAATACCTTTAGAAGTGATCAATTAAGCTTTTATGGTAATAATCCTAGGGTACGCATCATG	1500
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Qy	1501	TCATAAACCAATCGCGAATAGCTCTCAGCATCAATGTCAGCCGTTTCTTTTGTCTAAAGGT	1560
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Qy	2161	AATACATTAAACGGCTTTAGTGAATAAATACTAATAATTTATGAAATATTAATAAATAATA	2220
Dd	2179	AATACATTAAACGGCTTTAGTGAATAAATACTAATAATTTATGAAATATTAATAAATAATA	2238
Qy	2221	TTGGTTATTTCTTACATGTTGTAAGAATCATCTTACACAGATATCAAAAAAGAAATA	2280
Dd	2239	TTGGTTATTTCTTACATGTTGTAAGAATCATCTTACACAGATATCAAAAAAGAAATA	2298
Qy	2281	CTAGCCTTCTATCATAAACATCAAGTGAATTTTACTAAATATATGATATCTCATATTTAC	2340
Dd	2299	CTAGCCTTCTATCATAAACATCAAGTGAATTTTACTAAATATGATATCTCATATTTAC	2358
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Dd	2419	TTAAATCTTAATTTGTAATACATCATTTTGTAAATCATGACAGCCTTATTCGTTTAAAAAT	2478
Qy	2461	GACAGCTATGCTTATATGAAAAAATAATGATGTCGGCATGAATTTTCTCAGCATTTAACACAT	2520

GenCore version 5.1.6  
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9849.108 Million cell updates/sec

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Perfect score: 2920

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2108.8	72.2	2112	3	US-09-437-277-2
5	82.4	2.8	3292	3	US-09-662-254B-27
6	80.6	2.8	984	3	US-09-107-532A-2527
7	80.6	2.8	6865	3	US-09-900-038A-3
8	77	2.6	993	3	US-09-134-000C-2987
9	75.8	2.6	615	3	US-08-998-416-186
10	74.4	2.5	1141	3	US-09-806-708B-22
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22	70	2.4	891	3	US-10-303-134-30
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c 37	68.8	2.4	1785	3	US-09-601-198-156	Sequence 156, App
38	68.4	2.3	906	3	US-09-495-406-14	Sequence 14, Appl
39	68.4	2.3	906	3	US-09-816-028A-26	Sequence 26, Appl
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41	68.4	2.3	906	3	US-10-303-134-26	Sequence 26, Appl
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45	67.4	2.3	1039	3	US-09-902-540-1280	Sequence 1280, Ap

ALIGNMENTS

RESULT 1

US-09-469-200E-8  
; Sequence 8, Application US/09469200E  
; Patent No. 6833264  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Kumari, Kehama  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/09/469,200E  
; CURRENT FILING DATE: 1999-12-21  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 60/178,851  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: Pastuerella Multocida  
US-09-469-200E-8

Query Match	100.0%	Score	2919;	DB	3;	Length	2937;
Best Local Similarity	100.0%	Pred. No.	0;				
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Gaps	0;						
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QY	61	AAATTTATTTGAAAGTCGCGGAAATCTATGGACGAAATTTGTTGAATTTCAAAATTACC	120				
DB	79	AAATTTATTTGAAAGTCGCGGAAATCTATGGACGAAATTTGTTGAATTTCAAAATTACC	138				
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Best Local Similarity 86.9%; Pred. No. 0;  
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

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Job time : 123 secs

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Qy 841 DWTEKINAHPPFKLIIKTYFNDDLSKSNYKASQGMFTYALAHBLITIIKEVITSCOS 900
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QY      961 PUNKFIINSITL 972
Db      954 PUNKFIINSITL 965

RESULT 14
US-10-642-248-4
: Sequence 4, Application US/10642248
: Publication No. US20040132143A1
: GENERAL INFORMATION:
: APPLICANT: Deangelis, Paul
: TITLE OF INVENTION: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND METHO
: TITLE OF INVENTION: MAKING AND USING SAME
: FILE REFERENCE: 3554, 097
: CURRENT APPLICATION NUMBER: US/10/642,248
: CURRENT FILING DATE: 2003-08-15
: PRIOR APPLICATION NUMBER: 60/404,356
: PRIOR FILING DATE: 2002-08-16
: PRIOR APPLICATION NUMBER: 60/479,432
: PRIOR FILING DATE: 2003-06-18
: PRIOR APPLICATION NUMBER: 60/491,362
: PRIOR FILING DATE: 2003-07-31
: PRIOR APPLICATION NUMBER: 10/195,908
: PRIOR FILING DATE: 2002-07-15
: PRIOR APPLICATION NUMBER: 09/437,277
: PRIOR FILING DATE: 1999-11-01
: PRIOR APPLICATION NUMBER: 60/107,929
: PRIOR FILING DATE: 1998-11-11
: PRIOR APPLICATION NUMBER: 09/283,402
: PRIOR FILING DATE: 1999-04-01
: PRIOR APPLICATION NUMBER: 60/080,414
: PRIOR FILING DATE: 1998-04-02
: PRIOR APPLICATION NUMBER: 09/842,484
: PRIOR FILING DATE: 2001-04-25
: PRIOR APPLICATION NUMBER: 60/199,538
: PRIOR FILING DATE: 2000-04-25
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: SEQ ID NO 4
: LENGTH: 965
: TYPE: PRT
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US-10-642-248-4

Query Match      88.1%; Score 4502.5; DB 4; Length 965;
Best Local Similarity 86.9%; Pred. No. 0;
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

1 MNTLSGATGAYNSNDYQALAKLPEKSAETYGKRIYEFQITCKEKLSAHPVSNAHLSVN 60
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1 MNTLSGATGAYNSNDYQALAKLPEKSAETYGKRIYEFQITCKEKL---STNS--YVS 53
61 KEKVAVCDSPDIATQQLLSNVKVLVSDSEKNTLKNMKKLTEKSKSNAEVRVALVP 120
54 EDKSKVCCSSLDIAFQQLLSNVKVLVSDSEKNTLKNMKKSLTGGKSNNAEIRVELVP 113
121 KDFPKDLVLAPELDHVNDFTWYKRRKRLGIRKQHVGLSIIYTFNPAISITLACL 180
114 KDFPKDLVLAPELDHVNDFTWYKRRKRLGIRKQHVGLSIIYTFNPAISITLACL 173
181 VNQKTHYPPREVIVTDGSGQEDLSPIIKQYENKLDIRYVQKXNGPQASAAARMGRLACY 240
174 VNQKTHYPPREVIVVADGSGKENLITIVQKTEQKLDIRYVQKXNGPQASAAARMGRLACY 233

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QY 241 DFIGLDCDPA<sup>2</sup>NPLW<sup>2</sup>MSHYA<sup>2</sup>ELL<sup>2</sup>EDDL<sup>2</sup>ITIGRKY<sup>2</sup>IDPH<sup>2</sup>ODK<sup>2</sup>OF<sup>2</sup>LN<sup>2</sup>AS<sup>2</sup>LES<sup>2</sup>LP 300  
 Db 234 DFIGLDCDPA<sup>2</sup>POOL<sup>2</sup>WHSY<sup>2</sup>TELLE<sup>2</sup>EDND<sup>2</sup>IVLIGRKY<sup>2</sup>VDTH<sup>2</sup>NT<sup>2</sup>IA<sup>2</sup>BO<sup>2</sup>PL<sup>2</sup>ND<sup>2</sup>PYL<sup>2</sup>ES<sup>2</sup>LP 293  
 QY 301 EVK<sup>2</sup>NN<sup>2</sup>SV<sup>2</sup>AA<sup>2</sup>GE<sup>2</sup>GV<sup>2</sup>SL<sup>2</sup>DM<sup>2</sup>LE<sup>2</sup>OE<sup>2</sup>EKEN<sup>2</sup>RL<sup>2</sup>SD<sup>2</sup>PER<sup>2</sup>FA<sup>2</sup>GV<sup>2</sup>AA<sup>2</sup>PA<sup>2</sup>K<sup>2</sup>AL<sup>2</sup>N<sup>2</sup>KS<sup>2</sup>GF<sup>2</sup>PD 360  
 Db 294 ET<sup>2</sup>AT<sup>2</sup>NN<sup>2</sup>PS<sup>2</sup>IS<sup>2</sup>TK<sup>2</sup>NI<sup>2</sup>SL<sup>2</sup>DM<sup>2</sup>LE<sup>2</sup>HK<sup>2</sup>KT<sup>2</sup>D<sup>2</sup>RL<sup>2</sup>CS<sup>2</sup>PR<sup>2</sup>YP<sup>2</sup>SC<sup>2</sup>GV<sup>2</sup>AA<sup>2</sup>PS<sup>2</sup>K<sup>2</sup>EW<sup>2</sup>L<sup>2</sup>KN<sup>2</sup>GW<sup>2</sup>PD 353  
 QY 361 EE<sup>2</sup>FN<sup>2</sup>HW<sup>2</sup>GE<sup>2</sup>DE<sup>2</sup>FG<sup>2</sup>RL<sup>2</sup>FR<sup>2</sup>YS<sup>2</sup>FE<sup>2</sup>KT<sup>2</sup>IG<sup>2</sup>MA<sup>2</sup>YH<sup>2</sup>OE<sup>2</sup>PP<sup>2</sup>GE<sup>2</sup>KE<sup>2</sup>NET<sup>2</sup>RE<sup>2</sup>AG<sup>2</sup>NI<sup>2</sup>TL<sup>2</sup>DI<sup>2</sup>MR<sup>2</sup>K 420  
 Db 354 EE<sup>2</sup>FN<sup>2</sup>HW<sup>2</sup>GE<sup>2</sup>DE<sup>2</sup>FG<sup>2</sup>RL<sup>2</sup>FR<sup>2</sup>AK<sup>2</sup>CF<sup>2</sup>FE<sup>2</sup>VID<sup>2</sup>GC<sup>2</sup>MA<sup>2</sup>YH<sup>2</sup>OE<sup>2</sup>PP<sup>2</sup>GE<sup>2</sup>KE<sup>2</sup>NET<sup>2</sup>RE<sup>2</sup>AK<sup>2</sup>SI<sup>2</sup>TL<sup>2</sup>K<sup>2</sup>LV<sup>2</sup>KR 413  
 QY 421 VP<sup>2</sup>Y<sup>2</sup>Y<sup>2</sup>R<sup>2</sup>KL<sup>2</sup>LP<sup>2</sup>ED<sup>2</sup>SH<sup>2</sup>IN<sup>2</sup>VP<sup>2</sup>LS<sup>2</sup>Y<sup>2</sup>IP<sup>2</sup>AY<sup>2</sup>NC<sup>2</sup>ANY<sup>2</sup>OR<sup>2</sup>CV<sup>2</sup>DS<sup>2</sup>AL<sup>2</sup>NOT<sup>2</sup>VD<sup>2</sup>LE<sup>2</sup>VC<sup>2</sup>I<sup>2</sup>CND<sup>2</sup>ST 480  
 Db 414 VP<sup>2</sup>Y<sup>2</sup>Y<sup>2</sup>R<sup>2</sup>KL<sup>2</sup>LP<sup>2</sup>ED<sup>2</sup>SH<sup>2</sup>IR<sup>2</sup>I<sup>2</sup>PL<sup>2</sup>VS<sup>2</sup>IP<sup>2</sup>AY<sup>2</sup>NC<sup>2</sup>ANY<sup>2</sup>OR<sup>2</sup>CV<sup>2</sup>DS<sup>2</sup>AL<sup>2</sup>NOT<sup>2</sup>VD<sup>2</sup>LE<sup>2</sup>VC<sup>2</sup>I<sup>2</sup>CND<sup>2</sup>ST 473  
 QY 481 DNT<sup>2</sup>LE<sup>2</sup>VI<sup>2</sup>NK<sup>2</sup>L<sup>2</sup>CG<sup>2</sup>NN<sup>2</sup>PR<sup>2</sup>VR<sup>2</sup>IM<sup>2</sup>SK<sup>2</sup>PG<sup>2</sup>NG<sup>2</sup>IAS<sup>2</sup>AS<sup>2</sup>AA<sup>2</sup>VS<sup>2</sup>FA<sup>2</sup>K<sup>2</sup>Y<sup>2</sup>IG<sup>2</sup>OL<sup>2</sup>DS<sup>2</sup>D<sup>2</sup>YL<sup>2</sup>EP<sup>2</sup>D<sup>2</sup>AV<sup>2</sup>EL<sup>2</sup>C 540  
 Db 414 DNT<sup>2</sup>LE<sup>2</sup>VI<sup>2</sup>NK<sup>2</sup>L<sup>2</sup>CG<sup>2</sup>NN<sup>2</sup>PR<sup>2</sup>VR<sup>2</sup>IM<sup>2</sup>SK<sup>2</sup>PG<sup>2</sup>NG<sup>2</sup>IAS<sup>2</sup>AS<sup>2</sup>AA<sup>2</sup>VS<sup>2</sup>FA<sup>2</sup>K<sup>2</sup>Y<sup>2</sup>IG<sup>2</sup>OL<sup>2</sup>DS<sup>2</sup>D<sup>2</sup>YL<sup>2</sup>EP<sup>2</sup>D<sup>2</sup>AV<sup>2</sup>EL<sup>2</sup>C 533  
 QY 511 LKE<sup>2</sup>PL<sup>2</sup>KD<sup>2</sup>KT<sup>2</sup>LAC<sup>2</sup>V<sup>2</sup>Y<sup>2</sup>TT<sup>2</sup>NN<sup>2</sup>RV<sup>2</sup>NP<sup>2</sup>DG<sup>2</sup>SL<sup>2</sup>IANG<sup>2</sup>Y<sup>2</sup>WP<sup>2</sup>EP<sup>2</sup>SP<sup>2</sup>RE<sup>2</sup>K<sup>2</sup>LT<sup>2</sup>TA<sup>2</sup>IA<sup>2</sup>HH<sup>2</sup>PR<sup>2</sup>MT<sup>2</sup>RA<sup>2</sup>ML<sup>2</sup> 600  
 Db 534 LKE<sup>2</sup>PL<sup>2</sup>KD<sup>2</sup>KT<sup>2</sup>LAC<sup>2</sup>V<sup>2</sup>Y<sup>2</sup>TT<sup>2</sup>NN<sup>2</sup>RV<sup>2</sup>NP<sup>2</sup>DG<sup>2</sup>SL<sup>2</sup>IANG<sup>2</sup>Y<sup>2</sup>WP<sup>2</sup>EP<sup>2</sup>SP<sup>2</sup>RE<sup>2</sup>K<sup>2</sup>LT<sup>2</sup>TA<sup>2</sup>IA<sup>2</sup>HH<sup>2</sup>PR<sup>2</sup>MT<sup>2</sup>RA<sup>2</sup>ML<sup>2</sup> 593  
 QY 601 TDG<sup>2</sup>FE<sup>2</sup>RE<sup>2</sup>K<sup>2</sup>LE<sup>2</sup>NAV<sup>2</sup>DM<sup>2</sup>FL<sup>2</sup>KS<sup>2</sup>EV<sup>2</sup>GF<sup>2</sup>K<sup>2</sup>HL<sup>2</sup>NK<sup>2</sup>I<sup>2</sup>CY<sup>2</sup>RV<sup>2</sup>LH<sup>2</sup>GD<sup>2</sup>NT<sup>2</sup>SI<sup>2</sup>KK<sup>2</sup>G<sup>2</sup>I<sup>2</sup>OK<sup>2</sup>KN<sup>2</sup>H<sup>2</sup>V<sup>2</sup>V<sup>2</sup>N 660  
 Db 594 TDG<sup>2</sup>FE<sup>2</sup>RE<sup>2</sup>N<sup>2</sup>IE<sup>2</sup>NAV<sup>2</sup>DM<sup>2</sup>FL<sup>2</sup>KS<sup>2</sup>EV<sup>2</sup>GF<sup>2</sup>K<sup>2</sup>HL<sup>2</sup>NK<sup>2</sup>I<sup>2</sup>CY<sup>2</sup>RV<sup>2</sup>LH<sup>2</sup>GD<sup>2</sup>NT<sup>2</sup>SI<sup>2</sup>KK<sup>2</sup>G<sup>2</sup>I<sup>2</sup>OK<sup>2</sup>KN<sup>2</sup>H<sup>2</sup>V<sup>2</sup>V<sup>2</sup>N 653  
 QY 661 QSL<sup>2</sup>NR<sup>2</sup>Q<sup>2</sup>IT<sup>2</sup>Y<sup>2</sup>NY<sup>2</sup>Y<sup>2</sup>DE<sup>2</sup>FD<sup>2</sup>DL<sup>2</sup>DES<sup>2</sup>RKY<sup>2</sup>FNK<sup>2</sup>TA<sup>2</sup>Y<sup>2</sup>OE<sup>2</sup>BI<sup>2</sup>DL<sup>2</sup>KO<sup>2</sup>IK<sup>2</sup>IT<sup>2</sup>OK<sup>2</sup>NDA<sup>2</sup>K<sup>2</sup>AV<sup>2</sup>SI<sup>2</sup>FP<sup>2</sup> 720  
 Db 654 QSL<sup>2</sup>NR<sup>2</sup>Q<sup>2</sup>IT<sup>2</sup>Y<sup>2</sup>NY<sup>2</sup>Y<sup>2</sup>DE<sup>2</sup>FD<sup>2</sup>DL<sup>2</sup>DES<sup>2</sup>RKY<sup>2</sup>FNK<sup>2</sup>TA<sup>2</sup>Y<sup>2</sup>OE<sup>2</sup>BI<sup>2</sup>DL<sup>2</sup>KO<sup>2</sup>IK<sup>2</sup>IT<sup>2</sup>OK<sup>2</sup>NDA<sup>2</sup>K<sup>2</sup>AV<sup>2</sup>SI<sup>2</sup>FP<sup>2</sup> 713  
 QY 721 NT<sup>2</sup>LN<sup>2</sup>GL<sup>2</sup>V<sup>2</sup>KK<sup>2</sup>NN<sup>2</sup>IT<sup>2</sup>EY<sup>2</sup>NNKI<sup>2</sup>FI<sup>2</sup>YL<sup>2</sup>VD<sup>2</sup>HK<sup>2</sup>NH<sup>2</sup>L<sup>2</sup>TP<sup>2</sup>DI<sup>2</sup>KK<sup>2</sup>EL<sup>2</sup>LA<sup>2</sup>FY<sup>2</sup>HK<sup>2</sup>QV<sup>2</sup>NI<sup>2</sup>LL<sup>2</sup>ND<sup>2</sup>ISY<sup>2</sup> 780  
 Db 714 NT<sup>2</sup>LN<sup>2</sup>GL<sup>2</sup>V<sup>2</sup>KK<sup>2</sup>NN<sup>2</sup>IT<sup>2</sup>EY<sup>2</sup>NNKI<sup>2</sup>FI<sup>2</sup>YL<sup>2</sup>VD<sup>2</sup>HK<sup>2</sup>NH<sup>2</sup>L<sup>2</sup>TP<sup>2</sup>DI<sup>2</sup>KK<sup>2</sup>EL<sup>2</sup>LA<sup>2</sup>FY<sup>2</sup>HK<sup>2</sup>QV<sup>2</sup>NI<sup>2</sup>LL<sup>2</sup>ND<sup>2</sup>ISY<sup>2</sup> 773  
 QY 781 TS<sup>2</sup>NR<sup>2</sup>L<sup>2</sup>IK<sup>2</sup>TE<sup>2</sup>AH<sup>2</sup>LS<sup>2</sup>NI<sup>2</sup>NK<sup>2</sup>LS<sup>2</sup>Q<sup>2</sup>LN<sup>2</sup>CE<sup>2</sup>Y<sup>2</sup>IF<sup>2</sup>DN<sup>2</sup>HS<sup>2</sup>L<sup>2</sup>FE<sup>2</sup>V<sup>2</sup>ND<sup>2</sup>SV<sup>2</sup>AY<sup>2</sup>



Db 781 TSNRLIITEAHLNSINKLSQNLNCEYIIIDNHDLSLFVKNDSYAYMKKYDVGMNFSALTH 840  
Qy 841 DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSQS 900  
Db 841 DWIEKINAHPPFKKLIITYFNDNDLRSNNVKGASQGMFTYALAHALLTIIKEVITSQS 900  
Qy 901 IDSVPEYNTEDIWFQFALLIILEKKTGHVFNKTSTLTYPWPKLQWNTNEQIESAKRGNI 960  
Db 901 IDSVPEYNTEDIWFQFALLIILEKKTGHVFNKTSTLTYPWPKLQWNTNEQIXSARGNI 960  
Qy 961 PVNKFIIINSITL 972  
Db 961 PVNKFIIINSITL 972

RESULT 11  
US-09-842-484A-4  
; Sequence 4, Application US/09842484A  
; Publication No. US20030104601A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL L.  
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME  
; FILE REFERENCE: 4605.003  
; CURRENT APPLICATION NUMBER: US/09/842,484A  
; CURRENT FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 965  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-09-842-484A-4

Query Match 88.1%; Score 4502.5; DB 3; Length 965;  
Best Local Similarity 86.9%; Pred. No. 0;  
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

Qy 1 MNTLSQATKAYNSNDYQALALFKESAIEYGRKIVEFOITCKEKLSAHPSVNSAHLNVN 60  
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Db 54 EDKNSVCDSSDIATQALLSNVKKLVLSSEKSLKNKWSITCKKSSENAEIRKVELVP 113  
Qy 121 KDFPKDLVLAIPDHNDFWYKKRKLGLIKPEHQHVGSLSIIVTFNRPAILSLITLACL 180  
Db 114 KDFPKDLVLAIPDHNDFWYKKRKLGLIKPEHQHVGSLSIIVTFNRSRLIDITLACL 173  
Qy 181 VNQKTHYFEVITVDGSGEDSPIRQYENKLDIRYVRQKDNQFGQASARNMGLAKY 240  
Db 174 VNQKTHYFEVIVVADGSGENLITVQYEQKLDIKYVRQKDYQYQLCAVRNLGURTAKY 233  
Qy 241 DFIGLLDCDMPNPLVHVSVAELLEDLDTIIGRPKYDTHIDPKDPLNNASLLESILP 300  
Db 234 DFVSLDCDMPAQQLVHVSILYTELLEDNDIVLIGRPKYVDTHNITAEQFLNDPYLIESLP 293  
Qy 301 EYKTNNSVAAKGEGVSLDWLRLEQFTEKNTENLSDSPFRFFAAGNVAFKWLKNSKGFDD 360  
Db 294 ETATNNFSITSGNISLDWLRLEHFKKTDNLRLCDSPPRYFCGNGVAFSEKWLNVGWFD 353  
Qy 361 EEFNWGGEDEVFGYRLFRYSGFFKTDIGIMAYHQBPGKENETDREAGKNITLIMREK 420  
Db 354 EEFNWGGEDEVFGYRLFAKGCFFRVIDGGMAYHQBPGKENETDREAGKSIITLKIVREK 413  
Qy 421 VPYIYRKLLPIEDSHNRVPLVSIYIPAYNCANYIQRQVDSALNOTVVDLEVCINDGST 480  
Db 414 VPYIYRKLLPIEDSHNRVPLVSIYIPAYNCANYIQRQVDSALNOTVVDLEVCINDGST 473  
Qy 481 DNTLEVINKLYGNPRVIRMSKPGNGGIASASNAAVSFAKGYIYIGQLSDDDYLEPDAVELC 540

Db 474 DNTLEVINKLYGNPRVIRMSKPGNGGIASASNAAVSFAKGYIYIGQLSDDDYLEPDAVELC 533  
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Db 534 LKPEFLKDKTTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHHPMFRTIRAWHL 593  
Qy 601 TDGFNEKIENAVYDMFLKLSSEVGFPHLANKI CYNRVLHGDNTSI KKLGIQKKHFFVVVN 660  
Db 594 TDGFNEKIENAVYDMFLKLSSEVGFPHLANKI CYNRVLHGDNTSI KKLGIQKKHFFVVVN 653  
Qy 661 QSLNRQGITYYNDEDFDLDDESRRKIYFNKTAEOEEDILDKDIKIIQNKDAKIAVSIFYP 720  
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Qy 721 NTNLGLVKLNNIIEYNNKNI FVIVLHVDKXHLTPDIKKEILAFYHKHQVNILLNNDISYY 780  
Db 714 NTNLGLVKLNNIIEYNNKNI FVIVLHVDKXHLTPDIKKEILAFYHKHQVNILLNNDISYY 773  
Qy 781 TSNRLIITEAHLNSINKLSQNLNCEYIIIDNHDLSLFVKNDSYAYMKKYDVGMNFSALTH 840  
Db 774 TSNRLIITEAHLNSINKLSQNLNCEYIIIDNHDLSLFVKNDSYAYMKKYDVGMNFSALTH 833  
Qy 841 DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSQS 900  
Db 834 DWIEKINAHPPFKKLIITYFNDNDLRSNNVKGASQGMFTYALAHELLTIIKEVITSQS 893  
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Qy 961 PVNKFIIINSITL 972  
Db 954 PVNKFIIINSITL 965

RESULT 12

US-10-217-613-3  
; Sequence 3, Application US/10217613  
; Publication No. US20030113845A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL  
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND US  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 35541.081  
; CURRENT APPLICATION NUMBER: US/10/217,613  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3  
; LENGTH: 965  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-10-217-613-3

Query Match 88.1%; Score 4502.5; DB 4; Length 965;  
Best Local Similarity 86.9%; Pred. No. 0;  
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

Qy 1 MNTLSQATKAYNSNDYQALALFKESAIEYGRKIVEFOITCKEKLSAHPSVNSAHLNVN 60  
Db 1 MNTLSQATKAYNSNDYQALALFKESAIEYGRKIVEFOITCKEKL----STNS---YVS 53  
Qy 61 KEEKVNVCDSPDIATQALLSNVKKLVLSDSKNTLKNKWLLTEKKSSENAEVRALVLP 120  
Db 54 EDKNSVCDSSDIATQALLSNVKKLVLSSEKSLKNKWSITCKKSSENAEIRKVELVP 113

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/ US-10-217-613-9

Query Match 92.7%; Score 4733; DB 4; Length 972;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 901; Conservative 22; Mismatches 49; Indels 0; Gaps 0;

Qy	1	MNTLSQAIKAYNSNDYQALALKLFPEKSAEYGRKIVEFQITKCKEKLSAHPSVNSAHLNVN	60
Db	1	MNTLSQAIKAYNCNDYXALALKLFPEKSAEYGRKIVEFQIICKOEKLSANPSVNEANLSVN	60
Qy	61	KEEKNVCDSPDLDIATQLLLSNVKLVLSDSSEKNTLKNKWLKLTTEKSENAEYRAVALVP	120
Db	61	EEKKNVCDSPDLDIATQLLLSNVKLVLSKSEKNSLKNKWLKLTTEKSENAEYRAVALVP	120
Qy	121	KOPKDLVLAPLDHVNDETMYKKRIGIKPEHQHVGLSIIVTFNRPAILSLTACL	180
Db	121	KOPKDLVLAPLDHVNDETMYKKRIGIKPEHQHVGLSIIXPTFNRPAILDITACL	180
Qy	181	VNQKTHYPEVITDDGSOEDLSPIROYENKLDIRYVRQKONGFOASAARNMGLRLAKY	240
Db	181	VNQKTHYPEVAVDDGSOEXLLPIRXOYEXKLDIRYVRQKONGXQACARNAVGLRLAKY	240
Qy	241	DFIGLLDCDMAPNPLMVHSYVAELLEDLTTIGPRKYIDTQHDPKOFLNNALESPL	300
Db	241	DFXGILDCDMAPXQLMVHSYLAELLEDLTTIGPRKYDTQNDIAEXFLNXASLESPL	300
Qy	301	EVKTNNSVAAKGGTYSLDWRLQOEKTNLRSLSDSPFFPAAGNVAFKAKWLKSGFFD	360
Db	301	ETATNNPAKGGEXSLDWRLQEFKTXNLRCDSPFFXFAAGNVAFKAKWLKSGFFD	360
Qy	361	EEFNHWGGEDVEFGYRLFRYGSFFKTTIDGIMAYHQBPCKENETDREAGNITLDMREK	420
Db	361	EEFNHWGGEDVEFGYRLFRKGCFFRTIDGMAYHQBPCKENETXREAGNITLDMREK	420
Qy	421	VPIYVRKLLPIEDSHINRVPLSVIYIPAYNCANYIQRVCVDSALNQTVVLEVCICNDGST	480
Db	421	VPIYVRKLLPIEDSHINRPLSVIYIPAYNCANYIQRVCVDSALNQTVVLEVCICNDGST	480
Qy	481	DNTLEVINKLYGNPRVRIKSPKNGGIASANAASVFAKGYIIGOLDSDDYLEPDAVELC	540
Db	481	DNTIEVINKLYGNPRVRIKSPKNGGIASANAASVFAKGYIIGOLDSDDYLEPDAVELC	540
Qy	541	LKEFLKDKTCLACVYTTNRNVNPDGSLIANGYNWPFESREKLTTAMIAHFRMFTIRAWHL	600
Db	541	LKEFLKDKTCLACVYTTNRNVNPDGSLIANGYNWPFESREKLTTAMIAHFRMFTIRAWHL	600
Qy	601	TDFGNEKIEAVDYMFLKLSVGFKPKHLNKI CYNRVLHGDNTSIKKLGIQKQKHFVVVN	660
Db	601	TDFGFENIENAVDYMFLKLSVGFKPKHLNKI CYNRVLHGDNTSIKKLGIQKQKHFVVVN	660
Qy	661	QSLNRQGITYYNVDDEDDLDESRYIFNKTAEQBEIDILKDIKTONKDAKTAVSIFYP	720
Db	661	QSLNRQGINYYNVDDEDDLDESRYIFNKTAEQBEIDILKDIKTONKDAKTAVSIFYP	720
Qy	721	NTLGLVKKLNNIIEYNKNI FVILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY	780
Db	721	NTLGLVKKLNNIIEYNKNI FVILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY	780
Qy	781	TSNRLIKTEAHLNINKLSQLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMNFSALTH	840

Db781TSNRLIKTEAHLNINKLSQNLNCEYIIIDNHDLSLFVKNDSYAYMKKYDVGMMFSALTH840

Qy841DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSCQS900

Db841DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSCQS900

Qy901IDSVPEYNTEDIWFOFALLILEKKTGHVFNKTSITLTYMPWERKLOWTNEQIESAKRGENI960

Db901IDSVPEYNTEDIWFOFALLILEKKTGHVFNKTSITLTYMPWERKLOWTNEQIESAKRGENI960

Qy961PVNKFIIINSITL972

Db961PVNKFIIINSITL972

RESULT 9

US-11-096-190-9

Sequence 9, Application US/11096190

Publication No. US20050221446A1

GENERAL INFORMATION:

APPLICANT: Widner, William

APPLICANT: Sloma, Alan

APPLICANT: Thomas, Michael D.

APPLICANT: Tang, Maria

TITLE OF INVENTION: Methods For Producing A Hyaluronic Acid In A Bacillus Cell

FILE REFERENCE: 10596.200-US

CURRENT APPLICATION NUMBER: US/11/096,190

CURRENT FILING DATE: 2005-03-31

PRIOR APPLICATION NUMBER: 2005-03-31

PRIOR FILING DATE: 2004-03-31

NUMBER OF SEQ ID NOS: 73

SOFTWARE: PatentIn version 3.2

SEQ ID NO 9

LENGTH: 972

TYPE: PRT

ORGANISM: Pasteurella multocida

US-11-096-190-9

Query Match

Best Local Similarity 99.9%; Score 5104; DB 6; Length 972;

Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db1MNTLSQAIKAYNSNDYQLALKLFEKSABIYGRKIVEFOITKCEKLSAHPNSVNSAHLNVN60

Qy61KEEKVNVCDSPLDIATQALLSNVKKLVLSDSSEKNTLKNKWKLITTEKKSNAEVRVALVP120

Db61KEEKVNVCDSPLDIATQALLSNVKKLVLSDSSEKNTLKNKWKLITTEKKSNAEVRVALVP120

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Db121KDFPKDLVLAPLDHVNDFWTYKKRKRGLGKPEHQHVGSLSIIVTTFNRPALISITLACL180

Qy181VNQKTHYPFEVITVDGSGQEDLSPIIROQYENKLDIRYVRQKDNFGQASARNMGLRLAKY240

Db181VNQKTHYPFEVITVDGSGQEDLSPIIROQYENKLDIRYVRQKDNFGQASARNMGLRLAKY240

Qy241DFIGLLDCDMPNPLVWHSYVAELLEDDDLTTIIGRPKYIDTQHDIDPKDFLNNASLLESIP300

Db241DFIGLLDCDMPNPLVWHSYVAELLEDDDLTTIIGRPKYIDTQHDIDPKDFLNNASLLESIP300

Qy301EVTKTNSVAAKGGTGVSLDWRLEQPEKTEKNTLSDSPRFFFAAGNVAFPAKKNLKSFGFD360

Db301EVTKTNSVAAKGGTGVSLDWRLEQPEKTEKNTLSDSPRFFFAAGNVAFPAKKNLKSFGFD360

Qy361EEFNHWGGEDVFGYRLFRYGSFFKTIIDGIMAYHQEPKNETDREAGKNITLDMREK420

Db361EEFNHWGGEDVFGYRLFRYGSFFKTIIDGIMAYHQEPKNETDREAGKNITLDMREK420

Qy421VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRCDVSALNQTVDVLEVICNDGST480

Db421VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRCDVSALNQTVDVLEVICNDGST480

Qy481DNTLEVINKLYGNPRVRIMSKPNGGIASASNAVSPAKCVYIGQLSDDDYLBPDVAVELC540

Db481DNTLEVINKLYGNPRVRIMSKPNGGIASASNAVSPAKCVYIGQLSDDDYLBPDVAVELC540

Qy541LKEFLKDKTKLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFHFMFTIRAWHL600

Db541LKEFLKDKTKLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFHFMFTIRAWHL600

Qy601TDGFNEKIEANVDYDMFLKSEVKGFKHLNKICYNRVLHGDNTSIKKLGIOKQKHFFVVVN660

Db601TDGFNEKIEANVDYDMFLKSEVKGFKHLNKICYNRVLHGDNTSIKKLGIOKQKHFFVVVN660

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Db661QSLNRQGITTYNYDEFDLDESRYIFNKTAEQEEIDILKDKIIONKOAKIAVSIFYP720

Qy721NTLNLGLVKLNIIIEYNKNIFVIVLHVDKXHLTPDIKKEILAFYHKHQVNILLNNDISYY780

Db721NTLNLGLVKLNIIIEYNKNIFVIVLHVDKXHLTPDIKKEILAFYHKHQVNILLNNDISYY780

Qy781TSNRLIKTEAHLNINKLSQNLNCEYIIIDNHDLSLFVKNDSYAYMKKYDVGMMFSALTH840

Db781TSNRLIKTEAHLNINKLSQNLNCEYIIIDNHDLSLFVKNDSYAYMKKYDVGMMFSALTH840

Qy841DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSCQS900

Db841DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSCQS900

Qy901IDSVPEYNTEDIWFOFALLILEKKTGHVFNKTSITLTYMPWERKLOWTNEQIESAKRGENI960

Db901IDSVPEYNTEDIWFOFALLILEKKTGHVFNKTSITLTYMPWERKLOWTNEQIESAKRGENI960

Qy961PVNKFIIINSITL972

Db961PVNKFIIINSITL972

RESULT 10

US-10-217-613-9

Sequence 9, Application US/10217613

Publication No. US20030113845A1

GENERAL INFORMATION:

APPLICANT: DEANGELIS, PAUL

TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND US

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 35541.081

CURRENT APPLICATION NUMBER: US/10/217,613

CURRENT FILING DATE: 2002-08-12

PRIOR APPLICATION NUMBER: 09/283,402

PRIOR FILING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 60/080,414

PRIOR FILING DATE: 1998-04-02

PRIOR APPLICATION NUMBER: 09/178,851

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 972

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: consensus sequence

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (17)-(17)

OTHER INFORMATION: either Asn, Asp, Glu or Gln

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (62)-(62)

OTHER INFORMATION: either Asn, Asp, Glu or Gln

FEATURE:

US-10-217-613-9

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Qy 61 KEEKVNVCDSPLDIATOLLSSNVKLVLSDESKNTLKNKWLKTEKKSENAEYRAVALVP 120
Db 61 KEEKVNVCDSPLDIATOLLSSNVKLVLSDESKNTLKNKWLKTEKKSENAEYRAVALVP 120
Qy 121 KDFPKDLVLAPLDHVNDFTWYKKRKRGLGKPEHQHVGLSIIVTTFNRPAILSLTACL 180
Db 121 KDFPKDLVLAPLDHVNDFTWYKKRKRGLGKPEHQHVGLSIIVTTFNRPAILSLTACL 180
Qy 181 VNQKTHYPEVIVTDDGSQEDLSPIIROYENKLDIRYVQKONGFOASAARNMGLRLAKY 240
Db 181 VNQKTHYPEVIVTDDGSQEDLSPIIROYENKLDIRYVQKONGFOASAARNMGLRLAKY 240
Qy 241 DFIGLLDCMAPNPLVHVSVAELLEDDDLTIIGPRKYIDTQHIDPKDFLNNASLLESLP 300
Db 241 DFIGLLDCMAPNPLVHVSVAELLEDDDLTIIGPRKYIDTQHIDPKDFLNNASLLESLP 300
Qy 301 EVKTNNSVAAKGEVTSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFAKWLKSGFFD 360
Db 301 EVKTNNSVAAKGEVTSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFAKWLKSGFFD 360
Qy 361 EEPNHWGGEDVEFGYRLFYGSFFKTDGIMAYHQBPPEGKENTDREAGNITLDMREK 420
Db 361 EEPNHWGGEDVEFGYRLFYGSFFKTDGIMAYHQBPPEGKENTDREAGNITLDMREK 420
Qy 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQCVDNALQTVVLEVCICNDGST 480
Db 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQCVDNALQTVVLEVCICNDGST 480
Qy 481 DNTLEVINKLYGNPRVIMSKPENGASNAASVAFKGYIIGOLDSDDYLPDPAVELC 540
Db 481 DNTLEVINKLYGNPRVIMSKPENGASNAASVAFKGYIIGOLDSDDYLPDPAVELC 540
Qy 541 LKEFLKDKTLCACVYTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLCACVYTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIEANVDYDMFLKSEVGKPKHLNKICYNRVLHGDNTSIKKLGIOKKNHFVAVN 660
Db 601 TDGFNEKIEANVDYDMFLKSEVGKPKHLNKICYNRVLHGDNTSIKKLGIOKKNHFVAVN 660
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
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## RESULT 8

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US-10-309-560-8
; Sequence 8, Application US/10309560
; Publication No. US20030235893A1
; GENERAL INFORMATION:
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; APPLICANT: WEIGEL, PAUL H
; APPLICANT: KUMARI, KSHAMA
; TITLE OF INVENTION: HYALURONAN SYNTHASES AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 35541.082
; CURRENT APPLICATION NUMBER: US/10/309,560
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/336,105
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-10-309-560-8
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Query Match 99.9%; Score 5104; DB 4; Length 972;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MNTLSQAIKAYNSNDYQLALKLFKSAEYIGRKIVFQITKCKEKLSAHPSVNSAHSV 60
Qy 61 KEEKVNVCDSPLDIATOLLSSNVKLVLSDESKNTLKNKWLKTEKKSENAEYRAVALVP 120
Db 61 KEEKVNVCDSPLDIATOLLSSNVKLVLSDESKNTLKNKWLKTEKKSENAEYRAVALVP 120
Qy 121 KDFPKDLVLAPLDHVNDFTWYKKRKRGLGKPEHQHVGLSIIVTTFNRPAILSLTACL 180
Db 121 KDFPKDLVLAPLDHVNDFTWYKKRKRGLGKPEHQHVGLSIIVTTFNRPAILSLTACL 180
Qy 181 VNQKTHYPEVIVTDDGSQEDLSPIIROYENKLDIRYVQKONGFOASAARNMGLRLAKY 240
Db 181 VNQKTHYPEVIVTDDGSQEDLSPIIROYENKLDIRYVQKONGFOASAARNMGLRLAKY 240
Qy 241 DFIGLLDCMAPNPLVHVSVAELLEDDDLTIIGPRKYIDTQHIDPKDFLNNASLLESLP 300
Db 241 DFIGLLDCMAPNPLVHVSVAELLEDDDLTIIGPRKYIDTQHIDPKDFLNNASLLESLP 300
Qy 301 EVKTNNSVAAKGEVTSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFAKWLKSGFFD 360
Db 301 EVKTNNSVAAKGEVTSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFAKWLKSGFFD 360
Qy 361 EEPNHWGGEDVEFGYRLFYGSFFKTDGIMAYHQBPPEGKENTDREAGNITLDMREK 420
Db 361 EEPNHWGGEDVEFGYRLFYGSFFKTDGIMAYHQBPPEGKENTDREAGNITLDMREK 420
Qy 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQCVDNALQTVVLEVCICNDGST 480
Db 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQCVDNALQTVVLEVCICNDGST 480
Qy 481 DNTLEVINKLYGNPRVIMSKPENGASNAASVAFKGYIIGOLDSDDYLPDPAVELC 540
Db 481 DNTLEVINKLYGNPRVIMSKPENGASNAASVAFKGYIIGOLDSDDYLPDPAVELC 540
Qy 541 LKEFLKDKTLCACVYTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLCACVYTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
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Db 601 TDGFNEKIEANVDYDMFLKSEVGKPKHLNKICYNRVLHGDNTSIKKLGIOKKNHFVAVN 660
Qy 661 QSLNRQGITYYNYDEPDDLDESRRKIFNKTAEYQEBIDILKDIKIIQNKDIAVSI FYP 720
Db 661 QSLNRQGITYYNYDEPDDLDESRRKIFNKTAEYQEBIDILKDIKIIQNKDIAVSI FYP 720
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Db 721 NTNLGLVKKLNIIIEYNKNI FVILVHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY 780
Qy 781 TSNRLIKTEAHLNINKLSQLNLCBYIIPDNHDSL FVKND SYAYMKKYDVGMNFSAL TH 840
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Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIDNHDLSLFVKNDSYAYMKKYDVGWFSALTH 840  
Qy 841 DWIEKINAHPPFKKLIKTYFNDNDLKSVMNVKGSQGMFTYALAHELLTTIKEVITSCQS 900  
Db 841 DWIEKINAHPPFKKLIKTYFNDNDLKSVMNVKGSQGMFTYALAHELLTTIKEVITSCQS 900  
Qy 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKTSITLTYPWVERKLOWTNEQIESAKRGENI 960  
Db 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKTSITLTYPWVERKLOWTNEQIESAKRGENI 960  
Qy 961 PVNKFIIINSITL 972  
Db 961 PVNKFIIINSITL 972  
RESULT 6  
US-10-172-527-10  
; Sequence 10, Application US/10172527  
; Publication No. US20030092118A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H  
; APPLICANT: Kumari, Kahama  
; APPLICANT: Deangelis, Paul  
; TITLE OF INVENTION: HYALURONAN SYNTHASE GENES AND EXPRESSION THEREOF IN BACILLUS SUBTILIS  
; FILE REFERENCE: 3554.048  
; CURRENT APPLICATION NUMBER: US/10/172.527  
; CURRENT FILING DATE: 2002-06-13  
; PRIOR FILING DATE: 2002-06-13  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 60/297,744  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 09/469,200  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 10  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: pasteurella multocida  
US-10-172-527-10  
Query Match 99.9%; Score 5104; DB 4; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNTLSQAIKAYNSNDYQALALFEKSABYGRKIVEFOITKCKEKLSAHPSVNSAHLVSN 60  
Db 1 MNTLSQAIKAYNSNDYQALALFEKSABYGRKIVEFOITKCKEKLSAHPSVNSAHLVSN 60  
Qy 61 KEEKNVNCDSPLDIATQALLSNVKKLVLSDEKNTLKNKKLLTEKKSENAEVRVALVP 120  
Db 61 KEEKNVNCDSPLDIATQALLSNVKKLVLSDEKNTLKNKKLLTEKKSENAEVRVALVP 120  
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Qy 181 VNQKTHYPFEVITVDGQEDLSPIRQYENKLDIYVRQKNGFQASAARNMGLRLAKY 240  
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Db 241 DFIGLLDCDMPNLVWHSYVAELLEDDDLTIIGPRKIDTOHIDPKDFLNNASLESILP 300  
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Db 301 EVKTTNSVAAKGEVTVSLDWRLEQFEKTENLRSDSPFRFFAAGNVFAKWLKNSGFFD 360  
Qy 361 BEFNHWGGEDEVFGYRLFRYGSPFKTIDGIMAYHQBPCKENETDREAGKNTILDMREK 420

Db 361 BEFNHWGGEDEVFGYRLFRYGSPFKTIDGIMAYHQBPCKENETDREAGKNTILDMREK 420  
Qy 421 VPYIYRKLLPIEDSHINRVPPLSVIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480  
Db 421 VPYIYRKLLPIEDSHINRVPPLSVIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480  
Qy 481 DNTLEVINKLYGNPRVRJMSKPNKGGTASASNAVFAKGYIYIQLDSDDDYLEPDAVELC 540  
Db 481 DNTLEVINKLYGNPRVRJMSKPNKGGTASASNAVFAKGYIYIQLDSDDDYLEPDAVELC 540  
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Db 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNNPEFSREKLTTAMIAHFRMFTIRAWHL 600  
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Db 601 TDGFNEKIEANAVDYDMPLKLSYGVGKFHNLKICYNRVLHGDNTSIKKLGIOKKNHFVVVN 660  
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Db 661 QSLNRQGITYYNYDEPDLDDESRYIFNKTAEQEEDILDKIKIQNKDAKIAVSIFYP 720  
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Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIDNHDLSLFVKNDSYAYMKKYDVGWFSALTH 840  
Qy 841 DWIEKINAHPPFKKLIKTYFNDNDLKSVMNVKGSQGMFTYALAHELLTTIKEVITSCQS 900  
Db 841 DWIEKINAHPPFKKLIKTYFNDNDLKSVMNVKGSQGMFTYALAHELLTTIKEVITSCQS 900  
Qy 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKTSITLTYPWVERKLOWTNEQIESAKRGENI 960  
Db 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKTSITLTYPWVERKLOWTNEQIESAKRGENI 960  
Qy 961 PVNKFIIINSITL 972  
Db 961 PVNKFIIINSITL 972  
RESULT 7  
US-10-326-185-95  
; Sequence 95, Application US/10326185  
; Publication No. US20030175902A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloma, Alan  
; APPLICANT: Behr, Regine  
; APPLICANT: Widner, William  
; APPLICANT: Tang, Maria  
; APPLICANT: Sternberg, David  
; APPLICANT: Brown, Stephen  
; TITLE OF INVENTION: Methods for Producing Hyaluronan In a Recombinant Host Cell  
; FILE REFERENCE: 10241.200-US  
; CURRENT APPLICATION NUMBER: US/10/326.185  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US 60/342,644  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 95  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-10-326-185-95  
Query Match 99.9%; Score 5104; DB 4; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNTLSQAIKAYNSNDYQALALFEKSABYGRKIVEFOITKCKEKLSAHPSVNSAHLVSN 60

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Db 61 KEEKVNCDSPLDIATQALLSNVKKLVLSDEKNTLKNKWLTEKKSENAEVRVALVP 120
Qy 121 KDPKDLVLAPLPHVNDFTWYKRRKRLGKPEHGHVGLSIIVTTFNRPAILSIITLACL 180
Db 121 KDPKDLVLAPLPHVNDFTWYKRRKRLGKPEHGHVGLSIIVTTFNRPAILSIITLACL 180
Qy 181 VNQKTHYPEVIVTDDGSQEDLSPIIRQYENKLDIRYVRQKONGFOASARNMGLRLAKY 240
Db 181 VNQKTHYPEVIVTDDGSQEDLSPIIRQYENKLDIRYVRQKONGFOASARNMGLRLAKY 240
Qy 241 DFIGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTOHIIDPKDFLNNASLESPL 300
Db 241 DFIGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTOHIIDPKDFLNNASLESPL 300
Qy 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSDSPFRFAAGNAVAFKAKWLKNGSGFPD 360
Db 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSDSPFRFAAGNAVAFKAKWLKNGSGFPD 360
Qy 361 EEFNHWGGEDVEFGYRLFRYGSFFKTDIGIMAYHQBPPGKENETDREAGKNITLDMREK 420
Db 361 EEFNHWGGEDVEFGYRLFRYGSFFKTDIGIMAYHQBPPGKENETDREAGKNITLDMREK 420
Qy 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Db 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Qy 481 DNTLEVINKLIGNNPRVIMSKPENGGLASASNAVSAFAGYIIGOLDSDDDYLEPDAVELC 540
Db 481 DNTLEVINKLIGNNPRVIMSKPENGGLASASNAVSAFAGYIIGOLDSDDDYLEPDAVELC 540
Qy 541 LKEFLKDKTLACVYTTNRNPNVPGSLIANGYNWPFESREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLACVYTTNRNPNVPGSLIANGYNWPFESREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIEHAVDYDMFLKSEVGKPKHLNKICYNRVLHGDNTSIKKLGIGKQKHFVAVN 660
Db 601 TDGFNEKIEHAVDYDMFLKSEVGKPKHLNKICYNRVLHGDNTSIKKLGIGKQKHFVAVN 660
Qy 661 QSLNRQGITVYNDDEFDLDESRYIFNKTAEVQEBIDILKDIKIQNDKAKTAVSIFYP 720
Db 661 QSLNRQGITVYNDDEFDLDESRYIFNKTAEVQEBIDILKDIKIQNDKAKTAVSIFYP 720
Qy 721 NTNLGLVKKLNNIIEYNKNI FVILVHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY 780
Db 721 NTNLGLVKKLNNIIEYNKNI FVILVHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY 780
Qy 781 TSRLIKTEAHLNINKLSQLNLCYIIPDNHDSL FVKNDSYAYMKKYDVGMNFSALTH 840
Db 781 TSRLIKTEAHLNINKLSQLNLCYIIPDNHDSL FVKNDSYAYMKKYDVGMNFSALTH 840
Qy 841 DWTKEINAHPPPKLTKTYFNDNDLKSMMVKGASQGMWMTYALAHELLTIIEKVITSCOS 900
Db 841 DWTKEINAHPPPKLTKTYFNDNDLKSMMVKGASQGMWMTYALAHELLTIIEKVITSCOS 900
Qy 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKGENI 960
Db 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKGENI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
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## RESULT 5

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US-09-879-959-10
; Sequence 10, Application US/09879959
; Patent No. US20020160489A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H
; APPLICANT: Kumari, Kshama
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION
; TITLE OF INVENTION: IN BACILLUS SUBTILIS
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; FILE REFERENCE: 3554.049
; CURRENT APPLICATION NUMBER: US/09/879,959
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/469,200
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 972
; TYPE: PRT
; ORGANISM: pasteurella multocida
US-09-879-959-10
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 KEEKVNCDSPLDIATQALLSNVKKLVLSDEKNTLKNKWLTEKKSENAEVRVALVP 120
Db 61 KEEKVNCDSPLDIATQALLSNVKKLVLSDEKNTLKNKWLTEKKSENAEVRVALVP 120
Qy 121 KDPKDLVLAPLPHVNDFTWYKRRKRLGKPEHGHVGLSIIVTTFNRPAILSIITLACL 180
Db 121 KDPKDLVLAPLPHVNDFTWYKRRKRLGKPEHGHVGLSIIVTTFNRPAILSIITLACL 180
Qy 181 VNQKTHYPEVIVTDDGSQEDLSPIIRQYENKLDIRYVRQKONGFOASARNMGLRLAKY 240
Db 181 VNQKTHYPEVIVTDDGSQEDLSPIIRQYENKLDIRYVRQKONGFOASARNMGLRLAKY 240
Qy 241 DFIGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTOHIIDPKDFLNNASLESPL 300
Db 241 DFIGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTOHIIDPKDFLNNASLESPL 300
Qy 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSDSPFRFAAGNAVAFKAKWLKNGSGFPD 360
Db 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSDSPFRFAAGNAVAFKAKWLKNGSGFPD 360
Qy 361 EEFNHWGGEDVEFGYRLFRYGSFFKTDIGIMAYHQBPPGKENETDREAGKNITLDMREK 420
Db 361 EEFNHWGGEDVEFGYRLFRYGSFFKTDIGIMAYHQBPPGKENETDREAGKNITLDMREK 420
Qy 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Db 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Qy 481 DNTLEVINKLIGNNPRVIMSKPENGGLASASNAVSAFAGYIIGOLDSDDDYLEPDAVELC 540
Db 481 DNTLEVINKLIGNNPRVIMSKPENGGLASASNAVSAFAGYIIGOLDSDDDYLEPDAVELC 540
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; Sequence 2, Application US/10642248		
; Publication No. US20040132143A1		
; GENERAL INFORMATION:		
; APPLICANT: DeAngelis, Paul		
; APPLICANT: Jing, Wei		
; TITLE OF INVENTION: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND METHO		
; FILE REFERENCE: 3554.097		
; CURRENT APPLICATION NUMBER: US/10/642.248		
; CURRENT FILING DATE: 2003-08-15		
; PRIOR FILING DATE: 2002-08-16		
; PRIOR APPLICATION NUMBER: 60/404,356		
; PRIOR FILING DATE: 2003-06-18		
; PRIOR APPLICATION NUMBER: 60/491,362		
; PRIOR FILING DATE: 2003-07-31		
; PRIOR APPLICATION NUMBER: 10/195,908		
; PRIOR FILING DATE: 2002-07-15		
; PRIOR APPLICATION NUMBER: 09/437,277		
; PRIOR FILING DATE: 1999-11-01		
; PRIOR APPLICATION NUMBER: 60/107,929		
; PRIOR FILING DATE: 1998-11-11		
; PRIOR APPLICATION NUMBER: 09/283,402		
; PRIOR FILING DATE: 1999-04-01		
; PRIOR APPLICATION NUMBER: 60/080,414		
; PRIOR FILING DATE: 1998-04-02		
; PRIOR APPLICATION NUMBER: 09/842,484		
; PRIOR FILING DATE: 2001-04-25		
; PRIOR APPLICATION NUMBER: 60/199,538		
; PRIOR FILING DATE: 2000-04-25		
; Remaining Prior Application data removed - See File Wrapper or PALM.		
; NUMBER OF SEQ ID NOS: 71		
; SOFTWARE: PatentIn version 3.1		
; SEQ ID NO 2		
; LENGTH: 972		
; TYPE: PRT		
; ORGANISM: Pasteurella multocida		
US-10-642-248-2		
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Best Local Similarity 100.0%; Pred. No. 0;		
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db	1	MNTLSQAIKAYNSNDYQALALFKESABIIYGRKIVEFOITKCKEKLSAHPSVNSAHLVSN 60
Qy	61	KEEKVNVCDSPLDIATQALLSNVKKVLVSDSEKNTLKNKKWLLTEKKSENAEVRVALVP 120
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Qy	121	KDPKDLVLAPLDHVNDFTWYKKRKRGLIPEHQHVGSLSIIVTFNRPAILSLITLACL 180
Db	121	KDPKDLVLAPLDHVNDFTWYKKRKRGLIPEHQHVGSLSIIVTFNRPAILSLITLACL 180
Qy	181	VNQKTHYFEFVITDDGSOEDLSPIIROYENKLDIYVRQKDNFGQSAARNMGLRLAKY 240
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Qy	241	DFIGLLDCDMANPLVWHSYVAELLEDLTTIGPRKYIDTQHIIDPKDFLNNASLESIP 300
Db	241	DFIGLLDCDMANPLVWHSYVAELLEDLTTIGPRKYIDTQHIIDPKDFLNNASLESIP 300
Qy	301	EVKVTNSVAAKGEVTVSLDWRLEQEKTEKNTLRLSDSPRRFFAAGNVAFPAKWLKNSGFPD 360
Db	301	EVKVTNSVAAKGEVTVSLDWRLEQEKTEKNTLRLSDSPRRFFAAGNVAFPAKWLKNSGFPD 360
Qy	361	BEFNHWGGBDVEFGYRLFRYGSFFKTIIDGIMAYHQEPPEKNETDREAGKNTITLDMREK 420
Db	361	BEFNHWGGBDVEFGYRLFRYGSFFKTIIDGIMAYHQEPPEKNETDREAGKNTITLDMREK 420
Qy	421	VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCINDGST 480

Db	421	VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCINDGST 480
Qy	481	DNTLEVINKLYGNPRVRITMSKPNKGASASNAAVSFAGYYIIGQLSDDDYDLPDAVELC 540
Db	481	DNTLEVINKLYGNPRVRITMSKPNKGASASNAAVSFAGYYIIGQLSDDDYDLPDAVELC 540
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Db	541	LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Qy	601	TGDFNEKIENAVDDYDMFLKLSYGVKPKHLNKICYNRVLHGDNTSIKKLGIOKKNHFVVVN 660
Db	601	TGDFNEKIENAVDDYDMFLKLSYGVKPKHLNKICYNRVLHGDNTSIKKLGIOKKNHFVVVN 660
Qy	661	QSLNRQGITTYNYDEDFDDESRYIFNKTAEOEEDILKDIKIQNKDAKIAVSIFYP 720
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Db	721	NTLNGLVKLNIIIEYNKNI FVIVLHVDKNHLPDIKKEILAFYKHQVNLNNDISYY 780
Qy	781	TSNRLIKTEAHLNINKLSQNLNCEYIIIPDNHDSLPVKNDISYAYMKKYDVGMMFSALTH 840
Db	781	TSNRLIKTEAHLNINKLSQNLNCEYIIIPDNHDSLPVKNDISYAYMKKYDVGMMFSALTH 840
Qy	841	DWIEKINAHPPFKKLITKYTFNDNDLSKMNKYGASQGMFMTYALAHELLTTIKEVITSCQS 900
Db	841	DWIEKINAHPPFKKLITKYTFNDNDLSKMNKYGASQGMFMTYALAHELLTTIKEVITSCQS 900
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Db	901	IDSVPENTEDINWQFALLILEKKTGHVFNKTSITLYMPWERKLOWTNEQIESAKRGNI 960
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Db	961	PVKNFIINSITL 972
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; Sequence 9, Application US/11109855		
; Publication No. US20050202540A1		
; GENERAL INFORMATION:		
; APPLICANT: Weigel, Paul H.		
; APPLICANT: DeAngelis, Paul		
; APPLICANT: Kumari, Keshava		
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof		
; FILE REFERENCE: 3554.011		
; CURRENT APPLICATION NUMBER: US/11/109,855		
; CURRENT FILING DATE: 2005-04-20		
; PRIOR APPLICATION NUMBER: US 09/178,851		
; PRIOR FILING DATE: 1998-10-26		
; PRIOR APPLICATION NUMBER: US 60/064,435		
; PRIOR FILING DATE: 1997-10-31		
; NUMBER OF SEQ ID NOS: 10		
; SOFTWARE: PatentIn version 3.1		
; SEQ ID NO 9		
; LENGTH: 972		
; TYPE: PRT		
; ORGANISM: Pasteurella Multocida		
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Query Match 100.0%; Score 5108; DB 6; Length 972;		
Best Local Similarity 100.0%; Pred. No. 0;		
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db 421 VPYIYRKLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Qy 481 DNTLEVINKLYGNPRVIRMSKNGGASASNAASVFAKYYIGQLSDDDYLEPDAVELC 540
Db 481 DNTLEVINKLYGNPRVIRMSKNGGASASNAASVFAKYYIGQLSDDDYLEPDAVELC 540
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Qy 721 NTNLGLVKLNNIIEYNKNI FVIVLHVDKNHLPDIIKKEILAFYHKHQNVLNNDISYY 780
Db 721 NTNLGLVKLNNIIEYNKNI FVIVLHVDKNHLPDIIKKEILAFYHKHQNVLNNDISYY 780
Qy 781 TSRLIKTEAHLNINKLSQNLNCEYIIFDNHDSL FVKND SYAYMKKYDVGWNFSA LTH 840
Db 781 TSRLIKTEAHLNINKLSQNLNCEYIIFDNHDSL FVKND SYAYMKKYDVGWNFSA LTH 840
Qy 841 DWIEKINAHPPFKLKITFYNDNDLKSMMVKGASQGMFTYALAHELLTTIIKEVITSCOS 900
Db 841 DWIEKINAHPPFKLKITFYNDNDLKSMMVKGASQGMFTYALAHELLTTIIKEVITSCOS 900
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPMPWERKLOWTNEQIESAKRGENI 960
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Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
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Query Match 100.0%; Score 5108; DB 4; Length 972;  
Best Local Similarity 100.0%; Pred. No. 0;

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Qy 61 KEEKVNVCDSPLDIATQLLLSNVKLVLSDESKNTLKNKWLKTEKXSENAEVRVALVP 120
Db 61 KEEKVNVCDSPLDIATQLLLSNVKLVLSDESKNTLKNKWLKTEKXSENAEVRVALVP 120
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Db 121 KOPPKDLVLAPLDDHVNDSYTKRKRKRLGIRPEHGHVGLSIIIVTFNRPAILSIITLACL 180
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Qy 781 TSRLIKTEAHLNINKLSQNLNCEYIIFDNHDSL FVKND SYAYMKKYDVGWNFSA LTH 840
Db 781 TSRLIKTEAHLNINKLSQNLNCEYIIFDNHDSL FVKND SYAYMKKYDVGWNFSA LTH 840
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Db 841 DWIEKINAHPPFKLKITFYNDNDLKSMMVKGASQGMFTYALAHELLTTIIKEVITSCOS 900
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Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPMPWERKLOWTNEQIESAKRGENI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
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RESULT 3  
US-10-642-248-2

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:04:42 ; Search time 119 Seconds  
(without alignments)  
3412.858 Million cell updates/sec

Title: US-10-642-248-2  
Perfect score: 5108  
Sequence: 1 MNTLSQAIKAYNSDYQAL.....SAKGENIPVKNKFIINSITL 972

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.Main.\*  
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4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5108	100.0	972	4	US-10-011-768B-9
2	5108	100.0	972	4	US-10-011-771B-9
3	5108	100.0	972	4	US-10-642-248-2
4	5108	100.0	972	6	US-11-109-855-9
5	5104	99.9	972	3	US-09-879-959-10
6	5104	99.9	972	4	US-10-172-527-10
7	5104	99.9	972	4	US-10-326-185-95
8	5104	99.9	972	4	US-10-309-560-8
9	5104	99.9	972	6	US-11-096-190-9
10	4733	92.7	972	4	US-10-217-613-9
11	4502.5	88.1	965	3	US-09-842-484A-4
12	4502.5	88.1	965	4	US-10-217-613-3
13	4502.5	88.1	965	4	US-10-217-613-8
14	4502.5	88.1	965	4	US-10-642-248-4
15	4502.5	88.1	965	5	US-10-197-153-3
16	4502.5	88.1	965	6	US-11-042-530-4
17	4490.5	87.9	965	3	US-09-842-484A-2
18	4490.5	87.9	965	4	US-10-184-485-3
19	4490.5	87.9	965	6	US-11-042-530-2
20	3697	72.4	703	4	US-10-217-613-1
21	3697	72.4	703	4	US-10-217-613-7
22	3697	72.4	703	4	US-10-642-248-9
23	3697	72.4	703	5	US-10-197-153-1
24	3673.5	71.9	702	4	US-10-184-485-1
25	2209	43.2	686	4	US-10-216-289-2
26	2209	43.2	686	4	US-10-216-289-4
27	332.5	6.5	648	4	US-10-282-122A-47924

ALIGNMENTS

RESULT 1

US-10-011-768B-9  
; Sequence 9, Application US/10011768B  
; Publication No. US20030073221A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Kumari, Kshama  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/10/011.768B  
; CURRENT FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: Pastuerella Multocida  
US-10-011-768B-9

Query Match	100.0%	Score 5108	DB 4	Length 972
Best Local Similarity	100.0%	Pred. No. 0		
Mismatches	0	Conservative	0	Indels 0; Gaps 0
QY	1	MNTLSQAIKAYNSDYQALFKPKSAIYGRKIVEFOITCKEKLKLSAHPNSAHLSPV	60	
Db	1	MNTLSQAIKAYNSDYQALFKPKSAIYGRKIVEFOITCKEKLKLSAHPNSAHLSPV	60	
QY	61	KEEKVNCDSPLDITATOLLNSVKKLVLSDEKNTLKNWKLTKKSENAEVRVALVP	120	
Db	61	KEEKVNCDSPLDITATOLLNSVKKLVLSDEKNTLKNWKLTKKSENAEVRVALVP	120	
QY	121	KDFPKDLVLAPLPHVNDFTWYKKRKLGIKPEHQHVGLSIIVTTFNRPAILSTLACL	180	
Db	121	KDFPKDLVLAPLPHVNDFTWYKKRKLGIKPEHQHVGLSIIVTTFNRPAILSTLACL	180	
QY	181	VNQKTHYFEVITDDGSQEDLSPIIROYENKLDIYRQKNGFQASAAARMGLRLAKY	240	
Db	181	VNQKTHYFEVITDDGSQEDLSPIIROYENKLDIYRQKNGFQASAAARMGLRLAKY	240	
QY	241	DFIGLLDCDMPNPLWVHSYVAELLEDLTIIGPKYIDTQHDIDPKDFLNNASLESUP	300	
Db	241	DFIGLLDCDMPNPLWVHSYVAELLEDLTIIGPKYIDTQHDIDPKDFLNNASLESUP	300	
QY	301	EYKTNNSVAAKGEQTVSLDWRLEQPEKTENLRSLSPFRFFAAGNVFAFKWLNKSGPFD	360	

Db	1480	GATAATACCTAGAGTGATCAATAGCTTTATGGTAATAATCCTAGGGTAGCCATCATG	1539
Qy	1501	TCATAACCAATGGCGGAATAGCTCAGCATCAAAATGACGCGGTTCCTTTGCTAAAGGT	1560
Db	1540	TCATAACCAATGGCGGAATAGCTCAGCATCAAAATGACGCGGTTCCTTTGCTAAAGGT	1599
Qy	1561	TATTACATTGGCGAGTTAGATTAGATGATTATCTTGAGCCTGATGAGTTGAACCTGTGT	1620
Db	1600	TATTACATTGGCGAGTTAGATTAGATGATTATCTTGAGCCTGATGAGTTGAACCTGTGT	1659
Qy	1621	TTAAAAGAAATTTTAAAGAGATAAAACGCTAGCTTGTCTTTATACCACTAATAGAAAAGTC	1680
Db	1660	TTAAAAGAAATTTTAAAGAGATAAAACGCTAGCTTGTCTTTATACCACTAATAGAAAAGTC	1719
Qy	1681	AATCCGATGGTACCTTAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTCCAGGAGAAAA	1740
Db	1720	AATCCGATGGTACCTTAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTCCAGGAGAAAA	1779
Qy	1741	CTCACACGCTATGATTGCTCACCCTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTTA	1800
Db	1780	CTCACACGCTATGATTGCTCACCCTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTTA	1839
Qy	1801	ACTGATCGATTCAATGAAAAAATTTGAAAATGCGGTAGCATATGACATGTTTCTCCAAACTC	1860
Db	1840	ACGATCGATTCAATGAAAAAATTTGAAAATGCGGTAGCATATGACATGTTTCTCCAAACTC	1899
Qy	1861	AGTGAAGTTGGAAATTTAAACATCTTTAATAAATCTGCTATTAACCGTGTATTACATGGT	1920
Db	1900	AGTGAAGTTGGAAATTTAAACATCTTTAATAAATCTGCTATTAACCGTGTATTACATGGT	1959
Qy	1921	GATTAACATCAATTAAGAAACTTGGCAATTCBAAGGAAAAACCAATTTTGTGTAGTCAAT	1980
Db	1960	GATTAACATCAATTAAGAAACTTGGCAATTCBAAGGAAAAACCAATTTTGTGTAGTCAAT	2019
Qy	1981	CAGTCATTAAATAGACAAGGCATACTTATTATTAATTTATGACCAATTTTGATTTAGAT	2040
Db	2020	CAGTCATTAAATAGACAAGGCATACTTATTATTAATTTATGACCAATTTTGATTTAGAT	2079
Qy	2041	GAAGTAGAAGTATATTTTCAATAAACCCTGGAATATCAAGAAGAGATTGATCTTTA	2100
Db	2080	GAAGTAGAAGTATATCTTCAATAAACCCTGGAATATCAAGAAGAGATTGATCTTTA	2139
Qy	2101	AAAGATATTAATATCCAGAAATAAGATGCCAAATCCGAGTCAGTATTTTATATCCC	2160
Db	2140	AAAGATCTTAACTCATTTCAAAATTAAGATGCCAAATCCGAGTCAGTATTTTATATCCC	2199
Qy	2161	AATACATTAAACGGCTTAGTGAAAAAATTAACAATATTATTGAATATAATAAAAAATA	2220
Db	2200	AATACATTAAACGGCTTAGTGAAAAAATTAACAATATTATTGAATATAATAAAAAATA	2259
Qy	2221	TTGGTTATTGTTTACATGTTGATGAAATCATCTTACACAGATATCAAAAAAGAAATA	2280
Db	2260	TTGGTTATTGTTTACATGTTGATGAAATCATCTTACACAGATATCAAAAAAGAAATA	2319
Qy	2281	CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC	2340
Db	2320	TTGGCTTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC	2379
Qy	2341	ACGAGTAAATGATTAAATAAAACCTGAGCGCATTTTAAGTAATATAATAAATTAAGTCAG	2400
Db	2380	ACGAGTAAATGATTAAATAAAACCTGAGCGCATTTTAAGTAATATAATAAATTAAGTCAG	2439
Qy	2401	TTAAATCTAAATTTGTAATACATCATTTTGTGATTAATCATGACGCTTATCGTTAAAAAT	2460
Db	2440	TTAAATCTAAATTTGTAATACATCATTTTGTGATTAATCATGACGCTTATCGTTAAAAAT	2499
Qy	2461	GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTTCTCAGCATTAACACAT	2520
Db	2500	GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTTCTCAGCATTAACACAT	2559
Qy	2521	GATTGGATCGAGAAAAATCAATGCGCATCCACATTTTAAAAAGCTCATTTAAAACTTATTTT	2580

Search completed: January 8, 2006, 17:27:54  
Job time : 2080 secs

Db	2560	GATTGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAAAGCTGATTTAAACCTATTTT	2619
Qy	2581	AATGACAATGACTTTAAAAGATGATGAATGTGAAGGGGCGCATCAAGGTATGTTTATGACG	2640
Db	2620	AATGACAATGACTTTAAAAGATGATGAATGTGAAGGGGCGCATCAAGGTATGTTTATGACG	2679
Qy	2641	TATGCGCTAGCGCATGAGCTTCTGACGATTATTTAAAAGAGTCAATCACATCTTCCCAATCA	2700
Db	2680	TATGCGCTAGCGCATGAGCTTCTGACGATTATTTAAAAGAGTCAATCACATCTTCCCAATCA	2739
Qy	2701	ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCAATTTGCACTTTTAATC	2760
Db	2740	ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCAATTTGCACTTTTAATC	2799
Qy	2761	TTAGAAAAGAAAAACCGGCCATGTATTTAATAAAACATCGACCTGACTTATATGCGCTTGG	2820
Db	2800	TTAGAAAAGAAAAACCGGCCATGTATTTAATAAAACATCGACCTGACTTATATGCGCTTGG	2859
Qy	2821	GAACGAAAAATTACAATGGACAAATGAACAAATTTGAAAGTGCAAAAAGAGAGGAAAAATATA	2880
Db	2860	GAACGAAAAATTACAATGGACAAATGAACAAATTTGAAAGTGCAAAAAGAGGAAAAATATA	2919
Qy	2881	CCTGTTAAACAAAGTTTCATTTAATAATAGTATTAACCTCTATATAA	2920
Db	2920	CCGTTTAAACAAAGTTTCATTTAATAATAGTATTAACCTCTATATAA	2959

QY 1921 GATAACACATCAATTAGAACTTGGCAATCAAAAGAAAAACCATTGTTGTAGTCAAT 1980  
DB 1921 GATAACACATCAATTAGAACTTGGCAATCAAAAGAAAAACCATTGTTGTAGTCAAT 1980  
QY 1981 CAGTCATTAAATAGACAAGGCATCACTTATTATATATATGACGAATTTGATGATTTAGAT 2040  
DB 1981 CAGTCATTAAATAGACAAGGCATCACTTATTATATATGACGAATTTGATGATTTAGAT 2040  
QY 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
DB 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
QY 2101 AAAGATATTAATCAATCCAGATTAAGATGCCAAAATCGCAGTCAGTATTTTATCCC 2160  
DB 2101 AAAGATATTAATCAATCCAGATTAAGATGCCAAAATCGCAGTCAGTATTTTATCCC 2160  
QY 2161 AATACATTAAACGGCTTAGTGAAAAAATCTAAACAATATATTGAAATATAATAAAAAATATA 2220  
DB 2161 AATACATTAAACGGCTTAGTGAAAAAATCTAAACAATATATTGAAATATAATAAAAAATATA 2220  
QY 2221 TTCGTTATTGTTCTACATGTTGATGAAGATCATCTTTACACAGATATCAAA 2271  
DB 2221 TTCGTTATTGTTCTACATGTTGATGAAGATCATCTTTACACAGATATCTAA 2271

RESULT 15  
US-09-842-484A-3  
; Sequence 3, Application US/09842484A  
; Publication No. US20030104601A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL L.  
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME  
; FILE REFERENCE: 4605.003  
; CURRENT APPLICATION NUMBER: US/09/842,484A  
; CURRENT FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2979  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-09-842-484A-3

Query Match 77.6%; Score 2266.4; DB 3; Length 2979;  
Best Local Similarity 86.4%; Pred. No. 0;  
Matches 2523; Conservative 0; Mismatches 376; Indels 21; Gaps 1;

QY 1 ATGAATACATTATCAAGCAATAAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
DB 61 ATGAATACATTATCAAGCAATAAAAGCATATAACAGCAATGACTATGAATTAGCACTC 120  
QY 61 AAATATTGTAAGTTCGGCGGAATCTATGACGGAATAATTTGTCGAATTTCAAAATTACC 120  
DB 121 AAATATTGTAAGTTCGCTGAAACCTACGGCGGAAAAATCGTTGAAATTCAAAATATC 180  
QY 121 AAATGCAAGAAAAAATCTCTCAGCACATCTCTGTTAAATTCAGCACATCTTTCTGTAAT 180  
DB 181 AAATGTAAGAAAAAATCTCTGACCAATTC-----TTATGTAAGT 219  
QY 181 AAAGAGAAAAAGTCAATGTTTCGATAGTTCGGTAGATATTGCAACACAACTGTTACTTT 240  
DB 220 GAAGATAAAAAAACAAGTGTTCGATAGTCTCATTTAGATATCGCAACACAGCTCTTACTT 279  
QY 241 TCCAACGTAATAAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATCG 300  
DB 280 TCCAACGTAATAAATTAATCTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATCG 339  
QY 301 AAATGCTCACTGAGAAGAAATCTGAAAAATGCGAGGTGAAGCGGTGCGCCCTTGTACCA 360  
DB 340 AAATCTATCACTGGGAAAAAATCGGAGAACGCAAGAAATCAGAAAGGTGGAATAGTACCC 399

QY 361 AAAGATTTTCCCAAGATCTGGTTTATAGCCCTTTACCTGATCATGTAAATGATTTTACA 420  
DB 400 AAAGATTTTCTAAAGATCTTGTCTTGTCTCCATTGCGCAGATCATGTAAATGATTTTACA 459  
QY 421 TGGTACAAAAAGCGAAAGAAAGACTTGGCATATAAAACCTGAACATCAACATGTTGGTCTT 480  
DB 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATAAAGCCTGTAAATAAGAAATATCGGTCTT 519  
QY 481 TCTATTATCGTTACAAACATTCATCGACCGACCAAGCAATTTTATCGATTACATTAGCCTGTTTA 540  
DB 520 TCTATTATTAATTCCTACATTTAATCGTAGGCGGTATTTTAGATATAACGTTAGCCCTGTTG 579  
QY 541 GTAAACCAAAAAACACATTTACCCCTTTTCAAGTTATCGTGACAGATGATGGTAGTCAGAA 600  
DB 580 GTCAATCAGAAAAACAACACTACCCATTTGAAAGTCGTTGTGACAGATGATGGTAGTAAGAA 639  
QY 601 GATCTATCACCGATCATTTGCGCAATATGAAATAAATTTGATATTTGCTAGCTAGCAGACAA 660  
DB 640 AACTTACTTACCATTTGTCAAAAAATACGAAACAAAAAATGACATAAAGATATGTAAAGACAA 699  
QY 661 AAAGATTAACGGTTTTCAGCCAGTCCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 720  
DB 700 AAAGATTTATGGATATCAATTTGTGTGACAGTCAGAACTTAGGTTTTACGTACAGCAAAAGTAT 759  
QY 721 GACTTTATTGGCTTACTCGACTGTGATATGCGCAAAATCCATTTATGGGTTTCATTCTTTAT 780  
DB 760 GATTTTGTCTCGATTTCTAGACTGCGATATGSCACCAACAATTTATGSGTTTCATTCTTAT 819  
QY 781 GTTCAGAGCTATTAGAAAGATGATTTAAACAATCATTTGTTCCAGAAAAATATACATCGAT 840  
DB 820 CTTACAGAACTATTAGAAAGACAATGATTTGTTTAAATTTGACCTTAGAAAAATATGTGGAT 879  
QY 841 ACACAACATATTGACCCAAAGACTTCTTAATAATACGCGAGTTTTCGTTGAATCATTTACCA 900  
DB 880 ACTCATATATTACCGCAGAAACAATCTTAAACGATCCATTAATTAATAGAATCACTACTCT 939  
QY 901 GAAGTGAACCAATATAGTGTTCGCCAAAAAGGGAAGAAAGAGTTCTCTCGATTGG 960  
DB 940 GAAACCGCTACAATATACATCTCTCGATTACATCAAAAGGAAATATATCGTTGATTGG 999  
QY 961 CGCTTAGAACAAATTCGAAAAACAGAAATCTCCGTTATCCGATTCGCTTCGCTTTCCGTTT 1020  
DB 1000 AGATTAGAACATTTCAAAAAACCGATAATCTACGCTATGTGATTTCTCCGTTTCGTTAT 1059  
QY 1021 TTTGCGCGGGTAATGTTGCTTTTCGTAATAAATGGCTAAATAATCGGTTTCTTTTCGAT 1080  
DB 1060 TTTAGTTTCGCGTAATGTTGCAATTTCTAAAGAAATGGCTTAAATAAGTAGTGGTTGCTGAT 1119  
QY 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGGTTATTCGCTTAC 1140  
DB 1120 GAAGAAATTTAATCATTTGGGGGGCGAGATGTAGAAATTTGGTTACAGATTTATTTGCCAAA 1179  
QY 1141 GGTAGTTTCTTTTAAACCTATTGATGGCAATTTATGGCTTACCATTCAAGAGCCACAGGTAAA 1200  
DB 1180 GCGTGTCTTTTCAGAGTAATTTGACGGCGGAATGGCATACCATCAAGAAACCACTCGTAAA 1239  
QY 1201 GAAATGAAACCGATCGTGAACGGGAAAAAATATTTAGCTCGATTTATGAGAGAAAG 1260  
DB 1240 GAAATGAAACAGACCGGAAAGCTGTGTAAGAGTATTTACGCTTAAATTTGTGAAAGAAAAG 1299  
QY 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGATATCAATAGAGTACCT 1320  
DB 1300 GTACCTTTACATCTATAGAAAGCTTTTACCAATAGAAAGTTCACATATTCATAGAAATACCT 1359  
QY 1321 TTAGTTTCAATTTTATATCCAGCTTTAATCTGTGCAAACTATTTCAACGTTGCGGTAGAT 1380  
DB 1360 TTAGTTTCTATTATATCCCGCTTATAACTGTGCAAAATTAATTTCAAAGATGTGTAGAT 1419  
QY 1381 AGTCAGTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTCAACA 1440  
DB 1420 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAAACGATGGTCAACA 1479  
QY 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTTATGTTAAATAATCTCTAGGAGTACGCATCATG 1500

;  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 09/842,484  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 2271  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-10-642-248-20

Query Match 77.78; Score 2269.4; DB 7; Length 2271;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGATACATATATCACAGCAATAAAGCATATAACAGCAATGACATATCAATTAGCACTC	60
Db	1	ATGATACATATATCACAGCAATAAAGCATATAACAGCAATGACATATCAATTAGCACTC	60
Qy	61	AAATATTGAAAGTCGGCGGAAATCTATGACGGAATAATTTGTGAATTTCAAATPACC	120
Db	61	AAATATTGAAAGTCGGCGGAAATCTATGACGGAATAATTTGTGAATTTCAAATPACC	120
Qy	121	AAATGCAAGAAAGAACTCTCAGACATCTCTGTTAAATTCAGACATCTTCTGTAAAT	180
Db	121	AAATGCAAGAAAGAACTCTCAGACATCTCTGTTAAATTCAGACATCTTCTGTAAAT	180
Qy	181	AAAGAAAGAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACAACTGTTACTT	240
Db	181	AAAGAAAGAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACAACTGTTACTT	240
Qy	241	TCCAACTGAAAGAAATTTAGTACTTTCTGACTCGGAAAGAAACACGTTAAAGAAATGG	300
Db	241	TCCAACTGAAAGAAATTTAGTACTTTCTGACTCGGAAAGAAACACGTTAAAGAAATGG	300
Qy	301	AAATGCTCTAGAGAGAAATCTGAAATGCGGAGGTAGAGCGGTGCGCCCTGTACCA	360
Db	301	AAATGCTCTAGAGAGAAATCTGAAATGCGGAGGTAGAGCGGTGCGCCCTGTACCA	360
Qy	361	AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTAAATGATTTTACA	420
Db	361	AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTAAATGATTTTACA	420
Qy	421	TGGTACAAAAGCGAAAGAAAGACTTTGGCATATAAACCTGAAACATCAACATGTTGGTCTT	480
Db	421	TGGTACAAAAGCGAAAGAAAGACTTTGGCATATAAACCTGAAACATCAACATGTTGGTCTT	480
Qy	481	TCTATTATCGTTACAAACATTCATCGACCGCAATTTTATCGATTACATTAGCCTGTTTA	540
Db	481	TCTATTATCGTTACAAACATTCATCGACCGCAATTTTATCGATTACATTAGCCTGTTTA	540
Qy	541	GTAACCAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	600
Db	541	GTAACCAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	600
Qy	601	GATCTATCAGCGATCATTCGCAATATGAAATTAATTTGGATATTCGCTACGTCAGACAA	660
Db	601	GATCTATCAGCGATCATTCGCAATATGAAATTAATTTGGATATTCGCTACGTCAGACAA	660
Qy	661	AAAGATACGGTTTTCAGCCNGTCCGCTCGGAATATGGATTACGCTTAGCAAAATAT	720
Db	661	AAAGATACGGTTTTCAGCCNGTCCGCTCGGAATATGGATTACGCTTAGCAAAATAT	720
Qy	721	GACTTTTATGGCTTACTCGACTGTGATATGCGCCAAATCCATTTATGGGTTTCAATCTTAT	780
Db	721	GACTTTTATGGCTTACTCGACTGTGATATGCGCCAAATCCATTTATGGGTTTCAATCTTAT	780
Qy	781	GTTCCAGAGCTATTAGAGATGATGATTTAAACAATCATTTGTTCCAGAAATAATCATCGAT	840
Db	781	GTTCCAGAGCTATTAGAGATGATGATTTAAACAATCATTTGTTCCAGAAATAATCATCGAT	840

Qy	841	ACACAAATATTTGACCCAAAAGACTTCTTAAATAACGCGAGTTTGTCTTGAATCATTACCA	900
Db	841	ACACAAATATTTGACCCAAAAGACTTCTTAAATAACGCGAGTTTGTCTTGAATCATTACCA	900
Qy	901	GAAGTGAAGAACCAATTAATAGTGTGTCGCGCAAAAGGGAAGGAACAGTTTCTCTGGATTGG	960
Db	901	GAAGTGAAGAACCAATTAATAGTGTGTCGCGCAAAAGGGAAGGAACAGTTTCTCTGGATTGG	960
Qy	961	CGCTTAGAACCAATTCGAAAAAAGCAGAAAAATCTCCGCTTATCCGATTCCGCTTTCCGTTTT	1020
Db	961	CGCTTAGAACCAATTCGAAAAAAGCAGAAAAATCTCCGCTTATCCGATTCCGCTTTCCGTTTT	1020
Qy	1021	TTTTCGCGCGGGTAATGTTGCTTTTCGCTTAAAAATGCTTAAATTAATTCGCTTTCTTTGAT	1080
Db	1021	TTTTCGCGCGGGTAATGTTGCTTTTCGCTTAAAAATGCTTAAATTAATTCGCTTTCTTTGAT	1080
Qy	1081	GAGGAATTAATCACTCGGGGTGAGAGATGGAATTTGGATATCGCTTATTTCCGTTAC	1140
Db	1081	GAGGAATTAATCACTCGGGGTGAGAGATGGAATTTGGATATCGCTTATTTCCGTTAC	1140
Qy	1141	GGTAGTTTCTTTAAAACTATTGATGCATTTATGCGCTTACCATCAAGAGCCACCAAGTAAA	1200
Db	1141	GGTAGTTTCTTTAAAACTATTGATGCATTTATGCGCTTACCATCAAGAGCCACCAAGTAAA	1200
Qy	1201	GAAAAATGAACCCGATCGTGAAGCGGGAAGAAATATTAATCGCTCGATATTTATGAGAGAAAAG	1260
Db	1201	GAAAAATGAACCCGATCGTGAAGCGGGAAGAAATATTAATCGCTCGATATTTATGAGAGAAAAG	1260
Qy	1261	GTCCCTTATATCTATAGAAAATCTTTTACCAATAGAGATTTCCGATATCAATAGATGACCT	1320
Db	1261	GTCCCTTATATCTATAGAAAATCTTTTACCAATAGAGATTTCCGATATCAATAGATGACCT	1320
Qy	1321	TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTTCAACGTTGCGTAGAT	1380
Db	1321	TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTTCAACGTTGCGTAGAT	1380
Qy	1381	AGTGCACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGTTCAACA	1440
Db	1381	AGTGCACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGTTCAACA	1440
Qy	1441	GATAATACCTTTAGAGTGATCAATAGCTTTTATGGTAATTAATCTCTAGGTTACGATCATG	1500
Db	1441	GATAATACCTTTAGAGTGATCAATAGCTTTTATGGTAATTAATCTCTAGGTTACGATCATG	1500
Qy	1501	TCTAAACCAAAATCGCGAATAGCTCAGCATCAAAATGCGAGCTTCTTTTGTCTTAAAGGT	1560
Db	1501	TCTAAACCAAAATCGCGAATAGCTCAGCATCAAAATGCGAGCTTCTTTTGTCTTAAAGGT	1560
Qy	1561	TATTACATTTGGGAGTTTAGATTCAGATGATTTATCTTGGAGCTGATGCGATTTGAATCTGTT	1620
Db	1561	TATTACATTTGGGAGTTTAGATTCAGATGATTTATCTTGGAGCTGATGCGATTTGAATCTGTT	1620
Qy	1621	TTAAAGAAATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACATTAATAGAAAACGTC	1680
Db	1621	TTAAAGAAATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACATTAATAGAAAACGTC	1680
Qy	1681	AATCCGAGTGGTAGCTTAATCGCTTAATGTTTACAAATTTGGCCAGAAATTTTCCAGAGAAAA	1740
Db	1681	AATCCGAGTGGTAGCTTAATCGCTTAATGTTTACAAATTTGGCCAGAAATTTTCCAGAGAAAA	1740
Qy	1741	CTCACACCGCTATGATTTGCTCACCCTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTTA	1800
Db	1741	CTCACACCGCTATGATTTGCTCACCCTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTTA	1800
Qy	1801	ACTGATGGATTCATTAAGAAAAATTTGAAATTTGCGGTAGACTATGACATGTTCTCAAACTC	1860
Db	1801	ACTGATGGATTCATTAAGAAAAATTTGAAATTTGCGGTAGACTATGACATGTTCTCAAACTC	1860
Qy	1861	AGTCAGTTTGGAAAAATTTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT	1920
Db	1861	AGTCAGTTTGGAAAAATTTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT	1920

Db 1180 GGCTGTTTTTCAGAGTAATTTGACGGCGGAATGCCATCCATCAAGAACCCACCTGGTAAA 1239  
Qy 1201 GAAATGAAACCGATCGTGAACGGGAAAAATATATACGCTCGATATATATGAGAGAAAAAG 1260  
Db 1240 GAAATGAAACGAGAACCGAGCTGGTAAAAAGTATTACGCTTAAAAATTTGTGAAAGAAAAAG 1299  
Qy 1261 GTCCCTTATATCTATAGAAAACCTTTACCANTAGAGATTCGCCATATCAATAGAGTACCT 1320  
Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAGATTCACATATTCATAGAAATACCT 1359  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAAAGCTTGGGTAGAT 1380  
Db 1360 TTAGTTTCTATTTATATCCCGCTTATAACTGTGCAAAATATATTCAAAGATGTGTAGAT 1419  
Qy 1381 AGTCACCTGAATCAGACTGTTGTTGATCTCGAGGTTGTAATTTGPAACGATGGTTCAACA 1440  
Db 1420 AGTGCTCTTAATCAAACCTGTTGTGATCTCGAGGTTGTAATTTGPAACGATGGTTCAACA 1479  
Qy 1441 GATATACCTTAGAAGTATCAATTAAGCTTTATGTTAATATCTTAGGGTACGCATCATG 1500  
Db 1480 GATAATACCTTAGAAGTATCAATTAAGCTTTATGTTAATATCTTAGGGTACGCATCATG 1539  
Qy 1501 TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGACGCGTTCTTTTTCCTAAAGGT 1560  
Db 1540 TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGACGCGTTCTTTTTCCTAAAGGT 1599  
Qy 1561 TATTACATTTGGGCGAGTTAGATTCAGATGATTTATCTTGAGCCTGATGCGAGTTGAACTGTGT 1620  
Db 1600 TATTACATTTGGGCGAGTTAGATTCAGATGATTTATCTTGAGCCTGATGCGAGTTGAACTGTGT 1659  
Qy 1621 TTAAGAAGATTTTAAAAAGATAAAACGTCAGCTTGTGTTTATACCACTAAATAGAAACGTC 1680  
Db 1660 TTAAGAAGATTTTAAAAAGATAAAACGTCAGCTTGTGTTTATACCACTAAATAGAAACGTC 1719  
Qy 1681 AATCCGGATGGTAGCTTAATGCTAAATGTTACAAATGSCCAGAAATTTTCAGAGAAAAA 1740  
Db 1720 AATCCGGATGGTAGCTTAATGCTAAATGTTACAAATGSCCAGAAATTTTCAGAGAAAAA 1779  
Qy 1741 CTCACACGGCTATGATTTGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTTGGCATTTA 1800  
Db 1780 CTCACACGGCTATGATTTGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTTGGCATTTA 1839  
Qy 1801 ACTGATGATTCATGAAAGAAATGAAATGCGGTAGACTATGACATGTTCTCCTCAACCTC 1860  
Db 1840 ACGGATGGATTTAACGAAAAATTTGAAACCGCGGTGATATGACATGTTCTCTTAAACTC 1899  
Qy 1861 AGTGAAGTTGGAATTTTAAACATCTTAATAAAATCTGTATAACCGGTGTTATACATGTT 1920  
Db 1900 AGTGAAGTTGGAATTTTAAACATCTTAATAAAATCTGTATAACCGGTGTTATACATGTT 1959  
Qy 1921 GATAACACATCAATTAAGAAACCTTGCGCATTTCAAAAGAAAAACCATTTGTTGTAGTCAAT 1980  
Db 1960 GATAACACATCAATTAAGAAACCTTGCGCATTTCAAAAGAAAAACCATTTGTTGTAGTCAAT 2019  
Qy 1981 CAGTCATTAATATAGAACGGCATATCTTATTAATATATGACGAATTTGATGATTTAGAT 2040  
Db 2020 CAGTCATTAATATAGAACGGCATATCTTATTAATATATGACAAAAATTTGATGATTTAGAT 2079  
Qy 2041 GAAAGTAGAAGTATATCTTCAATTAACCGCTGAAATATCAAGAGAGAGATTCATATCTTA 2100  
Db 2080 GAAAGTAGAAGTATATCTTCAATTAACCGCTGAAATATCAAGAGAGAGATTCATATCTTA 2139  
Qy 2101 AAGAGATTTAAAAATCATCCAGAAATAAGATGCGCAAAATCGCAGTCAAGTATTTTATCCC 2160  
Db 2140 AAGATCTTAACCTCAATCAAAATAAGATGCCAAATCGCAGTCAAGTATTTTCTATCCC 2199  
Qy 2161 AATACATTAACCGCTTAGTGAAGAAACCTTAAACAATATTTATGAAATATATAAAATATA 2220  
Db 2200 AATACATTAACCGCTTAGTGAAGAAACCTTAAACAATATTTATGAAATATATAAAATATA 2259  
Qy 2221 TTGCGTATTTGTTCTACATGTTGATAGAAATCATCTTTACACCCAGATATCAAAAAAGAAATA 2280  
Db 2260 TTGCGTATTTATTTCTACATGTTGATAGAAATCATCTTTACACCCAGATATCAAAAAAGAAATA 2319

Qy 2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTTAC 2340  
Db 2320 TTGCTTCTTATCATAGCACCAAGTGATATTTTACTAAATATGATATGATATTTAC 2379  
Qy 2341 ACAGATTAATAGATTTAAATAAAACCTGAGCGCATTTAAAGTAAATATTAATAAATTAAGTCAG 2400  
Db 2380 ACAGATTAATAGACTAAATAAAACCTGAGGCACATTTAAAGTAAATAATAATAAATTAAGTCAG 2439  
Qy 2401 TTAATCTAAATTTGTGAATACATCATTTTGTGATATCATGACGCTTATTCGTTTAAATAT 2460  
Db 2440 TTAATCTAAATTTGTGAATACATCATTTTGTGATATCATGACGCTTATTCGTTTAAATAT 2499  
Qy 2461 GACAGCTATGCTTATATGAAAAATATGATCTCGGCATGAATTTCTCAGCATTTAACACAT 2520  
Db 2500 GACAGCTATGCTTATATGAAAAATATGATCTCGGCATGAATTTCTCAGCATTTAACACAT 2559  
Qy 2521 GATTGGATTCGAGAAAAATCAATGCGCATCCACCATTTTAAAAAGCTCATTTAAAACTTATTTT 2580  
Db 2560 GATTGGATTCGAGAAAAATCAATGCGCATCCACCATTTTAAAAAGCTGATTTAAAACTTATTTT 2619  
Qy 2581 AATGACATGACTTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTTATGACG 2640  
Db 2620 AATGACATGACTTTAAAGAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTTATGAA 2679  
Qy 2641 TATCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTATCAACATCTTGCCAGTCA 2700  
Db 2680 TATCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTATCAACATCTTGCCAGTCA 2739  
Qy 2701 ATTGATAGTGTCCAGAAATATAAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAAATC 2760  
Db 2740 ATTGATAGTGTCCAGAAATATAAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAAATC 2799  
Qy 2761 TTAGAAAAGAAAAACGGCCATGTTTAAATAAACATCGACCTGACTTATATGCTTTGG 2820  
Db 2800 TTAGAAAAGAAAAACGGCCATGTTTAAATAAACATCGACCTGACTTATATGCTTTGG 2859  
Qy 2821 GAACGAAATTTACATTTGACAAATGAAACAAATGAAAGTGCAGAAAGAGGAGAAATATA 2880  
Db 2860 GAACGAAATTTACATTTGACAAATGAAACAAATTTCAAGTGCAGAAAGAGGAGAAATATC 2919  
Qy 2881 CCTGTTAAACAAGTTTCATTATTATAGTATAACTCTATAAA 2920  
Db 2920 CCCGTTAAACAAGTTTCATTATTATAGTATAACGCTATAAA 2959

## RESULT 14

US-10-642-248-20  
; Sequence 20, Application US/10642248  
; Publication No. US20040132143A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Jing, Wei  
; TITLE OF INVENTION: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND METH  
; TITLE OF INVENTION: MAKING AND USING SAME  
; FILE REFERENCE: 3554.097  
; CURRENT APPLICATION NUMBER: US/10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414

Qy	2341	ACGAGTAATAGATTAAATAAAAACTGAGCGCAATTAAGTAATAATTAATAAATTAAGTCAG	2400
Db	2380	ACGAGTAATAGACTAATAAAAACTGAGCGCAATTAAGTAATAATTAATAAATTAAGTCAG	2439
Qy	2401	TTAAATCTAAATGTGTAATCATCATATTTTGTGTAATCATGACAGCCATTCGTTAAATAAT	2460
Db	2440	TTAAATCTAAATGTGTAATCATCATATTTTGTGTAATCATGACAGCCATTCGTTAAATAAT	2499
Qy	2461	GACAGCTATGCTTATATGAAAAATATGATGCGCATGAATTTCTCAGCATTAACACAT	2520
Db	2500	GACAGCTATGCTTATATGAAAAATATGATGCGCATGAATTTCTCAGCATTAACACAT	2559
Qy	2521	GATTGGATCGAGAAAAATCAATGCGCATCCACCAATTTAAAAAGGCTCATTTAAAACTTATTTT	2580
Db	2560	GATTGGATCGAGAAAAATCAATGCGCATCCACCAATTTAAAAAGGCTCATTTAAAACTTATTTT	2619
Qy	2581	AATGACAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTTATGACG	2640
Db	2620	AATGACAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTTATGACG	2679
Qy	2641	TATCGCTAGCGCATGAGCTTCTGACGATTAATTAAGAAGTCATCACATCTTGCCAGTCA	2700
Db	2680	TATCGCTAGCGCATGAGCTTCTGACGATTAATTAAGAAGTCATCACATCTTGCCAGTCA	2739
Qy	2701	ATTGATAGTGTCCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACATTTTAAATC	2760
Db	2740	ATTGATAGTGTCCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACATTTTAAATC	2799
Qy	2761	TTAGAAAAGAAAAACCGGCCATGTATTTAATAAAACATCGACCCCTGACTTATATGCTTTGG	2820
Db	2800	TTAGAAAAGAAAAACCGGCCATGTATTTAATAAAACATCGACCCCTGACTTATATGCTTTGG	2859
Qy	2821	GAACGAAATTTACAAATCGACAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTC	2880
Db	2860	GAACGAAATTTACAAATCGACAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTC	2919
Qy	2881	CCGTAAACAAAGTTCAATTAATTAATAGTAACTCTATAAA	2920
Db	2920	CCGTAAACAAAGTTCAATTAATTAATAGTAACTCTATAAA	2959

RESULT 13  
US-11-042-530-1  
; Sequence 1, Application US/11042530  
; Publication No. US20050164984A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL L.  
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME  
; FILE REFERENCE: 4605.007  
; CURRENT APPLICATION NUMBER: US/11/042,530  
; CURRENT FILING DATE: 2005-01-24  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/842,484  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patencin version 3.1  
; SEQ ID NO 1  
; LENGTH: 2979  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-042-530-1

Query Match 77.8%; Score 2271.2; DB 10; Length 2979;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;

Qy	1	ATGATACATTTATCACAGCAATTAAGCATATTAACAGCAATGACTATCAATTAAGTACGCTC	60
Db	61	ATGATACATTTATCACAGCAATTAAGCATATTAACAGCAATGACTATCAATTAAGTACGCTC	120
Qy	61	AAATTTATTTGAAAAGTCGGCGGAAATCTATGGAACGAAAAATTTGTTGAATTTTCAAAATTACC	120

Db	121	AAATTTATTTGAGAGTCTGCTGAAACCTAGCGGCGAAAAATCGTTGAATTTCCAAATATTC	180
Qy	121	AAATGCAAGAAAAAATCTCTCAGCACATCTCTCTGTTAAATTCAGCACATCTTTCTTGTAAT	180
Db	181	AAATGTAAGAAAAAATCTCTGACCAATTC-----TTATGTAAGT	219
Qy	181	AAAGAGAAAAAAGTCAATGTTTGGGATAGTCCGTTAGATATTTGCAACACAACTGTTACTT	240
Db	220	GAAGATAAAAAAACAAGTGTTCGATAGTCTCATTTAGATATCGCAACACACAGCTCTTACTT	279
Qy	241	TCCAAAGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAAGCTTTAAAAAATAAATGG	300
Db	280	TCCAAAGTAAAAAATTTAACTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG	339
Qy	301	AAATTTGCTCACTCAGAGAAATCTGAAAAATCGGAGGTAAAGCGCTCGCCCTTGTACCA	360
Db	340	AAATCTATCACTCGGAAAAAATCGAGNACGAGAAATCAGAAAGGTGGAACACTAGTACCC	399
Qy	361	AAAGATTTTCCCAAAGATCTGGTTTGTAGCCCTTTTACCTGATCATGTTAATGATTTTACA	420
Db	400	AAAGATTTTCTCTAAAGATCTGTTTCTGCTCCATTCGAGATCATGTTAATGATTTTACA	459
Qy	421	TGCTACAAAAAGGCAAGAAAAAGACTTGGCATTAACCTGAAACATCAACATGTTGCTCTT	480
Db	460	TGCTACAAAAATCGAAAAAAGCTTAGGTATAAAGCCTGTAAATAAGAAATATCGGCTCTT	519
Qy	481	TCATTATTCGTTACAAACATTCATCGACCAAGCAATTTATCGATTACATTAGCCTGTTTA	540
Db	520	TCATTATTAATCTCACTTAATCGTAGCGGTATTTTAGATATAAGCTTAGCCTGTTTG	579
Qy	541	GTAAACCAAAAAACACATTAACCGTTTGAAGTTATCGTGAAGATGTTAGTGTAGTACGAA	600
Db	580	GTCAATCAGAAAAAACAACACTACCAATTTGAAGTCGTTGTCAGATGATGTTAGTAAAGAA	639
Qy	601	GATCTATCACCGATCATTCGCCAATATGAAAAATAAATTGGATATTCGCTAGCTCAGACAA	660
Db	640	AACCTTACTTACCATTGTGCAAAATAAGCAACAAACCTTGACATAAAGTATGTAAAGCAA	699
Qy	661	AAAGATAACCGTTTCAAGCCAGTGCCTCGGAATAATGGGATTTACGCTTAGCAAAAATAT	720
Db	700	AAAGATTAAGATATCAATTTGTGTGAGTACAGAACTTAGGTTTACGTACAGCAAGTAT	759
Qy	721	GACTTTATTTGCTTACTCGATGTGATATCGGCCAAATCAATATGGGTTTCACTTTAT	780
Db	760	GATTTTGTCTCGATTTCTAGACTGCGATATGCGCACCAACAATTTATGGGTTTCACTTTAT	819
Qy	781	GTTGACAGCTTATTAAGATGATGATTTAAACATCAATTCGTTCCAGAAATATCATCGAT	840
Db	820	CTTACAGAACTATTAGAAGCAATGATTTGTTTAAATTTGACCTAGACCTAGAAAATATGTTGAT	879
Qy	841	ACACAACATATTGACCCCAAAAGACTCTTAAATAACCGAGTTTGTCTTGAATCATTTACCA	900
Db	880	ACTCATTAATTTATCCGAGAAACAACTCTTAACGATCCATATTTAATAGATCACTACCT	939
Qy	901	GAAGTGAAGAAACCAATAATAGTGTTCGCGCAAAAGGGGAGGAAACAGTTTCTCGATTGG	960
Db	940	GAACCCGCTACAAATAACAATCTCTCGATTACATCAAAAGGAAATATATCTGTTGATTGG	999
Qy	961	CGCTTAGAACAAATTCGAAAAAACHAGAAATCTCGCTTATCCGATTTCCGCTTTCCGTTT	1020
Db	1000	AGATTAGAACATTTCAAAAAAACCAGATAATCTACGCTATGTGATTTCCGTTTCCGTTAT	1059
Qy	1021	TTTTCGGCGGTATGTTGCTTTTCGCTAAAAAATGGCTTAATAAATCCGTTTCTTTTGAT	1080
Db	1060	TTTTCGGCGGTATGTTGCTTTTCGCTAAAAAATGGCTTAATAAATGGCTTTGTTGTTGAT	1119
Qy	1081	GAGGAATTTAATCACTGGGTGGAGAAAGATGTGGAATTTGGATATCGCTTATTCGTTTAC	1140
Db	1120	GAAGAAATTTAATCACTGGGTGGAGAAAGATGTAGAAATTTGGTTACAGATTTATTTGCCAAA	1179
Qy	1141	GGTATGTTTCTTTAAAACTATTGATGGCATTTATGCGCTTACCATCAAGAGCCACAGGTAAA	1200

181 AAAATGTAAGAAAAAAGCTCTCGACCAATTC-----TTATGTAAAGT 219 Db  
181 AAAGAAGAAAAAGTCAATGTTTGGGATAGTCGCTTAGATATATGCAACAACTGTACTT 240 Qy  
220 GAAGATAAAAAACAAGTGTGGATAGTCAATTAGATATCGCAACACAGCTCTACTT 279 Db  
241 TCCAACGTAAAAAATTAAGTACTTCTGACTCGGAAAAAACAAGTTAAAAAATAAATGG 300 Qy  
280 TCCAACGTAAAAAATTAAGTACTTCTGACTCGGAAAAAACAAGTTAAAAAATAAATGG 339 Db  
301 AAAATGCTCACTGAGAAGAAATCTGAAATGCGAGGTAAAGACGCTCGCCTCTGTACCA 360 Qy  
340 AAAATCTACTCTGGAAGAAAAATCGGAGAAACGAGAAATCAGAAAGGTGGAACGTAGTACCC 399 Db  
361 AAAAGATTTTCCAAAGATCTGGTTTTTAGCGCCTTTACCTGATCATGTTAAATGATTTTACA 420 Qy  
400 AAAGATTTTCTTAAGATCTTGTCTCTGCTCCATTTGCCAGATCATGTTAAATGATTTTACA 459 Db  
421 TGGTACAAAAAGCGAAAAAGAAAGACTTGGGCATAAAACCTGAAACATCAACATGTTGGTCTT 480 Qy  
460 TGGTACAAAAATCGAAAAAAGAGCTTAGGTATAAAGCCCTGTAATAAAGAAATATCGGTCTT 519 Db  
481 TCTATTATCGTTACAACTCAATCGAACCGCAATTTTATCGATTACATTTAGCCTGTTTFA 540 Qy  
520 TCTATTATTTTCTTACATTTAATCGTAGCCGTATTTTAGATATTAACGTTAGCCTGTTTG 579 Db  
541 GTAAACCAAAAAACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600 Qy  
580 GTCAATCAGAAAAAACAATACCCATTTGNAAGTCGTTGTTGACAGATGATGGTAGTAAGNA 639 Db  
601 GATCTATCACCGGATCATTTGCGCAATATAGAAAAATTAATGGATATTTGCTACGTCAGACAA 660 Qy  
640 AACTTACTTACCATTGTGCAAAAAATACGAAACAAAACCTTGACATAAAGTATGTAAGACAA 699 Db  
661 AAAGATACCGTTTTCAAGCCAGTCGCGCTCGAATATGGGATTTAGCTTAGCAAAATAT 720 Qy  
700 AAAGATTTAGGATATCAATTTGTGTGCGAGTCAGAAACCTTAGGTTTTACGTACAGCAAAAGTAT 759 Db  
721 GACTTTTATGGCTTACTGACGTGTGATATGGCGCAAAATCCATTTATGGGTTCAATCTTTAT 780 Qy  
760 GATTTTGTCTCGAATCTAGACTGCGATATGGCACCAACAATTTATGGGTTCAATCTTTAT 819 Db  
781 GTTCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT 840 Qy  
820 CTTACAGAACTATTAGAGACAATGATATGTTTTAAATGGACCTAGAAAAATATGTGGAT 879 Db  
841 ACACAACATATTGACCCAAAGACTTCTTAATACGCGAGTTGCTTGAATCATTTACCA 900 Qy  
880 ACTCATAATATTACCGCAGAACAAATTCCTTAAACGATCCCATTTTAAATAGAATCACATACCT 939 Db  
901 GAAGTGMAAACCAATAATAGTGTGGCGCAAAAGGGGAAGGAACAGTTTCTCTGGATTGG 960 Qy  
940 GAAACGGCTACAATAACAATCCTTCGATTACATCAAAAGGAAATATATCGTTGATTTGG 999 Db  
961 CGCTTAGAAACAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTTCCGCTTTCCGTTTT 1020 Qy  
1000 AGATTAGAACATTTCAAAAAAACCAGATAATCTACGCTATGTGATTTCTCCGTTTCCGTTAT 1059 Db  
1021 TTTGGCGGGTAATGTTGCTTTCGCTAAAAAATGCTTAATAATGCTCGGTTTCTTTGAT 1080 Qy  
1060 TTTGTTGCGGGTAATGTTGCAATTTCTAAAGAAATGSGCTAAATAAAGTAGTTGGTTTCGAT 1119 Db  
1081 GAGGAATTTAATCACTGGGTCGAGAGATGTGGAATTTGGATATCGCTTATTTCCGTTAC 1140 Qy  
1120 GAAGAAATTTAATCAATTTGGGGGGCGGAAGATGAGAATTTGGTTACGATTTATTTGCCAAA 1179 Db  
1141 GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCCTTACCATCAAGAGCCACCGGTAAA 1200 Qy  
1180 GCGTGTTTTTTACAGATTAATTGACGCGGGAATGGCCATCCATCAAGAAACCAACCTGGTAAA 1239 Db  
1201 GAAATGAAACCGATCGTGAAGCGGGAATAATTTTACGCTCGATATTATGAGAGAAAG 1260 Qy

1240 GAAATGAAACAGAAACGGAAGCTGGTAAAAAGTATTACGCTTAAAAATTTGTGAAAGAAAAG 1299 Db  
1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTTCGCATATCAATAGAGTACCT 1320 Qy  
1300 GTACCTTTACATCTATAGAAAGCTTTTACCAATAGAAGATTTCACATATTTCATAGAAATACCT 1359 Db  
1321 TTAGTTTCAATTTTATATCCCAAGCTTTATAAATGTCGCAAACTATATTCAACGTTTGCCTAGAT 1380 Qy  
1360 TTAGTTTCTATTATATCCCGCTTTATAAATGTCGCAAAATATTATCAAGATGTTGTAGAT 1419 Db  
1381 AGTCACCTGAATCAGACTGTTTGTGATCTCGAGGTTTGTATTGTTAAACGATGGTTCAACA 1440 Qy  
1420 AGTCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTGTTAAACGATGGTTCAACA 1479 Db  
1441 GATTAATCCTTTAGAGTGATCAATAAGCTTTTATGGTAAATATCTTAGGGTAGCATCATG 1500 Qy  
1480 GATAATACCTTTAGAAGTGATCAATAAGCTTTTATGGTAAATATCTTAGGGTAGCATCATG 1539 Db  
1501 TCTAAACCAAAATGCGGAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTCTAAAGGT 1560 Qy  
1540 TCTAAACCAAAATGCGGAAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTCTAAAGGT 1599 Db  
1561 TATTACATTTGGCGAGTTTAGATTTCAGATGATTATCTTGAGCCTGATGCAAGTTGAACTGTGT 1620 Qy  
1600 TATTACATTTGGCGAGTTTAGATTTCAGATGATTATCTTGAGCCTGATGCAAGTTGAACTGTGT 1659 Db  
1621 TTAAAGAAATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACTTAATAGAAACGTC 1680 Qy  
1660 TTAAAGAAATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACTTAATAGAAACGTC 1719 Db  
1681 AATCGGATGTGAGCTTAATCGTTAACTGCTAACTGCGCAGAAATTTTTCAGGAGAAAAA 1740 Qy  
1720 AATCGGATGTGAGCTTAATCGTTAACTGCTAACTGCGCAGAAATTTTTCAGGAGAAAAA 1779 Db  
1741 CTCACACGCTATGATTTGCTCACCACCTTTAGAATTTTTCAGGATTTAGAGCTTTGGCATTTA 1800 Qy  
1780 CTCACACGCTATGATTTGCTCACCACCTTTAGAATTTTTCAGGATTTAGAGCTTTGGCATTTA 1839 Db  
1801 ACTGATGATTTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAACCTC 1860 Qy  
1840 ACGGATGATTTTAAACGAAAAATTTGAAACCGCGGTGATTTAGACATGTTCTCTTAAACCTC 1899 Db  
1861 AGTGAAGTTGAAAAATTTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTTTACATGCT 1920 Qy  
1900 AGTGAAGTTGAAAAATTTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTTTACATGCT 1959 Db  
1921 GATAACACATCAATTTAAGAAACTTTGGCATTTCAAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980 Qy  
1960 GATAACACATCAATTTAAGAAACTTTGGCATTTCAAAAAGAAAAACCAATTTTGTGTAGTCAAT 2019 Db  
1981 CAGTCATTTAAATAGACAAGGCAATACCTTATTATAATTTATGACGAATTTGATGATTTAGAT 2040 Qy  
2020 CAGTCATTTAAATAGACAAGGCAATCAATTTATTATAATTTATGACAAAATTTGATGATTTAGAT 2079 Db  
2041 GAAAGTGAAGATGATTTTTCATATAAACCGCTGAATATCAAGAAGAGATTTGATATCTTTA 2100 Qy  
2080 GAAAGTGAAGATGATTTTTCATATAAACCGCTGAATATCAAGAAGAAATTTGATATCTTTA 2139 Db  
2101 AAAGATATTTAAATCATCCAGAAATTAAGATGCAAAAATCGCAGTCAGTATTTTTTATCCC 2160 Qy  
2140 AAAGATCTTAACTCAATTTCAAAATAAGATGCAAAAATCGCAGTCAGTATTTTTTATCCC 2199 Db  
2161 AATAATTTAAACCGCTTAGTGAAGAAAACTAAACAATTTATTGAAATATTAATAAATAATA 2220 Qy  
2200 AATAATTTAAACCGCTTAGTGAAGAAAACTAAACAATTTATTGAAATATTAATAAATAATA 2259 Db  
2221 TTTGCTTATTTGTTCTACATGTTGATGAATCATCTTTACACAGATATCAAAAAGAAAAATA 2280 Qy  
2260 TTTGCTTATTTTCTACATGTTGATGAAGATCATCTTTACACAGATATCAAAAAGAAAAATA 2319 Db  
2281 CTAGCCTTCTATCATATAAACATCAAGTGAATTTTTTACTAAATTAATGATATCTCATATTAC 2340 Qy  
2320 TTGGCTTCTTCTATCATATAAGCACCAGTGAATATTTTTTACTAAATAATGACATCTCATATTAC 2379 Db

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Qy 1261 GTCCTTATCTATAGAAAACCTTTTACCAATAGAGATTGCGATATCAATAGAGTACCT 1320
Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAGATTACATATTCATAGAAATACCT 1359
Qy 1321 TTAGTTTCAATTTATATCCAGCTTTTAACTGTCGCAAACTATATTTCAACGTTGGGTAGAT 1380
Db 1360 TTAGTTTCTATTTATATCCCGCTTTATAACTGTGCAAAATATATATTCAAAGATGTTGTAGAT 1419
Qy 1381 AGTCACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGCTAAACGATGGTTCAACA 1440
Db 1420 AGTCTCTTAATCAAACTGTTGTGCTGATCTCGAGGTTTGTATTTGCTAAACGATGGTTCAACA 1479
Qy 1441 GATAATACCTTTAGAAAGTATCAATTAAGCTTTATGCTTAATATCTCCTAGGATCGCATG 1500
Db 1480 GATAATACCTTTAGAAAGTATCAATTAAGCTTTATGCTTAATATCTCCTAGGATCGCATG 1539
Qy 1501 TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATCGAGCGGTTCTTTTGTCTAAAGGT 1560
Db 1540 TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATCGAGCGGTTCTTTTGTCTAAAGGT 1599
Qy 1561 TATTACATTTGGGAGTTAGATTGATTCAGATGATTATCTTGAGCCTGATGCAAGTTGAACCTGTG 1620
Db 1600 TATTACATTTGGGAGTTAGATTGATTCAGATGATTATCTTGAGCCTGATGCAAGTTGAACCTGTG 1659
Qy 1621 TTAAGAGAAATTTTAAAGATATAAACGCTAGCTTTGTGTTATATACCACTAATPAGAAACGTC 1680
Db 1660 TTAAGAGAAATTTTAAAGATATAAACGCTAGCTTTGTGTTATATACCACTAATPAGAAACGTC 1719
Qy 1681 AATCGGATGTTAGCTTTAATCGCTTAATGTTTACAAATTTGGCCAGAAATTTTCACGAGAAAAA 1740
Db 1720 AATCGGATGTTAGCTTTAATCGCTTAATGTTTACAAATTTGGCCAGAAATTTTCACGAGAAAAA 1779
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Qy 1801 ACTGATGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860
Db 1840 ACGGATGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1899
Qy 1861 AGTGAAGTTGAAAAATTTAAACATCTTTAAATATGCTATTAACCGTGTATTTACATGGT 1920
Db 1900 AGTGAAGTTGAAAAATTTAAACATCTTTAAATATGCTATTAACCGGTTATTTACATGGT 1959
Qy 1921 GATAACATCAATTTAAGAACTTGGCAATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980
Db 1960 GATAACATCAATTTAAGAACTTGGCAATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 2019
Qy 1981 CAGTCATTAAATAGACAGGCAATCTTATTAATTAATGATGCAATTTGATGATTTAGAT 2040
Db 2020 CAGTCATTAAATAGACAGGCAATCAATTTATTAATTAATGATGCAATTTGATGATTTAGAT 2079
Qy 2041 GAAAGTAGAAGTATATTTTCAATTAACCCCTGAATATCAAGAGAGATTTGATATCTTA 2100
Db 2080 GAAAGTAGAAGTATATTTTCAATTAACCCCTGAATATCAAGAGAGATTTGATATCTTA 2139
Qy 2101 AAAGATATTAATATCATCCAGATTAAGATGCAAAATCGCAGTCAGTATTTTATCTCC 2160
Db 2140 AAAGATATTAATATCATCCAGATTAAGATGCAAAATCGCAGTCAGTATTTTATCTCC 2199
Qy 2161 AATACATTTAAACGGCTTAGTGAAAAAACTAAACAAATATTTTGAATATAATATAAATA 2220
Db 2200 AATACATTTAAACGGCTTAGTGAAAAAACTAAACAAATATTTTGAATATAATATAAATA 2259
Qy 2221 TTCGTTATGTTCTACATGTTGATAAGATCATCTTACACAGATATCAAAAAAGAAATA 2280
Db 2260 TTCGTTATGTTCTACATGTTGATAAGATCATCTTACACAGATATCAAAAAAGAAATA 2319
Qy 2281 CTAGCCTTCTATATAACATCAAGTGAATTTTACTAATAATGATATCTCATATTTAC 2340
Db 2320 TTGGCTTCTTATCATTAAGCACAAGTGAATTTTACTAATAATGATATCTCATATTTAC 2379
Qy 2341 ACGAGTAATAGATTAAATAAAACCTGAGCGCAATTTAAGTAATATTAATAAATTAAGTCAG 2400
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Db 2380 ACAGTAATAGACTAATAAAACCTGAGGCACATTTAAGTAATATTAATAAATTAAGTCAG 2439
Qy 2401 TTAATCTAAATTTGTAATACATCATTTTGTGATAATCATGACAGCCTTATTCGTTAAAAAT 2460
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Qy 2461 GACAGCTATGCTTTATATGAAAAAATATGATGTCGGCATGAAATTTTCAGCATTAACACAT 2520
Db 2500 GACAGCTATGCTTTATATGAAAAAATATGATGTCGGCATGAAATTTTCAGCATTAACACAT 2559
Qy 2521 GATTGATCGAGAAATCAATGCGCATCCACCATTTTAAAAAGCTCATTAACCTTATTTT 2580
Db 2560 GATTGATCGAGAAATCAATGCGCATCCACCATTTTAAAAAGCTCATTAACCTTATTTT 2619
Qy 2581 AATGACAACTGACTTTAAAAAGTATGAATGTGAAAAAGGCGCATCAAGAGTATGTTTATGACG 2640
Db 2620 AATGACAACTGACTTTAAGAGTATGAATGTGAAAAAGGCGCATCAAGAGTATGTTTATGACG 2679
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGTCAATCATCATCTTGCAGTCA 2700
Db 2680 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGTCAATCATCATCTTGCAGTCA 2739
Qy 2701 ATTGATAGTGTGCGCAATATAACCTGAGGATATTTGGTTCCCAATTTGACACTTTTAATC 2760
Db 2740 ATTGATAGTGTGCGCAATATAACCTGAGGATATTTGGTTCCCAATTTGACACTTTTAATC 2799
Qy 2761 TTAGAAAAAGAAAAACCGCCCATGTATTTAATAAACAATCGACCTGACTTATATGCTTTGG 2820
Db 2800 TTAGAAAAAGAAAAACCGCCCATGTATTTAATAAACAATCGACCTGACTTATATGCTTTGG 2859
Qy 2821 GAACGAAAAATTTACAATGCGCAAAATGAACAAATTTGAAAGTGCAAAAAGAGAGAAAAATATA 2880
Db 2860 GAACGAAAAATTTACAATGCGCAAAATGAACAAATTTCAAAGTGCAAAAAGGCGAAAAATATC 2919
Qy 2881 CTTGTTTAAAGTTCAATTTAATTAATAGTATTAACCTATATAA 2920
Db 2920 CCGTTTAAACAGTTTCATTTAATTAATAGTATTAACGCTATAA 2959

RESULT 12
US-10-184-485-4
; Sequence 4, Application US/10184485
; Publication No. US2003007763A1
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
; FILE REFERENCE: 5820.551
; CURRENT APPLICATION NUMBER: US/10/184,485
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US/09/437,277
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
; SEQ ID NO 4
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-10-184-485-4

Query Match 77.8%; Score 2271.2; DB 5; Length 2979;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;

Qy 1 ATGATATCATTTATCACAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
Db 61 ATGATATCATTTATCACAGCAATAAAGCATATAAAGCAATGACTATGATGATGACTC 120
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Qy 121 AAATGCAAGAAAAAATCTCTCAGCACATCTCTTCTGTTTAATTCAGCACATCTTTCTGTAAT 180
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361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTACCTGATCATGTTAATGATTTTACA 420  
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721 GACTTTATGCTTACTCGACTGTGATATGCGCCAAATCCATTTATGGGTTCACTTTAT 780  
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841 ACACAAACATATTGACCCAAAGACTTCTTAATAACCGAGTTGCTTGAATCATTTACCA 900  
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1081 GAGGAATTTAATCACTCGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTCGGTTTAC 1140  
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1921 GATAACACATCAATTAAGAACTTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
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1981 CAGTCATTAATAGACAAGGCATTAATTTATTAATTTATGACGATTTGATGATTTAGAT 2040  
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2881 CCTGTTAAACAAAGTTCATTTTAAATAGTATAACTCTA 2916  
2881 CCTGTTAAACAAAGTTCATTTTAAATAGTATAACTCTA 2916

RESULT 10  
US-11-096-190-8  
; Sequence 8, Application US/11096190  
; Publication No. US20050221446A1  
; GENERAL INFORMATION:  
; APPLICANT: Widner, William  
; APPLICANT: Sloma, Alan  
; APPLICANT: Thomas, Michael D.  
; APPLICANT: Tang, Maria  
; TITLE OF INVENTION: Methods For Producing A Hyaluronic Acid In A Bacillus Cell  
; FILE REFERENCE: 10596.200-US  
; CURRENT FILING DATE: 2005-03-31  
; PRIOR FILING DATE: 2004-03-31  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-096-190-8

Query Match 99.8%; Score 2914.4; DB 10; Length 2916;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGATACATATATCAAGCAATTAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
DB 1 ATGATACATATATCAAGCAATTAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
QY 61 AAATATTATTGAAAGTCGCGGAAATCTATGAGCGGAAATTTGTTGAAATTTCAAAATTACC 120  
DB 61 AAATATTATTGAAAGTCGCGGAAATCTATGAGCGGAAATTTGTTGAAATTTCAAAATTACC 120  
QY 121 AAATGCAAGAAAACTCTCAGCACTATCTTCTGTTTAAATTCAGCACTCTTTCTGTAAT 180  
DB 121 AAATGCAAGAAAACTCTCAGCACTATCTTCTGTTTAAATTCAGCACTCTTTCTGTAAT 180  
QY 181 AAAGAGAAAAAGTCAATGTTTGGCATGATCGCTTAGATATATTGCAACACAACTGTACTT 240

QY 2641 TATGGCTAGCGCATGAGCTTCTGACGATTATTAAAGAGTTCATCACATCTTGGCAGTCA 2700  
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QY 2701 ATTGATAGTGGCAGAAATATAACACATGAGGATATTTGGTTCCAAATTTGCACTTTTAAATC 2760  
Db 2719 ATTGATAGTGGCAGAAATATAACACATGAGGATATTTGGTTCCAAATTTGCACTTTTAAATC 2778  
QY 2761 TTAGAAAAGAAAACCGGCCATGTATTTAATAAATCATCGACCTGACTTATATGCTTGG 2820  
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QY 2821 GAACGAAATTTACAAATGACAAATGAACAAATTCGAAAGTGCAGAAAGAGGAGGAGAAATATA 2880  
Db 2839 GAACGAAATTTACAAATGACAAATGAACAAATTCGAAAGTGCAGAAAGAGGAGGAGAAATATA 2898  
QY 2881 CCTGTTAAACAGTTTCATTATTAATAGTATATACTCTATAA 2919  
Db 2899 CCTGTTAAACAGTTTCATTATTAATAGTATATACTCTATAA 2937

RESULT 9  
US-10-326-185-94  
; Sequence 94, Application US/10326185  
; Publication No.: US20030175902A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloma, Alan  
; APPLICANT: Behr, Regine  
; APPLICANT: Widner, William  
; APPLICANT: Tang, Maria  
; APPLICANT: Sternberg, David  
; APPLICANT: Brown, Stephen  
; TITLE OF INVENTION: Methods for Producing Hyaluronan In a Recombinant Host Cell  
; FILE REFERENCE: 10241.200-US  
; CURRENT APPLICATION NUMBER: US/10/326.185  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US 60/342,644  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 94  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2916)  
; OTHER INFORMATION:  
US-10-326-185-94

Query Match 99.8%; Score 2914.4; DB 6; Length 2916;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATACATTTATCACAGCAATTAAGCAATATACAGCAATGACTATCAATTAGCACTC 60  
Db 1 ATGATACATTTATCACAGCAATTAAGCAATATACAGCAATGACTATCAATTAGCACTC 60  
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Db 241 TCCACGTTAAAAAAATTTAGTACTTTCTGACTCGGAAAAAACACGTTAAAAAATAAATGG 300  
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QY 481 TCTATTATCGTTTCAACATTTCAATCGAACAGCAATTTTATCGATTACATTAGCTGTTTAA 540  
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US-10-309-560-7  
; Sequence 7, Application US/10309560  
; Publication No. US20030235893A1  
; GENERAL INFORMATION:  
; APPLICANT: WEIGEL, PAUL H  
; APPLICANT: KUMARI, KSHAWA  
; TITLE OF INVENTION: HVALURONAN SYNTHASES AND METHODS OF MAKING AND USING SAME  
; FILE REFERENCE: 35541.082  
; CURRENT APPLICATION NUMBER: US/10/309,560  
; PRIOR FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: 60/336,105  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
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Db 2899 CCTGTTAAACAGTTCAATTAATAGTATTAACCTATAA 2937

RESULT 6

US-09-879-959-9  
; Sequence 9, Application US/09879959  
; Patent No. US20020160489A1

GENERAL INFORMATION:

; APPLICANT: Weigel, Paul H  
; APPLICANT: Kumari, Kshama  
; APPLICANT: Deangelis, Paul  
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION  
; FILE REFERENCE: 3554.049  
; CURRENT APPLICATION NUMBER: US/09/879,959  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: 09/469,200  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9

; LENGTH: 2937

; TYPE: DNA

; ORGANISM: pasteurella multocida

US-09-879-959-9

Query Match 99.9%; Score 2917.4; DB 3; Length 2937;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 79 AAATTTATTTGAAAAGTCGGCGAAATCTATGAGCGGAAAAATTTGTGAATTTCAAATTACC 138  
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Db 259 TCCACGTAATAAATAATAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 318  
Qy 301 AAATGCTCCTCAGAGAAGAAATCTGAAAATGCGGAGGTAAGAGCGGTCGCCCTTGTACCA 360  
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Qy 361 AAAGATTTTCCAAAGATCTGTTTTAGCGCTTTTACCTGATCATGTTAAATGATTTTACA 420  
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Db 439 TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAAAACCTGAACATCAACATGTTGGTCTTT 498  
Qy 481 TCTATTATCGTTTAAACATTTCAATCGACCAAGCAATTTTATCGATTACATTTAGCCTGTTTA 540  
Db 499 TCTATTATCGTTTAAACATTTCAATCGACCAAGCAATTTTATCGATTACATTTAGCCTGTTTA 558  
Qy 541 GTAAACCAAAAAACAATTTACCCGTTTGAAGTTTATCGTACAGATGATGTTAGTCAGGAA 600  
Db 559 GTAAACCAAAAAACAATTTACCCGTTTGAAGTTTATCGTACAGATGATGTTAGTCAGGAA 618  
Qy 601 GATCTATCACCGATCATTTCCGCAATATGAAAAATAAATTTGGATATTTTCGCTACGTCAGACAA 660

GENERAL INFORMATION:									
; APPLICANT: Weigel, Paul H.									
; APPLICANT: DeAngelis, Paul									
; APPLICANT: Kumari, Kahana									
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof									
; FILE REFERENCE: 3554.011									
; CURRENT APPLICATION NUMBER: US/11/109,855									
; CURRENT FILING DATE: 2005-04-20									
; PRIOR APPLICATION NUMBER: US 09/178,851									
; PRIOR FILING DATE: 1998-10-26									
; PRIOR APPLICATION NUMBER: US 60/064,435									
; PRIOR FILING DATE: 1997-10-31									
; NUMBER OF SEQ ID NOS: 10									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 8									
; LENGTH: 2937									
; TYPE: DNA									
; ORGANISM: Pastuerella Multocida									
US-11-109-855-8									
Query Match 100.0%; Score 2919; DB 10; Length 2937;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Qy	61	AAATTTTGAAGTGGCGGAATCTATGGACGGAATTTGTAATTTCAATTTACC	120						
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Qy	121	AAATGCAAGAAATCTCTGACACATCTTCTGTAAATTCAGCACATCTTCTGTAAAT	180						
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Qy	181	AAAGAAGAAAGTCAATTTTGGTAGTCCGTTAGATATTTGCAACACACTGTACTT	240						
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Qy	241	TCCAAGTAAAAAATTTAGTACTTCTGACTCGGAAAAAACAAGTAAAAAATTAATGG	300						
Db	259	TCCAAGTAAAAAATTTAGTACTTCTGACTCGGAAAAAACAAGTAAAAAATTAATGG	318						
Qy	301	AAATTTGCTCACTGAGAGAAATCTGAAATTCGGAGGTGAAGCGCTTGTGTACCA	360						
Db	319	AAATTTGCTCACTGAGAGAAATCTGAAATTCGGAGGTGAAGCGCTTGTGTACCA	378						
Qy	361	AAAGATTTTCCCAAGATCTGGTTTATAGCGCTTTACCTGATCATGTTAATGATTTTACA	420						
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Qy	421	TGGTACAAAAAGCGAAGAAAGACTTGGCAATAAAACCTGAAACATCAACATGTTGGTCTT	480						
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Qy	481	TCTATTATCGTTTACAACTCAATCGACAGCAATTTTATCGATTACATTTAGCCTGTTTGA	540						
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Qy	661	AAAGATTAACGTTTCAAGCCAGTCCGCTCGGAATATGGGATATACGCTTAGCAAAATAT	720						
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Qy	721	GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAAAATCCATTATTTGGTTTCAATTTAT	780						

Db	739	GACTTTATTTGGCTTACTCGACTGTGATATGGCGCCAAATCCATTATGGGTTCAATTTTAT	798						
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Db 2899 CCTGTTAAACAGTTCAATTTAATAGTATAACTCTATAA 2937
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## RESULT 4

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US-10-011-771B-8
; Sequence 8, Application US/10011771B
; Publication No. US20030082780A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H.
; APPLICANT: DeAngelis, Paul
; APPLICANT: Kumari, Khama
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof
; FILE REFERENCE: 3554.011
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; CURRENT APPLICATION NUMBER: US/10/011,771B
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 09/178,851
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: US 60/064,435
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Pasteurella Multocida
; US-10-011-771B-8

Query Match 100.0%; Score 2919; DB 5; Length 2937;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 79 AAATTATTTGAAAAGTCCGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAATTACC 138
Qy 121 AAATGCAAGAAAAAATCTCTCAGCACATCTCTCTGTTAAATTCAGCACATCTTTCTGTAAT 180
Db 139 AAATGCAAGAAAAAATCTCTCAGCACATCTCTCTGTTAAATTCAGCACATCTTTCTGTAAT 198
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Db 319 AAATTGCTCACTGAGAAGAAATCTGAAAATCCGAGAGTAAGAGCGGTCCGCTTTGTACCA 378
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Db 379 AAAGATTTTCCCAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTAATGATTTTACA 438
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Qy 661 AAAGATAACGGTTTTTCAAGCCAGTCCGCTCGGAATATGGGATTAACGTTAGCAAAAATAT 720
Db 679 AAAGATAACGGTTTTTCAAGCCAGTCCGCTCGGAATATGGGATTAACGTTAGCAAAAATAT 738
Qy 721 GACTTTTATGGCTTACTCGACTGTGATATGCGCCAAATCCATTTATGGGTTCACTTTTAT 780
Db 739 GACTTTTATGGCTTACTCGACTGTGATATGCGCCAAATCCATTTATGGGTTCACTTTTAT 798
Qy 781 GTTCGACAGCTATTAGAGATGATGATTTAAACATCATTTGTTCCAGAAAAATACATCAT 840
Db 799 GTTCGACAGCTATTAGAGATGATGATTTAAACATCATTTGTTCCAGAAAAATACATCAT 858
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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Pastuerella Multocida
US-10-011-768B-8

Query Match      100.0%; Score 2919; DB 5; Length 2937;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAATATTATTGAAAGCTCGCGGAAATCTATGACCGGAAATATGTTGAAATTTCAAAATTACC 120
DB 79 AAATATTATTGAAAGCTCGCGGAAATCTATGACCGGAAATATGTTGAAATTTCAAAATTACC 138

QY 121 AAATGCAAGAAATCTCTAGCACATCTTCTGTTAAATTCAGCACATCTTTCTGTTAAAT 180
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QY 181 AAAGAAAGAAATGTTTGGCATAGTCGTTAGATATATGCAACACACTGTTACTT 240
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QY 301 AAATGCTCAGTACAGAGAAATCTGAAATATGCGAGGTAAGAGCGGTGCGCCCTGTACCA 360
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QY 361 AAAGATTTTCCAAAGATCTGTTTGGCGCTTTTACCTGATCATGTTAAATGATTTTACA 420
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QY 421 TGGTACAAAGCGGAAAGAAAGACTTGGCATATAAACCCTGAAACATCAACATGTTGGTCTT 480
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QY 481 TCTATTATCGTTTACCAATTCATCGACAGCAATTTTATCGATTACATTTAGCCTGTTTA 540
DB 499 TCTATTATCGTTTACCAATTCATCGACAGCAATTTTATCGATTACATTTAGCCTGTTTA 558

QY 541 GTAAACCAAAACACATTTACCGGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600
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QY 601 GATCTATCACCGATCATTCGCGCAATATGAATAAATAATTCGCTACGTCAGACAA 660
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## RESULT 3

US-10-011-768B-8  
; Sequence 8, Application US/10011768B  
; Publication No. US20030073221A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: Deangelis, Paul  
; APPLICANT: Kumar, Kehana  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/10/011,768B  
; CURRENT FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; PRIOR FILING DATE: 1997-10-31

2461 GACAGCTATGCTTATATGCAAAATATATGATCGGCATGAATTTCTCAGCAATTAACACAT 2520  
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RESULT 2

US-10-642-248-1  
; Sequence 1, Application US/10642248  
; Publication No. US20040132143A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Jing, Wei  
; TITLE OF INVENTION: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND METHO  
; TITLE OF INVENTION: MAKING AND USING SAME  
; FILE REFERENCE: 3554.097  
; CURRENT APPLICATION NUMBER: US/10/642,248  
; CURRENT FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 09/842,484  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2920  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida

US-10-642-248-1

Query Match 100.0%; Score 2920; DB 7; Length 2920;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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GenCore version 5.1.6  
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Run on: January 8, 2006, 10:04:45 ; Search time 2070 Seconds

(without alignments)  
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Title: US-10-642-248-1

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Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2919	100.0	2937	10	US-11-109-855-8
6	2917.4	99.9	2937	3	US-09-879-959-9
7	2917.4	99.9	2937	5	US-10-172-527-9
8	2917.4	99.9	2937	6	US-10-309-560-7
9	2914.4	99.8	2916	6	US-10-326-185-94
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11	2271.2	77.8	2979	3	US-09-842-484A-1
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14	2269.4	77.7	2271	7	US-10-642-248-20
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17	2266.4	77.6	2979	9	US-10-197-153-4
18	2266.4	77.6	2979	10	US-11-042-530-3
19	2110.4	72.3	2112	7	US-10-642-248-71
20	2110.4	72.3	2112	5	US-10-197-153-2
21	2108.8	72.2	2112	5	US-10-184-485-2
22	2108.8	72.2	2112	7	US-10-642-248-11
23	2108.8	72.2	2112	7	US-10-642-248-12

ALIGNMENTS

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; Sequence 2, Application US/10217613

; Publication No. US20030113845A1

; GENERAL INFORMATION:

; APPLICANT: DEANGELIS, PAUL

; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND US

; FILE REFERENCE: 35541.081

; CURRENT APPLICATION NUMBER: US/10/217,613

; CURRENT FILING DATE: 2002-08-12

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 09/283,402

; PRIOR FILING DATE: 1998-04-02

; PRIOR APPLICATION NUMBER: 09/178,851

; PRIOR FILING DATE: 1998-10-26

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 2

; LENGTH: 2920

; TYPE: DNA

; ORGANISM: Pasteurella multocida

US-10-217-613-2

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DB	181	AAAGAAGAAAAAGTCAATGTTTCCGATAGTCCGTTAGATATTCGCAACACAACTGTTACTT	240
QY	241	TCCACGTAATAAAATAGTACTTTCTGACTCGGAAAAAACACGCTTAAAAATAAATG	300

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 12:56:41 ; Search time 388 Seconds  
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5485.817 Million cell updates/sec

Title: US-10-642-248-1

Perfect score: 2920  
Sequence: 1 atgaatcattatcacaagc.....taatagcattactctataaa 2920

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4637609 seqs, 364468668 residues

Total number of hits satisfying chosen parameters: 9275218

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of residues predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2917.4	99.9	2937	7	US-11-124-215-2
3	2917.4	99.9	2937	7	US-11-120-422-9
4	2266.4	77.6	2979	7	US-11-172-145-3
5	2110.4	72.3	2112	7	US-11-172-145-11
6	2108.8	72.2	2112	7	US-11-172-145-17
7	2108.8	72.2	2112	7	US-11-172-145-18
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9	2108.8	72.2	2112	7	US-11-172-145-20
10	1975.4	67.7	1980	7	US-11-172-145-13
11	1898.4	65.0	1902	7	US-11-172-145-14
12	1826.8	62.6	1830	7	US-11-172-145-15
13	1759.4	60.3	1764	7	US-11-172-145-16
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15	68.6	2.3	171486	7	US-11-121-086-105
16	65.2	2.2	6156	6	US-10-240-708-60
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24	60.8	2.1	171486	7	US-11-121-086-105	Sequence 105, App
25	60.6	2.1	49979	6	US-10-995-561-13443	Sequence 13443, A
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29	59.6	2.0	6866	6	US-10-240-708-20	Sequence 20, Appl
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34	57.6	2.0	3645	6	US-10-793-626-4110	Sequence 4110, Ap
35	57.4	2.0	5455	6	US-10-240-708-33	Sequence 33, Appl
36	57.2	2.0	5076	9	US-11-077-550-135	Sequence 135, App
37	56.8	1.9	2509	6	US-10-750-185-27479	Sequence 27479, A
38	56.8	1.9	2509	6	US-10-750-623-37479	Sequence 37479, A
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42	55.2	1.9	139054	7	US-11-121-086-96	Sequence 96, Appl
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44	54.2	1.9	6669	6	US-10-240-708-6	Sequence 6, Appl
45	53.8	1.8	2739	9	US-11-077-550-115	Sequence 115, Appl

## ALIGNMENTS

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RESULT 1
US-11-172-145-1
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; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; FILE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-1
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Matches 2920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1501 TCTAAACCAATGCGGAAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTCTAAAGST 1560  
Dh 1501 TCTAAACCAATGCGGAAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTCTAAAGST 1560  
Qy 1561 TATTACATTTGGCGATTAGATTAGATGATTAATCTTGAGCCTGATGACGATTGAATCTGTG 1620  
Dh 1561 TATTACATTTGGCGATTAGATTAGATGATTAATCTTGAGCCTGATGACGATTGAATCTGTG 1620  
Qy 1621 TTAAAAAGATTTTAAAAAGATTAAGAAAGCTTGTGTTTATATACCTAATATGAAGATC 1680  
Dh 1621 TTAAAAAGATTTTAAAAAGATTAAGAAAGCTTGTGTTTATATACCTAATATGAAGATC 1680  
Qy 1681 AATCCGATGATGATTAATCGCTTAATGTTACAAATGGCCAGAAATTTTCAAGGAAAAA 1740  
Dh 1681 AATCCGATGATGATTAATCGCTTAATGTTACAAATGGCCAGAAATTTTCAAGGAAAAA 1740  
Qy 1741 CTCAACAACGCTATGATTTGCTCACACTTTAGAAATGTTCAAGATTAAGCTTGCAATTTA 1800  
Dh 1741 CTCAACAACGCTATGATTTGCTCACACTTTAGAAATGTTCAAGATTAAGCTTGCAATTTA 1800  
Qy 1801 ACTGATGATTTCAATGAAAAATTTGAAAATGCGCTTAACATTAATGATTTCTTCAATCTC 1860  
Dh 1801 ACTGATGATTTCAATGAAAAATTTGAAAATGCGCTTAACATTAATGATTTCTTCAATCTC 1860  
Qy 1861 AGTGAAGTGGAAAAATTTAAACATCTTAATTAATTTGCTATAACGCTGATTAATCATGCT 1920  
Dh 1861 AGTGAAGTGGAAAAATTTAAACATCTTAATTAATTTGCTATAACGCTGATTAATCATGCT 1920  
Qy 1921 GATTAACATCAATTAAGAAAACCTTGCAATCAAAAAGAAAAACATTTTGTGTAGTCAT 1980  
Dh 1921 GATTAACATCAATTAAGAAAACCTTGCAATCAAAAAGAAAAACATTTTGTGTAGTCAT 1980  
Qy 1981 CAGTCATTAATTAAGCAAGGATTAATTAATTAATTAATTAAGCAAGATTTGATAGAT 2040  
Dh 1981 CAGTCATTAATTAAGCAAGGATTAATTAATTAATTAATTAAGCAAGATTTGATAGAT 2040  
Qy 2041 GAAAGTGAAGATTAATTTTCAATTAAGAAACGCTGATATCAAGAAAGATGATATCTTAA 2100  
Dh 2041 GAAAGTGAAGATTAATTTTCAATTAAGAAACGCTGATATCAAGAAAGATGATATCTTAA 2100  
Qy 2101 AAAGATATTAATCAATCAAGATTAAGATGCAAAAATGCGAGTCAGATATTTTATATCC 2160  
Dh 2101 AAAGATATTAATCAATCAAGATTAAGATGCAAAAATGCGAGTCAGATATTTTATATCC 2160  
Qy 2161 AATACATTTAAACGCTTAGTGAAGAAAACTAAACAATTTATTTGATATTAATTAATTAAT 2220  
Dh 2161 AATACATTTAAACGCTTAGTGAAGAAAACTAAACAATTTATTTGATATTAATTAATTAAT 2220

Oy	2221	TTCGTTATGTCTTCAACAGTTGGATAAAGAATCATCTTAACCGAGATTGCAAAAAGAATA	2280
Dd	2221	TTCCGTAATGTCTCAACAGTTGGATAAAGAATCATCTTAACCGAGATTGCAAAAAGAATA	2280
Oy	2281	CTAGCCTTCTATCAATAAACATCAAGTAGAATATTTACTAAATGAATATCTCATATTAC	2340
Dd	2281	CTAGCCTTCTATCAATAAACATCAAGTAGAATATTTACTAAATGAATATCTCATATTAC	2340
Oy	2341	ACGAGTAAATAGATTAAATAAAACTGAGGCCATTAAAGTAATVTTAATAAATTAACTCAG	2400
Dd	2341	ACGAGTAAATAGATTAAATAAAACTGAGGCCATTAAAGTAATVTTAATAAATTAACTCAG	2400
Oy	2401	TTAAATCTAAATTGGGAATACAATCATTTTTTGATTAATCAACAGCCGATTCGTTAAAT	2460
Dd	2401	TTAAATCTAAATTGGGAATACAATCATTTTTTGATTAATCAACAGCCGATTCGTTAAAT	2460
Oy	2461	GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTPAACACAT	2520
Dd	2461	GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTPAACACAT	2520
Oy	2521	GATTGATCGAGAAAATCAATGCGCATCCACCATTTPAAAAAGTCATTAAAACTTATTTT	2580
Dd	2521	GATTGATCGAGAAAATCAATGCGCATCCACCATTTPAAAAAGTCATTAAAACTTATTTT	2580
Oy	2581	AATGACAAATGACTTTAAAAAGTATGAAATGTGMAAGGGGCACTCACAGGTATGTTATACG	2640
Dd	2581	AATGACAAATGACTTTAAAAAGTATGAAATGTGMAAGGGGCACTCACAGGTATGTTATACG	2640
Oy	2641	TATGGCTAGGGCATGAGCTTCTGACGATTTATPAAAGAAAGTCATCACAATCTTGCCACTCA	2700
Dd	2641	TATGGCTAGGGCATGAGCTTCTGACGATTTATPAAAGAAAGTCATCACAATCTTGCCACTCA	2700
Oy	2701	ATTGATAGTGTCGCAAAATATAACACTGAGATATTTGGTTCCAAATTGCACTTTTAATC	2760
Dd	2701	ATTGATAGTGTCGCAAAATATAACACTGAGATATTTGGTTCCAAATTGCACTTTTAATC	2760
Oy	2761	TTAGAAAAAGAAACCGCGCATGTATTTAATPAAACATCGACCCTGACTTATATGCTTGG	2820
Dd	2761	TTAGAAAAAGAAACCGCGCATGTATTTAATPAAACATCGACCCTGACTTATATGCTTGG	2820
Oy	2821	GAAGCAAATTTCAATGACCAAAATGAAAGAAATGAAAGTCAAAAAGAGAGAAATATA	2880
Dd	2821	GAAGCAAATTTCAATGACCAAAATGAAAGAAATGAAAGTCAAAAAGAGAGAAATATA	2880
Oy	2881	CCTGTTAACAAAGTTCATTATTAATAGTATTAATTAACCTATATAA	2920
Dd	2881	CCTGTTAACAAAGTTCATTATTAATAGTATTAATTAATTAACCTATATAA	2920
<b>RESULT 2</b>			
US-11-124-215-2			
Sequence 2, Application US/11124215			
Publication No. US20050266460A1			
GENERAL INFORMATION:			
APPLICANT: DEANBELIS, PAUL			
TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLIA MULTOCIDA AND			
FILE REFERENCE: 35541.101			
CURRENT APPLICATION NUMBER: US/11/124,215			
PRIOR FILING DATE: 2005-05-09			
PRIOR FILING DATE: 2002-08-12			
PRIOR APPLICATION NUMBER: 09/283,402			
PRIOR FILING DATE: 1999-04-01			
PRIOR APPLICATION NUMBER: 60/080,414			
PRIOR FILING DATE: 1998-04-02			
PRIOR APPLICATION NUMBER: 09/178,851			
NUMBER OF SEQ ID NOS: 28			
SOFTWARE: PatentIn version 3.3			
SEQ ID NO 2			
LENGTH: 2937			
TYPE: DNA			

i: ORGANISM: Pasteurella multocida									
US-11-124-215-2									
Query Match	99.9%	Score 2917.4;	DB 7;	Length 2937;					
Best Local Similarity	100.0%	Pred. No. 0;							
Matches 2918;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;					
QY	1	ATGAATCATATATACAAGCAATAAAGCATATATAAGCATATGATCATATATGACACTC	60						
DB	19	ATGAATCATATATACAAGCATATAAAGCATATATAAGCATATGATCATATATGACACTC	78						
QY	61	AAATATATTTGAAAAAGTCGGCGGAATCTATGACGGAATAATGTTGAATTTCAAAATACC	120						
DB	79	AAATATATTTGAAAAAGTCGGCGGAATCTATGACGGAATAATGTTGAATTTCAAAATACC	138						
QY	121	AAATGCAAGAAAACTCTCAGCACATCTTCTGTATTAATTCAGACATCTTTCGTAAAT	180						
DB	139	AAATGCAAGAAAACTCTCAGCACATCTTCTGTATTAATTCAGACATCTTTCGTAAAT	198						
QY	181	AAAGAGAAAAAGTCATGTTTGAGATAGTCGGTTAGATATTGCAACAACACTGTACTT	240						
DB	199	AAAGAGAAAAAGTCATGTTTGAGATAGTCGGTTAGATATTGCAACAACACTGTACTT	258						
QY	241	TCCAACGTAAAAAATTTAGTACTTCTGTGACTCGAAAAAACAAGTTAAAAAATTAATGG	300						
DB	259	TCCAACGTAAAAAATTTAGTACTTCTGTGACTCGAAAAAACAAGTTAAAAAATTAATGG	318						
QY	301	AAATTTGCTACTGAGAGAAAACTTGAAATGCGAGGTTAAGAGCGGTCGCCCTTGTAACA	360						
DB	319	AAATTTGCTACTGAGAGAAAACTTGAAATGCGAGGTTAAGAGCGGTCGCCCTTGTAACA	378						
QY	361	AAAGATTTTCCCAAAAGATCTGTTTTGAGCGCTTTACCTGATCATGTTAATGATTTTACA	420						
DB	379	AAAGATTTTCCCAAAAGATCTGTTTTGAGCGCTTTACCTGATCATGTTAATGATTTTACA	438						
QY	421	TGCTACAAAAAGCGAANAAGAAAGACTTGCGCATTAACCTGAAACATCAATGTTGCTTT	480						
DB	439	TGCTACAAAAAGCGAANAAGAAAGACTTGCGCATTAACCTGAAACATCAATGTTGCTTT	498						
QY	481	TCTATTTATCGTTACCAACTTCATTCGACAGCAATTTTATGATTTACTTATGCTGTTTA	540						
DB	499	TCTATTTATCGTTACCAACTTCATTCGACAGCAATTTTATGATTTACTTATGCTGTTTA	558						
QY	541	GTTAAACCAAAAAACGACATTAACCGGTTTAAAGTTATCGAGAGATGATGATGACAGAA	600						
DB	559	GTTAAACCAAAAAACGACATTAACCGGTTTAAAGTTATCGAGAGATGATGATGACAGAA	618						
QY	601	GATCATATACCGATCATTTGCGCAATATGAAATTAATTTGATTTGCTATCGCTACAGCAA	660						
DB	619	GATCATATACCGATCATTTGCGCAATATGAAATTAATTTGATTTGCTATCGCTACAGCAA	678						
QY	661	AAAGATTAACGGTTTTCAAGCCAGTCGCGCTCGGAATATGGAATTAACGTTTAGCAAAATAT	720						
DB	679	AAAGATTAACGGTTTTCAAGCCAGTCGCGCTCGGAATATGGAATTAACGTTTAGCAAAATAT	738						
QY	721	GACTTTATTTGCTTTCTGACATCTGATATATGCGCCCAATTCATTAATGAGTTCAATCTTAT	780						
DB	739	GACTTTATTTGCTTTCTGACATCTGATATATGCGCCCAATTCATTAATGAGTTCAATCTTAT	798						
QY	781	GTTGACAGAGCTTTATGAGATATGATTAACAATCATTTGGTTCGAAGAAAAATACATCGAT	840						
DB	799	GTTGACAGAGCTTTATGAGATATGATTAACAATCATTTGGTTCGAAGAAAAATACATCGAT	858						
QY	841	ACACAACATATTGACCCAAAGAATCTTTAAATTAACGCGAGTTTGCTTGAATCATTAACA	900						
DB	859	ACACAACATATTGACCCAAAGAATCTTTAAATTAACGCGAGTTTGCTTGAATCATTAACA	918						
QY	901	GAAATGAAAAACCAATATATATGTTGTCGCCCAAAAGGGGAAAGAAACAAGTTTCTGATATGG	960						
DB	919	GAAATGAAAAACCAATATATATGTTGTCGCCCAAAAGGGGAAAGAAACAAGTTTCTGATATGG	978						
QY	961	CGCTTAGAACATTTGAGAAAAACAGAAAAATCTCCGCTTATCGATTCGCTTCGGTTT	1020						

Dh 979 CGCTAGACAACTTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTCCTTCCTTTT 1038  
Qy 1021 TTTCGGGGGGGTAAATGTTGCTTTCGCTTAAATAATGGCTAAATATCGGTTCTTTGAT 1080  
Dh 1039 TTTCGGGGGGGTAAATGTTGCTTTCGCTTAAATAATGGCTAAATATCGGTTCTTTGAT 1098  
Qy 1081 GAGGAATTTAATCACTGGGGGTGAGAAAGATGTGAAATTTGGATATCGCTTATTCCTGTAC 1140  
Dh 1099 GAGGAATTTAATCACTGGGGGTGAGAAAGATGTGAAATTTGGATATCGCTTATTCCTGTAC 1158  
Qy 1141 GGTATGTTCTTTAAACTATTTGATGTGCAATTTGGCTTACCATCAAGAGCCCAAGGTAAA 1218  
Dh 1159 GGTATGTTCTTTAAACTATTTGATGTGCAATTTGGCTTACCATCAAGAGCCCAAGGTAAA 1218  
Qy 1201 GAAATGAAACCGATTCGGAAGCGGGAATAATATTCGCTGATATTATGAGAAAG 1260  
Dh 1219 GAAATGAAACCGATTCGGAAGCGGGAATAATATTCGCTGATATTATGAGAAAG 1278  
Qy 1261 GTCCCTTATATCTATAGAAAACCTTTTACAAATAGAAATTCGCAATATGAGTACCT 1320  
Dh 1279 GTCCCTTATATCTATAGAAAACCTTTTACAAATAGAAATTCGCAATATGAGTACCT 1338  
Qy 1321 TTAGTTCAATTTATATCCAGCTTATATAGTGTCAAACTATTAATCAAGCTTGTAGT 1380  
Dh 1339 TTAGTTCAATTTATATCCAGCTTATATAGTGTCAAACTATTAATCAAGCTTGTAGT 1398  
Qy 1381 AGTGCACGTATCAAGCTGTGTGATCTCGAGGTGTGATTTGTAACGATGTTCAACA 1440  
Dh 1399 AGTGCACGTATCAAGCTGTGTGATCTCGAGGTGTGATTTGTAACGATGTTCAACA 1458  
Qy 1441 GATAATACCTTAGAAGTATCAATAGCTTTATGGTAAATATCTAGGGTACGATCATG 1500  
Dh 1459 GATAATACCTTAGAAGTATCAATAGCTTTATGGTAAATATCTAGGGTACGATCATG 1518  
Qy 1501 TCTAAACCAAAATGGCGGAATAGCTCAGCATCAAAATGCAAGCCGTTCTTTGCTAAAGT 1560  
Dh 1519 TCTAAACCAAAATGGCGGAATAGCTCAGCATCAAAATGCAAGCCGTTCTTTGCTAAAGT 1578  
Qy 1561 TATTAATTTGGGCGATTGATTCAGATGATTAATCTGAGCCGATGAGTGAACGTGCT 1620  
Dh 1579 TATTAATTTGGGCGATTGATTCAGATGATTAATCTGAGCCGATGAGTGAACGTGCT 1638  
Qy 1621 TTAATAAGATTTTAAAGATTAACGCTAGCTGTGTATATACCACTAATAGAAACGTC 1680  
Dh 1639 TTAATAAGATTTTAAAGATTAACGCTAGCTGTGTATATACCACTAATAGAAACGTC 1698  
Qy 1681 AATCCGATGTAGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTA 1740  
Dh 1699 AATCCGATGTAGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTA 1758  
Qy 1741 CTCACAGGCGTATGATGCTCACCACTTTAGAAATGTTACGATTAAGAGCTTGGCATTTA 1800  
Dh 1759 CTCACAGGCGTATGATGCTCACCACTTTAGAAATGTTACGATTAAGAGCTTGGCATTTA 1818  
Qy 1801 ACTGATGATTCATGAGAAAAATGAAAAATGCGGTAGACTATGACATGCTTCTCAAACTC 1860  
Dh 1819 ACTGATGATTCATGAGAAAAATGAAAAATGCGGTAGACTATGACATGCTTCTCAAACTC 1878  
Qy 1861 AGTGAAGTTGAAAAATTTAAACATCTTAATAAAATCTGCTAATCCGCTGATTTACATGCT 1920  
Dh 1879 AGTGAAGTTGAAAAATTTAAACATCTTAATAAAATCTGCTAATCCGCTGATTTACATGCT 1938  
Qy 1921 GATAACATCAATTAAGAAATCTTGCAATCAAAAGAAAAACATTTGTGTGTGATCAAT 1980  
Dh 1939 GATAACATCAATTAAGAAATCTTGCAATCAAAAGAAAAACATTTGTGTGTGATCAAT 1998  
Qy 1981 CAGTATTAATAATAGCAAGCATATCTTAATTAATTAATTAATGAAGATTTGATTAATGAT 2040  
Dh 1999 CAGTATTAATAATAGCAAGCATATCTTAATTAATTAATTAATGAAGATTTGATTAATGAT 2058  
Qy 2041 GAAAGTAAAGATATTTTCAATTAATAAAACCGCTGAATATCAAGAAAGATTAATCTTA 2100  
Dh 2059 GAAAGTAAAGATATTTTCAATTAATAAAACCGCTGAATATCAAGAAAGATTAATCTTA 2118

Qy 2101 AAGATATTAATAATCAATCCAGAAATTAAGATGCCAAATCGCAGTCAATATTTTATCCC 2160  
Dh 2119 AAGATATTAATAATCAATCCAGAAATTAAGATGCCAAATCGCAGTCAATATTTTATCCC 2178  
Qy 2161 AATACATTAACGGCTTAATGAAAAAACTTAACAAATTTATTTGATTAATTAATAAATATA 2220  
Dh 2179 AATACATTAACGGCTTAATGAAAAAACTTAACAAATTTATTTGATTAATTAATAAATATA 2238  
Qy 2221 TTGCTATGTTCTACATGTTGATTAAGAAATCATCTTACCAAGATATCAAAAAAGAAATA 2280  
Dh 2239 TTGCTATGTTCTACATGTTGATTAAGAAATCATCTTACCAAGATATCAAAAAAGAAATA 2298  
Qy 2281 CTAGCTTCTATCAATTAACATCAAGTGAATTTTATCTAAATAATGATATCTCATATTAC 2340  
Dh 2299 CTAGCTTCTATCAATTAACATCAAGTGAATTTTATCTAAATAATGATATCTCATATTAC 2358  
Qy 2341 ACAGATTAATGATTAATAAACTGAGGCCATTTAAGTAAATTAATTAATAATTAAGTCAG 2400  
Dh 2359 ACAGATTAATGATTAATAAACTGAGGCCATTTAAGTAAATTAATTAATAATTAAGTCAG 2418  
Qy 2401 TTAATCTAATTTGTAATCATCATTTTGTATATCATGACAGCTAATCGTTAAAT 2460  
Dh 2419 TTAATCTAATTTGTAATCATCATTTTGTATATCATGACAGCTAATCGTTAAAT 2478  
Qy 2461 GACAGCTATGCTTATATGAAAAAAATATGATGTGGCATGAAATTTCTCAGCATTAACAT 2520  
Dh 2479 GACAGCTATGCTTATATGAAAAAAATATGATGTGGCATGAAATTTCTCAGCATTAACAT 2538  
Qy 2521 GATTGATGCAAAAAATCAATGCGCATCCACATTTAAAAAGCTCAATTAATACTTATTTT 2580  
Dh 2539 GATTGATGCAAAAAATCAATGCGCATCCACATTTAAAAAGCTCAATTAATACTTATTTT 2598  
Qy 2581 AATGACAATGACTTAAAAAGATGAATGTGAAAGGGGATCACAAAGGTATGTTATAGC 2640  
Dh 2599 AATGACAATGACTTAAAAAGATGAATGTGAAAGGGGATCACAAAGGTATGTTATAGC 2658  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTAATTAAGAAATGATCATCTTGCAGTCA 2700  
Dh 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTAATTAAGAAATGATCATCTTGCAGTCA 2718  
Qy 2701 ATTGATATGTTGCCAGAAATTAACACTGAGATATTTGGTTCCAAATTTGCACTTTTATC 2760  
Dh 2719 ATTGATATGTTGCCAGAAATTAACACTGAGATATTTGGTTCCAAATTTGCACTTTTATC 2778  
Qy 2761 TTGAAAAAGAAACCGGCAATGATTAATTAATAACATCGAACCTGACTTATATGCTTGG 2820  
Dh 2779 TTGAAAAAGAAACCGGCAATGATTAATTAATAACATCGAACCTGACTTATATGCTTGG 2838  
Qy 2821 GAACGAAAAATTAACAATGACAAATGAACAATTTGAAAAGTGCAAAAGAGGAAAAATATA 2880  
Dh 2839 GAACGAAAAATTAACAATGACAAATGAACAATTTGAAAAGTGCAAAAGAGGAAAAATATA 2898  
Qy 2881 CCTGTTAAACAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2918  
Dh 2899 CCTGTTAAACAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2937

RESULT 3  
US-11-120-422-9  
; Sequence 9, Application US/11120422  
; Publication No. US20050287646A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H  
; APPLICANT: Kumari, Khama  
; APPLICANT: Deangelis, Paul  
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION  
; FILE REFERENCE: 3554, 049  
; CURRENT APPLICATION NUMBER: US/11/120,422  
; PRIOR APPLICATION NUMBER: 2005-05-02  
; PRIOR APPLICATION NUMBER: US/09/879,959  
; PRIOR FILING DATE: 2001-09-12

;; PRIOR APPLICATION NUMBER: 09/469,200  
;; PRIOR FILING DATE: 1999-12-21  
;; PRIOR APPLICATION NUMBER: 09/178,851  
;; PRIOR FILING DATE: 1998-10-26  
;; NUMBER OF SEQ ID NOS: 10  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 9  
;; LENGTH: 2937  
;; TYPE: DNA  
;; ORGANISM: pasteurella multocida  
US-11-120-422-9

Query Match 99.9%; Score 2917.4; DB 7; Length 2937;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGAATACATTATCACAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC	60
Db	19	ATGAATACATTATCACAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC	78
Qy	61	AAATTTTGAAGTCGGCGGAATCTATCGACGGAATAATGTTGAATTTCAAAATTACC	120
Db	79	AAATTTTGAAGTCGGCGGAATCTATCGACGGAATAATGTTGAATTTCAAAATTACC	138
Qy	121	AAATGCAAGAAAACCTCTGACGACATCTTCTGTTAATTCAGCACATCTTTCTGTAAAT	180
Db	139	AAATGCCAAGAAAACCTCTGACGACATCTTCTGTTAATTCAGCACATCTTTCTGTAAAT	198
Qy	181	AAAGAAGAAAAGTCAATGTTTGGATAGTCCGTTAGATATGCAACAACAACCTGTTACTT	240
Db	199	AAAGAAGAAAAGTCAATGTTTGGATAGTCCGTTAGATATGCAACAACAACCTGTTACTT	258
Qy	241	TCCAACGTAAAAAATTAGTACTTCTGACTCGGAAAAAACAAGTTAAAAATAAATGG	300
Db	259	TCCAACGTAAAAAATTAGTACTTCTGACTCGGAAAAAACAAGTTAAAAATAAATGG	318
Qy	301	AAATGCTCAGTGAAGAAATCTGAAATGCGAGGTAAAGCGGTGCGCCCTGTACCA	360
Db	319	AAATGCTCAGTGAAGAAATCTGAAATGCGAGGTAAAGCGGTGCGCCCTGTACCA	378
Qy	361	AAAGATTTTCCAAAGATCTGGTTTGTAGCGCTTTACTGATCATGTTTAATGATTTACA	420
Db	379	AAAGATTTTCCAAAGATCTGGTTTGTAGCGCTTTACTGATCATGTTTAATGATTTACA	438
Qy	421	TGGTACAAAAGCGAAGAAAGACTTGGCATAAACCTGACATCAACATGTTGGTCTT	480
Db	439	TGGTACAAAAGCGAAGAAAGACTTGGCATAAACCTGACATCAACATGTTGGTCTT	498
Qy	481	TCTATTATCGTTACAACTTCAATCGACGCAATTTTATCGATTACATTAGCCCTGTTTA	540
Db	499	TCTATTATCGTTACAACTTCAATCGACGCAATTTTATCGATTACATTAGCCCTGTTTA	558
Qy	541	GTAAACCAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	600
Db	559	GTAAACCAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	618
Qy	601	GATCTATCACCCGATCATTCGCAATATGAAATAAATTTGGATATTCGCTACGTACAGAA	660
Db	619	GATCTATCACCCGATCATTCGCAATATGAAATAAATTTGGATATTCGCTACGTACAGAA	678
Qy	661	AAAGATAACGGTTTCAAGCCAGTCGCGTCCGGAATATGGGATATAGCTTAGCAAAATAT	720
Db	679	AAAGATAACGGTTTCAAGCCAGTCGCGTCCGGAATATGGGATATAGCTTAGCAAAATAT	738
Qy	721	GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAAAATCCATTATGGGTTCATTCTTAT	780
Db	739	GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAAAATCCATTATGGGTTCATTCTTAT	798
Qy	781	GTTGCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT	840
Db	799	GTTGCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT	858
Qy	841	ACACAACATATTGACCCAAAAGACTTCTTAATAATAACGCGAGTTTGTGTTGAATCATTACCA	900

Db	859	ACACAACATATTGACCCAAAAGACTTCTTAATAAACCGAGTTTGTCTGTAATCATTACCA	918
Qy	901	GAAGTGAACCAATAATAGTGTTCGCGCAAAAGGGGAAGAAACAGTTTCTCTGGATTGG	960
Db	919	GAAGTGAACCAATAATAGTGTTCGCGCAAAAGGGGAAGAAACAGTTTCTCTGGATTGG	978
Qy	961	CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCCCTTCCGTTT	1020
Db	979	CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCCCTTCCGTTT	1038
Qy	1021	TTTCGCGCGGGTAATGTTGCTTTCGCTAAAAAATGCGTAATAATCGGTTTCTTTGAT	1080
Db	1039	TTTCGCGCGGGTAATGTTGCTTTCGCTAAAAAATGCGTAATAATCGGTTTCTTTGAT	1098
Qy	1081	GAGGAATTTAATCACTCGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC	1140
Db	1099	GAGGAATTTAATCACTCGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC	1158
Qy	1141	GGTAGTTTCTTTAAAACTATTGATGGCATTTATAGCCCTACCAATCAAGAGCCACAGGTAAA	1200
Db	1159	GGTAGTTTCTTTAAAACTATTGATGGCATTTATAGCCCTACCAATCAAGAGCCACAGGTAAA	1218
Qy	1201	GAATAATGAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATCAGAGAAAAG	1260
Db	1219	GAATAATGAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATCAGAGAAAAG	1278
Qy	1261	GTCCCTTATATCTATAGAAAATCTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT	1320
Db	1279	GTCCCTTATATCTATAGAAAATCTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT	1338
Qy	1321	TTAGTTTCAATTTATATCCCAAGCTTTATAAATGTCGAACTATATTCAACGTTGCGTAGAT	1380
Db	1339	TTAGTTTCAATTTATATCCCAAGCTTTATAAATGTCGAACTATATTCAACGTTGCGTAGAT	1398
Qy	1381	AGTGCACTGAATCAGACTGTTGTTGATCTCAGAGTTTGTATTTGTAACGATGGTTCAACA	1440
Db	1399	AGTGCACTGAATCAGACTGTTGTTGATCTCAGAGTTTGTATTTGTAACGATGGTTCAACA	1458
Qy	1441	GATTAATACCTTAGAAGTGATCAATAAGCTTTATGTAATAATCTTAGGGTACGCATCATG	1500
Db	1459	GATTAATACCTTAGAAGTGATCAATAAGCTTTATGTAATAATCTTAGGGTACGCATCATG	1518
Qy	1501	TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTAAAGGT	1560
Db	1519	TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTAAAGGT	1578
Qy	1561	TATTACATTTGGCGAGTTAGATTGATGATGATGATGATGATGATGATGATGATGATGATG	1620
Db	1579	TATTACATTTGGCGAGTTAGATTGATGATGATGATGATGATGATGATGATGATGATGATG	1638
Qy	1621	TTAAAGAAATTTTAAAGATAAACGCTAGCTGTGTTTATACCACTAAATAGAAAACGTC	1680
Db	1639	TTAAAGAAATTTTAAAGATAAACGCTAGCTGTGTTTATACCACTAAATAGAAAACGTC	1698
Qy	1681	AATCCGATGTTAGCTTAAATCGCTAAATGTTTACAAATGGCCAGAAATTTTTCAGAGAAAA	1740
Db	1699	AATCCGATGTTAGCTTAAATCGCTAAATGTTTACAAATGGCCAGAAATTTTTCAGAGAAAA	1758
Qy	1741	CTCAACACGGCTATGATTGCTCACCACTTTTGAATGTTTCAAGATTAGAGCTTTGGCATTTA	1800
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Qy	1801	ACTGATGATTCNAATGAAAAAATGAAAAATGCGGTAGACTATGACATGTTCTCAAACTC	1860
Db	1819	ACTGATGATTCNAATGAAAAAATGAAAAATGCGGTAGACTATGACATGTTCTCAAACTC	1878
Qy	1861	AGTGAAGTTGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGGTGTTATTACATGT	1920
Db	1879	AGTGAAGTTGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGGTGTTATTACATGT	1938
Qy	1921	GATAACACATCAATTAAGAAACTTCGCAATTTCAAAAAAAGAAACCAATTTGTTGTAGTCAAT	1980

Db 1939 GATAACACATCAATTAAGAAACCTTGGCATTCAAAGAAAACCAATTTTGTGTAGTCAAT 1998  
Qy 1981 CAGTCATTAATAGACAAAGCATAACTTATTAATATGACGAATTTGATGATTTAGAT 2040  
Db 1999 CAGTCATTAATAGACAAAGCATAACTTATTAATATGACGAATTTGATGATTTAGAT 2058  
Qy 2041 GAAAGTAGAAGTATATTTTCAATAAAGCGCTGAATATCAAGAAAGAGATTGATATCTTA 2100  
Db 2059 GAAAGTAGAAGTATATTTTCAATAAAGCGCTGAATATCAAGAAAGAGATTGATATCTTA 2118  
Qy 2101 AAAGATATTAATATCATCCAGAAATAAGAGATGCCAAAATCGCAGTCAGTATTTTATCCC 2160  
Db 2119 AAAGATATTAATATCATCCAGAAATAAGAGATGCCAAAATCGCAGTCAGTATTTTATCCC 2178  
Qy 2161 AATACATTAACCGCTTAGTGAAAAAATCTAAACAATATTTATGAATATATAAATAATATA 2220  
Db 2179 AATACATTAACCGCTTAGTGAAAAAATCTAAACAATATTTATGAATATATAAATAATATA 2238  
Qy 2221 TTGGTTATTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db 2239 TTGGTTATTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2298  
Qy 2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2358  
Qy 2341 ACGAGTAAATAGATTAATAAATACTGAGCGCATTTAAAGTAAATATAATAAATTAAGTCAG 2400  
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Qy 2521 GATTGGATCGAGAAAAATCAATCGCGCATCCACCATTTTAAAGGCTCATTAACCTTATTTT 2580  
Db 2539 GATTGGATCGAGAAAAATCAATCGCGCATCCACCATTTTAAAGGCTCATTAACCTTATTTT 2598  
Qy 2581 AATGACATGACTTTAAAGAGTATGAATCTGAAAGGGGATCACAAGGTATGTTTATGACG 2640  
Db 2599 AATGACATGACTTTAAAGAGTATGAATCTGAAAGGGGATCACAAGGTATGTTTATGACG 2658  
Qy 2641 TATCGCTAGCGCATGAGCTTCTGACGATTAATAAGAAAGTCATCACATCTTGCCAGTCA 2700  
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Qy 2701 ATTGATAGTGGCCAGAAATATAACA CTGAGGATATTTGGTTCCAAATTTTGCACTTTTAAATC 2760  
Db 2719 ATTGATAGTGGCCAGAAATATAACA CTGAGGATATTTGGTTCCAAATTTTGCACTTTTAAATC 2778  
Qy 2761 TTAGAAAAGAAAACCGGCCATGTTTAAATAAACAATCGACCTTATATGCTTTGG 2820  
Db 2779 TTAGAAAAGAAAACCGGCCATGTTTAAATAAACAATCGACCTTATATGCTTTGG 2838  
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Db 2839 GAACGAAAATTAATGACAAAATGAACAAAATTTGAAAGTGAAGAGGAGGAGAAAATATA 2898  
Qy 2881 CCTGTTAAAGATTCATTTAATAGTATATACTCTATAA 2919  
Db 2899 CCTGTTAAAGATTCATTTAATAGTATATACTCTATAA 2937

RESULT 4

US-11-172-145-3  
; Sequence 3, Application US/11172145  
; Publication No. US2005027696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul

; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 2979  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-172-145-3

Query Match 77.6%; Score 2266.4; DB 7; Length 2979;  
Best Local Similarity 86.4%; Pred. No. 0;  
Matches 2523; Conservative 0; Mismatches 376; Indels 21; Gaps 1;  
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Qy 61 AAATTTATTTTAAAAAGTCGGCGGAAATCTATGAGCGGAAAAATTTGTTGAATTTTCAAAATPACC 120  
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Qy 301 AAATTTGCTCATCTGAGAGAAATCTGAAAAATTCGGAGGTAAAGCGGTTCGCCCTTTGTACCA 360  
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Qy 481 TCTATTATCGTTACAAACATTTCAATTCGACAGCAATTTTATCGATTACATTAGCCTGTTTA 540  
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QY 541 GTAAACCAAAACACATTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
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QY 580 GTCAATCAGAAACAACTACCCATTTGAAAGTCGTTGTCAGATGATGGTAGGAA 639  
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QY 601 GATCTATCACCAGATCATTCGCGCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA 660  
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QY 2701 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTTGCATTTTAAATC 2760  
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1321 TTAGTTTCAATTTATNCCAGCTTATTAACCTGTCGCAATATATTTCAACGTTGCGTAGAT 1380  
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2041 GAAAGTAGAAGTATATTTTCAATTAACCGCTGATATCAAGAGAGATTTGATATCTTTA 2100  
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2101 AAAGATATTAA 2112  
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RESULT 6  
US-11-172-145-17  
; Sequence 17, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; PRIOR FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248

; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
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; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 17  
; LENGTH: 2112  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-172-145-17  
  
Query Match 72.2%; Score 2108.8; DB 7; Length 2112;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
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DB 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
  
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DB 601 GATCTATCACCGCATCAATTCGCCAATATGAAAATAAATTTGGATATTCGCTACCTCAGCAA 660

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 1381 AGTGACATGAATCAGACTGTTGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1440  
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RESULT 7

US-11-172-145-18  
 ; Sequence 18, Application US/11172145  
 ; Publication No. US20050272696A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DeAngelis, Paul  
 ; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
 ; FILE REFERENCE: 3554.104  
 ; CURRENT APPLICATION NUMBER: US/11/172,145  
 ; CURRENT FILING DATE: 2005-06-30  
 ; PRIOR APPLICATION NUMBER: 60/584,442  
 ; PRIOR FILING DATE: 2004-06-30  
 ; PRIOR APPLICATION NUMBER: 10/642,248  
 ; PRIOR FILING DATE: 2003-08-15  
 ; PRIOR APPLICATION NUMBER: 60/404,356  
 ; PRIOR FILING DATE: 2002-08-16  
 ; PRIOR APPLICATION NUMBER: 60/479,432  
 ; PRIOR FILING DATE: 2003-06-18  
 ; PRIOR APPLICATION NUMBER: 60/491,362  
 ; PRIOR FILING DATE: 2003-07-31  
 ; PRIOR APPLICATION NUMBER: 10/195,908  
 ; PRIOR FILING DATE: 2002-07-15  
 ; PRIOR APPLICATION NUMBER: 09/437,277  
 ; PRIOR FILING DATE: 1999-11-01  
 ; PRIOR APPLICATION NUMBER: 60/107,929  
 ; PRIOR FILING DATE: 1998-11-11  
 ; PRIOR APPLICATION NUMBER: 09/283,402  
 ; PRIOR FILING DATE: 1999-04-01  
 ; PRIOR APPLICATION NUMBER: 60/080,414  
 ; PRIOR FILING DATE: 1998-04-02  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 18  
 ; LENGTH: 2112  
 ; TYPE: DNA  
 ; ORGANISM: Paeteurella multocida  
 US-11-172-145-18

Query Match 72.2%; Score 2108.8; DB 7; Length 2112;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 61 AAATTTATTTGAAAGTTCGGCGGAAATCTATGAGCGGAAATTTGTTGAATTTCAAATTAACC 120  
QY 121 AAATGCAAGGAAATCTCAGCACATCTCTCTGTTAATTCAGCACATCTTTCTGTTAAAT 180  
DB 121 AAATGCAAGGAAATCTCAGCACATCTCTCTGTTAATTCAGCACATCTTTCTGTTAAAT 180  
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DB 181 AAAGAAGGAAATCAATTTGCGATAGTCCGTTAGATATTTGCAACACACTGTTACTT 240  
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DB 241 TCCAACGTAATAAATAGTACTTCTGACTGAGTCTCGGAAAGGAAACACGTTAAAAAATAAATGG 300  
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DB 301 AAATGCTCACTGAGAGAAATCTGAAATCGGAGGTAAGAGCGTCCGCTTGTACCA 360  
QY 361 AAAGATTTTCCAAAGATCTGTTTACGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
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DB 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGCTTAC 1140  
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DB 2101 AAAGATATTTAA 2112

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US-11-172-145-19
; Sequence 19, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172.145
; CURRENT FILING DATE: 2005-06-30
; PRIOR FILING DATE: 2005-06-30
; PRIOR FILING DATE: 2004-06-30
; PRIOR FILING DATE: 2003-08-15
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-07-15
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-19

Query Match 72.2%; Score 2108.8; DB 7; Length 2112;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAATCATTTATCACAGCAATTAAGCATATATACAGCAATGACTATCAATTAGCACTC 60
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Qy 361 AAAGATTTTCCAAAGATCTGGTTTTAGCGCTTTACCTGATCATGTTAAATGATTTACA 420
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2041 GAAAGTAGAAGTATATTTTCAATTAACCGCTGATATCAAGAGAGATTTGATATCTTA 2100  
2041 GAAAGTAGAAGTATATTTTCAATTAACCGCTGATATCAAGAGAGATTTGATATCTTA 2100  
2101 AAAGATATTTAA 2112  
2101 AAAGATATTTAA 2112

RESULT 9  
US-11-172-145-20  
; Sequence 20, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngellis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; FILE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02

; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20  
; LENGTH: 2112  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-172-145-20

Query Match 72.2%; Score 2108.8; DB 7; Length 2112;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAATACATTTATCACAAGCAATAAAGAGCATATATACAGCAATGACTATCAATTAGCACTC 60  
Db 1 ATGAATACATTTATCACAAGCAATAAAGAGCATATATACAGCAATGACTATCAATTAGCACTC 60  
Qy 61 AATTTATTTGAAAGTTCGGCGGAAATCTATGGACGAAATTTGTTGAATTTCAAATTAACC 120  
Db 61 AATTTATTTGAAAGTTCGGCGGAAATCTATGGACGAAATTTGTTGAATTTCAAATTAACC 120  
Qy 121 AATGCAAGAAAAAATCTCTCAGCACATCCCTTCTGTTAAATTCAGCACATCTTTCTGTAAAT 180  
Db 121 AATGCAAGAAAAAATCTCTCAGCACATCCCTTCTGTTAAATTCAGCACATCTTTCTGTAAAT 180  
Qy 181 AAAGAAGAAAAAAGTCAATGTTTGGCGATAGTCGCTTGTAGATTTGCAACAACTGTTACTT 240  
Db 181 AAAGAAGAAAAAAGTCAATGTTTGGCGATAGTCGCTTGTAGATTTGCAACAACTGTTACTT 240  
Qy 241 TCCAAAGCTAAAAAATTTAGTACTTTCTGACTCGCGAAAAAACAAGTAAAAAATAAATGG 300  
Db 241 TCCAAAGCTAAAAAATTTAGTACTTTCTGACTCGCGAAAAAACAAGTAAAAAATAAATGG 300  
Qy 301 AAATTTGCTCACTGAGAGAAATCTGAAATTCGGGAGGTAAAGCGGTCGCCCTTGTACCA 360  
Db 301 AAATTTGCTCACTGAGAGAAATCTGAAATTCGGGAGGTAAAGCGGTCGCCCTTGTACCA 360  
Qy 361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTTAATGATTTTACA 420  
Db 361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTTAATGATTTTACA 420  
Qy 421 TGGTACAAAAAGCGAAGAAAGACTTGGCATTAACCTGAACATCAACATGTTGCTCTT 480  
Db 421 TGGTACAAAAAGCGAAGAAAGACTTGGCATTAACCTGAACATCAACATGTTGCTCTT 480  
Qy 481 TCTATTATCGTTTACAAATTCATCGACCAAGCAATTTTATCGATTACATTTAGCCTGTTTA 540  
Db 481 TCTATTATCGTTTACAAATTCATCGACCAAGCAATTTTATCGATTACATTTAGCCTGTTTA 540  
Qy 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGNA 600  
Db 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGNA 600  
Qy 601 GATCTATCACCAGATCATTTCCGCAATATGAAAATAAATTTGGATTTTCGCTAGCTAGACAA 660  
Db 601 GATCTATCACCAGATCATTTCCGCAATATGAAAATAAATTTGGATTTTCGCTAGCTAGACAA 660  
Qy 661 AAAGATACGGTTTTCAGCCAGTCGCCCTCGGAATATGGGATTAACGTTAGCAAAATAT 720  
Db 661 AAAGATACGGTTTTCAGCCAGTCGCCCTCGGAATATGGGATTAACGTTAGCAAAATAT 720  
Qy 721 GACTTTTATGGCTTACTCGACTGTGATATGGCCCAAAATCCATTAATGGGTTCACTTTAT 780  
Db 721 GACTTTTATGGCTTACTCGACTGTGATATGGCCCAAAATCCATTAATGGGTTCACTTTAT 780  
Qy 781 GTTGACAGCTATTAGAGAGATGATTTAACATCATTGTTCCCAAGAAATACATCGAT 840  
Db 781 GTTGACAGCTATTAGAGAGATGATTTAACATCATTGTTCCCAAGAAATACATCGAT 840  
Qy 841 ACACAACATATTGACCCCAAGAGCTTTTAAATAACGGGAGTTTCTGTTGAATCATTTACCA 900  
Db 841 ACACAACATATTGACCCCAAGAGCTTTTAAATAACGGGAGTTTCTGTTGAATCATTTACCA 900

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QY 901 GAGTGAACCAACCAATAGTGTGCGCAAAAGGGAAGCAAGTTCCTCTGATTGG 960
DB 901 GAAAGTGAACCAACCAATAGTGTGCGCAAAAGGGAAGCAAGTTCCTCTGATTGG 960
QY 961 CGCTTAGAACCAATTCGAAAAACACAGAAATCTCCGCTTATTCGGAATTCGCCCTTCCTCGGTTTT 1020
DB 961 CGCTTAGAACCAATTCGAAAAACACAGAAATCTCCGCTTATTCGGAATTCGCCCTTCCTCGGTTTT 1020
QY 1021 TTTCGCGCGGGTAATGTGCTTTCGCTPAAAAATATGCGCTAAATAATCCGGTTTCCTTTGAT 1080
DB 1021 TTTCGCGCGGGTAATGTGCTTTCGCTPAAAAATATGCGCTAAATAATCCGGTTTCCTTTGAT 1080
QY 1081 GAGGAATTTAATCACTCGGCTGGAGAGATGTGAAATTTGGATATCGCTTATTCCTGTTAC 1140
DB 1081 GAGGAATTTAATCACTCGGCTGGAGAGATGTGAAATTTGGATATCGCTTATTCCTGTTAC 1140
QY 1141 GGTAGTTTCTTTAAACACTATTGATGGCAATATGCGCTTACCATCAAGAGCCACCAAGGTAAA 1200
DB 1141 GGTAGTTTCTTTAAACACTATTGATGGCAATATGCGCTTACCATCAAGAGCCACCAAGGTAAA 1200
QY 1201 GAAAAAGAACCGATCGTGAAGCGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG 1260
DB 1201 GAAAAAGAACCGATCGTGAAGCGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG 1260
QY 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAATTCGCATATCAATAGATACCT 1320
DB 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAATTCGCATATCAATAGATACCT 1320
QY 1321 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACGTTGGGTAGAT 1380
DB 1321 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACGTTGGGTAGAT 1380
QY 1381 AGTGCACTGAATCAGACTGTGTTGATCTCGAGGTTTGTATTGTTGAACGATGGTTCAACA 1440
DB 1381 AGTGCACTGAATCAGACTGTGTTGATCTCGAGGTTTGTATTGTTGAACGATGGTTCAACA 1440
QY 1441 GATATACCTTAGAAGTGAATCAATAGCTTTATGTTATGTTATTAATCTAGGTAACGATCATG 1500
DB 1441 GATATACCTTAGAAGTGAATCAATAGCTTTATGTTATGTTATTAATCTAGGTAACGATCATG 1500
QY 1501 TCTAAACCAATGCGGAATAGCCTCAGCACTCAATATGAGCGGTTCTTTTGTCTAAAGGT 1560
DB 1501 TCTAAACCAATGCGGAATAGCCTCAGCACTCAATATGAGCGGTTCTTTTGTCTAAAGGT 1560
QY 1561 TATTACATGGCGAGTTAGATTGATGATTAATCTTGAGCCTGATGAGTTGAATCTGTGT 1620
DB 1561 TATTACATGGCGAGTTAGATTGATGATTAATCTTGAGCCTGATGAGTTGAATCTGTGT 1620
QY 1621 TTTAAAGAAATTTTAAAGATTAACCGTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680
DB 1621 TTTAAAGAAATTTTAAAGATTAACCGTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680
QY 1681 AATCCGGATGGTAGCTTAATCGCTTAATGTTTACAAATTTGGCCAGAAATTTTACAGAGAAAA 1740
DB 1681 AATCCGGATGGTAGCTTAATCGCTTAATGTTTACAAATTTGGCCAGAAATTTTACAGAGAAAA 1740
QY 1741 CTCAACACGGCTATGATTGCTCACCACTTTAGAAATGTTACGATAGAGCTTGGCATTTA 1800
DB 1741 CTCAACACGGCTATGATTGCTCACCACTTTAGAAATGTTACGATAGAGCTTGGCATTTA 1800
QY 1801 ACTGATGGATCAATGAATAATTTGAAATGCGCTAGACTATGACATGTTCCCTCAAACTC 1860
DB 1801 ACTGATGGATCAATGAATAATTTGAAATGCGCTAGACTATGACATGTTCCCTCAAACTC 1860
QY 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTTACATGGT 1920
DB 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTTACATGGT 1920
QY 1921 GATAACACATCAATTAAGAAACTTTGGCATTCAAAAGAAAAACCAATTTGTTGTAGTCAAT 1980
DB 1921 GATAACACATCAATTAAGAAACTTTGGCATTCAAAAGAAAAACCAATTTGTTGTAGTCAAT 1980
QY 1981 CAGTCATTAAATAGCAAGGCAATCAATTTATTAATATGACGAATTTTGATGATTTAGAT 2040
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DB 1981 CAGTCATTAAATAGCAAGGCAATCAATTTATTAATATGACGAATTTGATGATTTAGAT 2040
QY 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTGATATCTTA 2100
DB 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTGATATCTTA 2100
QY 2101 AAAGATATTAAA 2112
DB 2101 AAAGATATTAAA 2112

RESULT 10
US-11-172-145-13
; Sequence 13, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; ; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Pasteurella multocida
; US-11-172-145-13
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Query Match 67.7%; Score 1975.4; DB 7; Length 1980;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1976; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 136 CTCTCAGCACATCCTTCTGTAAATTCAGCACATCTTCTCTGTAATAAAGAGAAAAAGTC 195
DB 4 CTCTCAGCACATCCTTCTGTAAATTCAGCACATCTTCTCTGTAATAAAGAGAAAAAGTC 63

QY 196 AATGTTTGGCATAGTCGCTTTAGATATTTGCAACACAACTGTTACTTTTCCAACTGAAAAAAA 255
DB 64 AATGTTTGGCATAGTCGCTTTAGATATTTGCAACACAACTGTTACTTTTCCAACTGAAAAAAA 123

QY 256 TTAGTACTTTCTGACTCGGAAAAAACACAGCTTTAAAAATAAATGGAATTTGCTCACTGAG 315
DB 124 TTAGTACTTTCTGACTCGGAAAAAACACAGCTTTAAAAATAAATGGAATTTGCTCACTGAG 183

QY 316 AAGAAATCTGAAATCGGAGAGTAAGAGCGGTGCGCCCTTGTACCAAAAGATTTTCCCAA 375
DB 184 AAGAAATCTGAAATCGGAGAGTAAGAGCGGTGCGCCCTTGTACCAAAAGATTTTCCCAA 243

QY 376 GATCTGGTTTTAGCGCCTTTTACCTGATCATGTTTAATGATTTTACATGTTACAAAGGCGA 435
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Db 244 GATCTGGTTTGTAGCGCTTTACCTGATCATGTTAATGATTTTACATGGTACAAAAGCGA 303  
Qy 436 AAGAAAGACTTGGCATATAAACCCTGAACATCAACATGTTGGTCTTTCTATTATCGTTACA 495  
Db 304 AAGAAAGACTTGGCATATAAACCCTGAACATCAACATGTTGGTCTTTCTATTATCGTTACA 363  
Qy 496 ACATTTCAATGACACAGCAAAATTTTATCGATTACATTTAGCTGCTTTTGTAGTAAACCAAAAACA 555  
Db 364 ACATTTCAATGACACAGCAAAATTTTATCGATTACATTTAGCTGCTTTTGTAGTAAACCAAAAACA 423  
Qy 556 CATTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAAGATCTATACCGATC 615  
Db 424 CATTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAAGATCTATACCGATC 483  
Qy 616 ATTCGCCAATGATAAATAAATTTGGATTATCGCTACGTCAGACAAAAGATAACCGTTTT 675  
Db 484 ATTCGCCAATGATAAATAAATTTGGATTATCGCTACGTCAGACAAAAGATAACCGTTTT 543  
Qy 735 CAAGCCAGTGGCGCTCGGAATATGGATTATCGCTTAGCAAAATATGACTTTATTGGCTTA 735  
Db 544 CAAGCCAGTGGCGCTCGGAATATGGATTATCGCTTAGCAAAATATGACTTTATTGGCTTA 603  
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Db 604 CTCGACTGTGATATGGCGCCAAATCCATTATGGGTTCAATCTTATGTTGGCAGAGCTATTA 663  
Qy 855 GAAGATGATGATTAAACAATCATTTGGTCCAGAAAATACATCGATACACACATATTGAC 855  
Db 723 GAAGATGATGATTAAACAATCATTTGGTCCAGAAAATACATCGATACACACATATTGAC 723  
Qy 915 CCAAAAGACTTCTTAAATAAGCGAGTTTGTGTAATCATTTACAGAGAGTGAAGAACCAAT 915  
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Qy 1035 GAAAAACAGAAAATCTCGCTTATCCGATTCGCGCTTTCCGTTTTCGCGCGGGTAAT 1035  
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Qy 1095 GTTGCTTTCGCTTAAATAAGTCTTAAATAAATCCGCTTTCTTTGTAGAGGAATTTAATCAC 1095  
Db 963 GTTGCTTTCGCTTAAATAAGTCTTAAATAAATCCGCTTTCTTTGTAGAGGAATTTAATCAC 963  
Qy 1155 TGGGCTGGAGAGATGTGGAATTTGGATATCGCTTATTCGCTTACGGTAGTTTCTTTAAA 1155  
Db 1023 TGGGCTGGAGAGATGTGGAATTTGGATATCGCTTATTCGCTTACGGTAGTTTCTTTAAA 1023  
Qy 1215 ACTATGATGCGATTATGCGCTTACCATCAAGAGCCACAGGTAAGAAAATGAAGCCGAT 1215  
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Qy 1335 AGAAAACTTTTACCAATAGAAATTCGATATCAATAGATACCTTTTAGTTTCAATTTAT 1335  
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Db 1263 ATCCAGCTTATAAATGTCGAAATATTTTCAAGCTTGGTAGATGCTGAATCAG 1263  
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Db 1323 ACTGTTGTTGATCTCGAGTTTGTATTTGTAAACGATGTTTCAACAGATAATACCTTAGAA 1323  
Qy 1515 GTGATCAATAAGCTTTATGGTAATATCTTAGGGTACGATCATGTCTTAAACCAATGGC 1515

Db 1324 GTGATCAATAAGCTTTATGGTAATATCTTAGGGTACGATCATGTCTTAAACCAATGGC 1383  
Qy 1516 GGAATAGCCTCAGCATCAAAATGAGCGCTTTCTTTTCTTAAAGGTTATTAATTTGGGAG 1575  
Db 1384 GGAATAGCCTCAGCATCAAAATGAGCGCTTTCTTTTCTTAAAGGTTATTAATTTGGGAG 1443  
Qy 1576 TTAGATTGATGATGATTTATCTTGAGCCTGATGCGAGTGTGAACTGTTTAAAGAAATTTTA 1635  
Db 1444 TTAGATTGATGATGATTTATCTTGAGCCTGATGCGAGTGTGAACTGTTTAAAGAAATTTTA 1503  
Qy 1636 AAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTCATCCGGATGGTAGC 1695  
Db 1504 AAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTCATCCGGATGGTAGC 1563  
Qy 1696 TTATCGCTAATGTTTACAATTTGGCCAGAAATTTTCACGAGAGAAAACCTCACACGCTATG 1755  
Db 1564 TTATCGCTAATGTTTACAATTTGGCCAGAAATTTTCACGAGAGAAAACCTCACACGCTATG 1623  
Qy 1756 ATTGCTCACCACCTTAGAATGTTTACGATTTAGAGCTTTGGCAATTTAACTGATGGATTCAAT 1815  
Db 1624 ATTGCTCACCACCTTAGAATGTTTACGATTTAGAGCTTTGGCAATTTAACTGATGGATTCAAT 1683  
Qy 1816 GAAAAAATGAAAAATGCGTAGACTATGACATGTTCTCAAACTCAGTGAAGTTGGAAAA 1875  
Db 1684 GAAAAAATGAAAAATGCGTAGACTATGACATGTTCTCAAACTCAGTGAAGTTGGAAAA 1743  
Qy 1876 TTTAAACATCTTAATAAAATCTGCTATAACCGTGTATTTACATGTTGATGATCAATCAAT 1935  
Db 1744 TTTAAACATCTTAATAAAATCTGCTATAACCGTGTATTTACATGTTGATGATCAATCAAT 1803  
Qy 1936 AAGAAACTTGGCATTTCAAAAGAAAAACCAATTTGTTGTTGATGATCAATCAATCAATCAAT 1995  
Db 1804 AAGAAACTTGGCATTTCAAAAGAAAAACCAATTTGTTGTTGATGATCAATCAATCAATCAAT 1863  
Qy 1996 CAAGGCTAATCTTATTAATTTATGAGAAATTTGATGATTTAGTGAAGTAGAAGTAT 2055  
Db 1864 CAAGGCTAATCTTATTAATTTATGAGAAATTTGATGATTTAGTGAAGTAGAAGTAT 1923  
Qy 2056 ATTTTCAATAAAACCGCTGAATATCAAGAGAGATTTGATATCTTAAAGATATTAA 2112  
Db 1924 ATTTTCAATAAAACCGCTGAATATCAAGAGAGATTTGATATCTTAAAGATATTAA 1980

RESULT 11

US-11-172-145-14  
; Sequence 14, Application US/11172145  
; Publication No: US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414

; PRIOR FILING DATE: 1998-04-02									
; Remaining Prior Application data removed - See File Wrapper or PALM.									
; NUMBER OF SEQ ID NOS: 25									
; SOFTWARE: PatentIn version 3.3									
; SEQ ID NO 14									
; LENGTH: 1902									
; TYPE: DNA									
; ORGANISM: Pasteurella multocida									
US-11-172-145-14									
Query Match 65.0%; Score 1898.4; DB 7; Length 1902;									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 1899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
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Db	3	GTTAGATATTGCAACACAACTGTTTACCTTTCCAAAGTAAATAAATAGTACTTTCTGACTC	62						
Qy	273	GGAAAAACACGTTAAATAATGAAATGCTCACTGAGAGAAATCTGAAATGC	332						
Db	63	GGAAAAACACGTTAAATAATGAAATGCTCACTGAGAGAAATCTGAAATGC	122						
Qy	333	GGAGGTAAAGCGGTGCGCCCTGTACCAAAAGATTTTCCAAAGATCTGGTTTTCAGGCC	392						
Db	123	GGAGGTAAAGCGGTGCGCCCTGTACCAAAAGATTTTCCAAAGATCTGGTTTTCAGGCC	182						
Qy	393	TTTACCTGATCATGTTAATGATTTTACATGTTACAAAGCGAAAGAAAGCTTGGCAT	452						
Db	183	TTTACCTGATCATGTTAATGATTTTACATGTTACAAAGCGAAAGAAAGCTTGGCAT	242						
Qy	453	AAACCTGAAACATCAACATGTTGCTCTTCTATTATGTTTACACATTTCAATCACCAGC	512						
Db	243	AAACCTGAAACATCAACATGTTGCTCTTCTATTATGTTTACACATTTCAATCACCAGC	302						
Qy	513	AAATTTTACGATTACATTTAGCTGCTTTAGTAAACCAAAACACATTAACCGTTTGAAGT	572						
Db	303	AAATTTTACGATTACATTTAGCTGCTTTAGTAAACCAAAACACATTAACCGTTTGAAGT	362						
Qy	573	TATCGTGACAGATGATGGTAGTCAGGAAGATCTATACCGATCATTCGCCAATATGAAA	632						
Db	363	TATCGTGACAGATGATGGTAGTCAGGAAGATCTATACCGATCATTCGCCAATATGAAA	422						
Qy	633	TAAATGGATATTCGCTACGTCAGACAAAGATAACGGTTTTCACCGCAGTCGCTCG	692						
Db	423	TAAATGGATATTCGCTACGTCAGACAAAGATAACGGTTTTCACCGCAGTCGCTCG	482						
Qy	693	GAATATGGGATTACGCTTAGCAAAATATGACTTTATGGCTTACTCGACTGTGATATGGC	752						
Db	483	GAATATGGGATTACGCTTAGCAAAATATGACTTTATGGCTTACTCGACTGTGATATGGC	542						
Qy	753	GCCAAATCCATTATGGGTTTCACTTTATGTTGCGAGCTATTAGAAGATGATTTAAC	812						
Db	543	GCCAAATCCATTATGGGTTTCACTTTATGTTGCGAGCTATTAGAAGATGATTTAAC	602						
Qy	813	AATCAATGGTCCAGAAAAATACATCGATACACACATATTGACCCAAAGACTTCTTAAA	872						
Db	603	AATCAATGGTCCAGAAAAATACATCGATACACACATATTGACCCAAAGACTTCTTAAA	662						
Qy	873	TACCGGAGTTTGTCTGAATCATTTACCAAGAGTGAACCAATATATAGTGTTCGCGAAA	932						
Db	663	TACCGGAGTTTGTCTGAATCATTTACCAAGAGTGAACCAATATATAGTGTTCGCGAAA	722						
Qy	933	AGGGGAAGGAACAGTTTCTCTGAGTTGCGCTTAGAACCAATTCGAAAAAACAAGAAATCT	992						
Db	723	AGGGGAAGGAACAGTTTCTCTGAGTTGCGCTTAGAACCAATTCGAAAAAACAAGAAATCT	782						
Qy	993	CCGCTTATCCGATTCGCTTTCCGTTTTCGCGCGGGTAATGTTGCTTTCGCTTAAAA	1052						
Db	783	CCGCTTATCCGATTCGCTTTCCGTTTTCGCGCGGGTAATGTTGCTTTCGCTTAAAA	842						
Qy	1053	ATGGCTAAATAAATCCCGTTTCTTTTGTATGAGGAATTTAATCACTGGGGTGGAGAGATGT	1112						
Db	843	ATGGCTAAATAAATCCCGTTTCTTTTGTATGAGGAATTTAATCACTGGGGTGGAGAGATGT	902						

Qy	1113	GGAAATTTGGATATCGCTTATTCGGTTACGGTAGCTTCTTTTAAACATATTTCATGSCATTAT	1172						
Db	903	GGAAATTTGGATATCGCTTATTCGGTTACGGTAGCTTCTTTTAAACATATTTCATGSCATTAT	962						
Qy	1173	GGCTTACCATCAAGAGCCACCGGTAAAGAAAAATGAACCGATCGTGAACGGGAAAAAA	1232						
Db	963	GGCTTACCATCAAGAGCCACCGGTAAAGAAAAATGAACCGATCGTGAACGGGAAAAAA	1022						
Qy	1233	TATTACGCTCGATATTATAGAGAAAGGTCCTTATATCTATAGAAAACTTTTACCAAT	1292						
Db	1023	TATTACGCTCGATATTATAGAGAAAGGTCCTTATATCTATAGAAAACTTTTACCAAT	1082						
Qy	1293	AGAAGATTCCCATATCAATAGACTACTTTAGTTTCAATTTATATCCCAGCTTATACTG	1352						
Db	1083	AGAAGATTCCCATATCAATAGACTACTTTAGTTTCAATTTATATCCCAGCTTATACTG	1142						
Qy	1353	TGCAAACTATATTCAACGTTGCGTAGATAGTGCACCTGAATCAGACTGTTGTCATCTCGA	1412						
Db	1143	TGCAAACTATATTCAACGTTGCGTAGATAGTGCACCTGAATCAGACTGTTGTCATCTCGA	1202						
Qy	1413	GGTTTGTATTGTAACGATGGTTCAACAGATAATACCTTTAGAAAGTGATCAATAGCTTTTA	1472						
Db	1203	GGTTTGTATTGTAACGATGGTTCAACAGATAATACCTTTAGAAAGTGATCAATAGCTTTTA	1262						
Qy	1473	TGTAATTAATCCTAGGTAGCGATCATGCTAAACCAAAATGGCGGATAGCCTCAGCATC	1532						
Db	1263	TGTAATTAATCCTAGGTAGCGATCATGCTAAACCAAAATGGCGGATAGCCTCAGCATC	1322						
Qy	1533	AAATGACGCGCTTCTTTTCTAAAGGTTATTACATTTGGGCAGTTAGATTTCAGATGATTA	1592						
Db	1323	AAATGACGCGCTTCTTTTCTAAAGGTTATTACATTTGGGCAGTTAGATTTCAGATGATTA	1382						
Qy	1593	TCTTGAGCCTGATGCGAGTTGAACTGTTTTPAAAAGAAATTTTAAAAGATAAAAAGCTAGC	1652						
Db	1383	TCTTGAGCCTGATGCGAGTTGAACTGTTTTPAAAAGAAATTTTAAAAGATAAAAAGCTAGC	1442						
Qy	1653	TTGTGTTTATACCACTAATAGAAAAAGTCAATCCGGATGGTAGCTTAATCCGTAATGCTTA	1712						
Db	1443	TTGTGTTTATACCACTAATAGAAAAAGTCAATCCGGATGGTAGCTTAATCCGTAATGCTTA	1502						
Qy	1713	CAATTTGCCAGAAATTTTTCACGAGAAAACTCACAACGGCTATGATTGCTCACCACTTTAG	1772						
Db	1503	CAATTTGCCAGAAATTTTTCACGAGAAAACTCACAACGGCTATGATTGCTCACCACTTTAG	1562						
Qy	1773	AATGTTTCAAGATTAGAGCTTTGGCAATTTAACTGATGGAATCAATGAAAAAATGAAAAATGC	1832						
Db	1563	AATGTTTCAAGATTAGAGCTTTGGCAATTTAACTGATGGAATCAATGAAAAAATGAAAAATGC	1622						
Qy	1833	CGTAGACTATGACATGTTTCTCAAACTCAGTGAAGTTGGAAAAATTTTAAACATCTTAATAA	1892						
Db	1623	CGTAGACTATGACATGTTTCTCAAACTCAGTGAAGTTGGAAAAATTTTAAACATCTTAATAA	1682						
Qy	1893	AACTGCTATAACCGGTATTATACATGCTGATTAACACATCAATTTAAAGAAACTTGGCAATCA	1952						
Db	1683	AACTGCTATAACCGGTATTATACATGCTGATTAACACATCAATTTAAAGAAACTTGGCAATCA	1742						
Qy	1953	AAAGAAAAACCAATTTTGTGTTAGTCAATCAGTCAATTAATAATAGAACGCACTTAATTA	2012						
Db	1743	AAAGAAAAACCAATTTTGTGTTAGTCAATCAGTCAATTAATAATAGAACGCACTTAATTA	1802						
Qy	2013	TAATATGACGAATTTGATGATTTAGTGAAGTAGAAAGTATATTTTCAATAAACCAGC	2072						
Db	1803	TAATATGACGAATTTGATGATTTAGTGAAGTAGAAAGTATATTTTCAATAAACCAGC	1862						
Qy	2073	TGAATATCAAGAGAGATTCATATCTTAAAGATATTAAA 2112							
Db	1863	TGAATATCAAGAGAGATTCATATCTTAAAGATATTAAA 1902							

RESULT 12  
US-11-172-145-15  
; Sequence 15, Application US/11172145



Db	1204	GCTAAAGGTTATTACATTGGCGCAGTTAGATT	CAGATGATTTATCTTGAGCGTGAATGAGTT	1263
Qy	1612	GAACGTGTTTTAAAGAAATTTTTAAAGATAAAACGCTAGCTTGCTGTTTATACCACTAAT	1671	
Db	1264	GAACGTGTTTTAAAGAAATTTTTAAAGATAAAACGCTAGCTTGCTGTTTATACCACTAAT	1323	
Qy	1672	AGAAACGTCAATCCGGATGGTAGCTTAATCGCTAAATGGTTACAAATGGCGCAGAAATTTTCA	1731	
Db	1324	AGAAACGTCAATCCGGATGGTAGCTTAATCGCTAAATGGTTACAAATGGCGCAGAAATTTTCA	1383	
Qy	1732	CGAGAAAACTCAACCGGCTATGATGTCTCAACACTTAGAATGTTTCAGATTAGAGCT	1791	
Db	1384	CGAGAAAACTCAACCGGCTATGATGTCTCAACACTTAGAATGTTTCAGATTAGAGCT	1443	
Qy	1792	TGGCATTTAACTGATGATTCATGAAAAAATTTGAAATGCCGTAGACTATGACATGTTTC	1851	
Db	1444	TGGCATTTAACTGATGATTCATGAAAAAATTTGAAATGCCGTAGACTATGACATGTTTC	1503	
Qy	1852	CTCAAACTCAGTGAAGTTGGAAAAATTTAAAAACATCTTAAATAAAATCTGCTATAACCGTGTA	1911	
Db	1504	CTCAAACTCAGTGAAGTTGGAAAAATTTAAAAACATCTTAAATAAAATCTGCTATAACCGTGTA	1563	
Qy	1912	TTACATGGTGATTAACACATCAATCAATTAAGAAACTTGGCAATCAAAAGAAAAACCAATTTTGGT	1971	
Db	1564	TTACATGGTGATTAACACATCAATCAATTAAGAAACTTGGCAATCAAAAGAAAAACCAATTTTGGT	1623	
Qy	1972	GTAGTCAATCAGTCAATTAATAGACAGGCATTAACCTTAAATTAATATGACGAATTTGAT	2031	
Db	1624	GTAGTCAATCAGTCAATTAATAGACAGGCATTAACCTTAAATTAATATGACGAATTTGAT	1683	
Qy	2032	GATTTAGATGAAGGTAGAAAGTATATTTTCAATAAAAAACCGCTGAATATCAAGAAGAGATT	2091	
Db	1684	GATTTAGATGAAGGTAGAAAGTATATTTTCAATAAAAAACCGCTGAATATCAAGAAGAGATT	1743	
Qy	2092	GATATCTTAAAGATATATAA	2112	
Db	1744	GATATCTTAAAGATATTTAA	1764	

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RESULT 14
US-10-995-561-13443/c
; Sequence 13443, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995.561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13443
; LENGTH: 49979
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(49979)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-14)
US-10-995-561-13443

```

	Query Match	2.5%	Score 73.6;	DB 6;	Length 49979;
	Best Local Similarity	45.2%;	Pred. No. 4.8e-05;		
	Matches 336;	Conservative	3;	Mismatches 402;	Indels 3; Gaps 2;
Qy	1872	AAATTTAAACATCTTAATAAAATCTGTATACCGTGATTATCATGTGTGATACACATC	1931		
Db	29239	AAATGTTATATATATATGTTATATAAATATATATGTTATATAATATATATATATATTT	29180		
Qy	1932	AATTAAGAAACTTGGCATTTCAAAAGAAAAACATTTTGGTTAGTCATCATGTCATTAAA	1991		

[illegible]

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RESULT 15
US-11-121-086-105/c
; Sequence 105, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105
; LENGTH: 171486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-105

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Query Match 2.3%; Score 68.6; DB 7; Length 171486;  
Best Local Similarity 47.1%; Pred. No. 0.00063;  
Matches 282; Conservative 0; Mismatches 309; Indels 8; Gaps 2;  
QY 1889 ATAAAACTGCTATACCGTGTTATTCATGGTGATTAACATCAATTAAGAACTGGCA 1948

Db 1561 GACATGTTCTCAAACTCAGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTAT 1620  
Qy 1903 AACCGTGTATACATGTGTATACACATCAATTAAGAACTTGGCATTTCAAAAGAAAAC 1962  
Db 1621 AACCGTGTATACATGTGTATACACATCAATTAAGAACTTGGCATTTCAAAAGAAAAC 1680  
Qy 1963 CATTTTGTGTAGTCAATCAATCAATTAAGAACTTGGCATTTCAAAAGAAAAC 2022  
Db 1681 CATTTTGTGTAGTCAATCAATCAATTAAGAACTTGGCATTTCAAAAGAAAAC 1740  
Qy 2023 GAATTTGATGATTTAGATGAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATCAAA 2082  
Db 1741 GAATTTGATGATTTAGATGAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATCAAA 1800  
Qy 2083 GAAGAGATTGATATCTTTAAAGATATTTAA 2112  
Db 1801 GAAGAGATTGATATCTTTAAAGATATTTAA 1830

## RESULT 13

US-11-172-145-16  
; Sequence 16, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16  
; LENGTH: 1764  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-172-145-16

Query Match 60.3%; Score 1759.4; DB 7; Length 1764;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1760; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 352 CTTGTACCAAAAGATTTTCCAAAGATCTGGTTTGTAGCGCTTTTACCTGATCATGTTAAT 411  
Db 4 CTTGTACCAAAAGATTTTCCAAAGATCTGGTTTGTAGCGCTTTTACCTGATCATGTTAAT 63  
Qy 412 GATTTTACATGGTACAAAAGCGAAGAAAGACTTGGCATTAACCTGACATCAACAT 471  
Db 64 GATTTTACATGGTACAAAAGCGAAGAAAGACTTGGCATTAACCTGACATCAACAT 123  
Qy 472 GTTGTCTTTCTTATCTTATCTTACAACTTCAATCGACCAGCAATTTTATCGATTACATTA 531

Db 124 GTTGTCTTTCTTATCTTATCTTACAACTTCAATCGACCAGCAATTTTATCGATTACATTA 183  
Qy 532 GCGTGTATAGTAAACCAAAACACATTAACCGTGTGAAAGTTATCTGTCAGACAGATGATGGT 591  
Db 184 GCGTGTATAGTAAACCAAAACACATTAACCGTGTGAAAGTTATCTGTCAGACAGATGATGGT 243  
Qy 592 AGTCAGGAAGATCTATCACCGATCATTTGCGCAATATGAAATTAATTTGGATATTCGCTAC 651  
Db 244 AGTCAGGAAGATCTATCACCGATCATTTGCGCAATATGAAATTAATTTGGATATTCGCTAC 303  
Qy 652 GTCAGACAAAAGATTAACCGTGTTCAGCCAGTGGCGCTCGGAATATGGGATTAACGCTTA 711  
Db 304 GTCAGACAAAAGATTAACCGTGTTCAGCCAGTGGCGCTCGGAATATGGGATTAACGCTTA 363  
Qy 712 GCAAAATATGACTTTTATGCTTACTCGACTGTGATATGCGCGCAAAATCCATTTATGGTT 771  
Db 364 GCAAAATATGACTTTTATGCTTACTCGACTGTGATATGCGCGCAAAATCCATTTATGGTT 423  
Qy 772 CATTTCTTATGTCAGAGCTTATTAGAAGATGATGATTTAAACAATCATTTGTCAGAAATA 831  
Db 424 CATTTCTTATGTCAGAGCTTATTAGAAGATGATGATTTAAACAATCATTTGTCAGAAATA 483  
Qy 832 TACATCGATACACAAATATGACCCAAAGACTTCTTAATTAACCGGAGTTTGTCTGAA 891  
Db 484 TACATCGATACACAAATATGACCCAAAGACTTCTTAATTAACCGGAGTTTGTCTGAA 543  
Qy 892 TCATTACCAGAAGTGAACCAATATAGTGTGTCGCGCAAAAGGGGAAGAAACAGTTTCT 951  
Db 544 TCATTACCAGAAGTGAACCAATATAGTGTGTCGCGCAAAAGGGGAAGAAACAGTTTCT 603  
Qy 952 CTGGATTGGCGCTTAGAACCAATTCGAAACAAAGAAATCTCGCTTATCCGATTCGCT 1011  
Db 604 CTGGATTGGCGCTTAGAACCAATTCGAAACAAAGAAATCTCGCTTATCCGATTCGCT 663  
Qy 1012 TTCGTTTTTTCGCGCGGTAAATGTTGCTTTCGCTTAAATAAGGCTTAATTAATTCGCT 1071  
Db 664 TTCGTTTTTTCGCGCGGTAAATGTTGCTTTCGCTTAAATAAGGCTTAATTAATTCGCT 723  
Qy 1072 TTCCTTGATCAGGAATTTAATCACTGGGTGGAGAGATGTGGAATTTGGATATCGCTTA 1131  
Db 724 TTCCTTGATCAGGAATTTAATCACTGGGTGGAGAGATGTGGAATTTGGATATCGCTTA 783  
Qy 1132 TTCGTTTACGCTAGTTTCTTTTAAACCTATTTATGATGGCAATTTATGGCTTACCATCAAGAGCCA 1191  
Db 784 TTCGTTTACGCTAGTTTCTTTTAAACCTATTTATGATGGCAATTTATGGCTTACCATCAAGAGCCA 843  
Qy 1192 CCAGGTAAGAAAATGAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATG 1251  
Db 844 CCAGGTAAGAAAATGAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATG 903  
Qy 1252 AGAGAAAAGGTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAAGATTTCGCATATCAAT 1311  
Db 904 AGAGAAAAGGTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAAGATTTCGCATATCAAT 963  
Qy 1312 AGAGTACCTTTTAGTTTCAATTTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGT 1371  
Db 964 AGAGTACCTTTTAGTTTCAATTTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGT 1023  
Qy 1372 TGCCTAGATAGTCACTGAATCAGACTGTTGTTGATCTCGAGTTTGTATTTGTAACGAT 1431  
Db 1024 TGCCTAGATAGTCACTGAATCAGACTGTTGTTGATCTCGAGTTTGTATTTGTAACGAT 1083  
Qy 1432 GGTTCACACAGATAATACCTTAGAAGTGAATCAATAAGCTTTTATGTAATAATATCTTAGGTA 1491  
Db 1084 GGTTCACACAGATAATACCTTAGAAGTGAATCAATAAGCTTTTATGTAATAATATCTTAGGTA 1143  
Qy 1492 CGCATCATGTCTAAACCAAAATGGCGAATAGCCCTCAGCATCAAAATGACGCGTTCTTTT 1551  
Db 1144 CGCATCATGTCTAAACCAAAATGGCGAATAGCCCTCAGCATCAAAATGACGCGTTCTTTT 1203  
Qy 1552 GCTAAAGGTTATTACATTTGGCGAGTTAGATTTAGATTTAGATTTATCTTTAGACCTGATGCGAGTT 1611



November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New). Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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